

From: Swope, Sheridan
Sent: Friday, January 28, 2005 3:36 PM
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Subject: 10/029,345

For 10/029,345, pls interference search only:

SID 108, residues 538-2532, against the NT data bases
SID 108, residues 538-1443, against the NT data bases
SID 108, full-length, oligo search (at least 1419 NTs), against the NT data bases

SID 109, full-length, against the NT & AA data bases
SID 109, residues 1-302, against the NT & AA data bases
SID 109, full-length, oligo search (at least 473 AAs), against the NT & AA data bases

Sheridan Swope, Ph.D.
Patent Examiner, AU 1652
Recombinant Enzymes
571-272-0943 (voice)
E02B71 Remsen Bld (Office)
E02C70 Remsen Bld (Mailbox)

5/1/2001

Scan this page

109: 1/2-665
1/2-302
>473

108: 538-2532
541-2532
538-1443
541-1443
>1419

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JAN 28 2005
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Toby Port

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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Db 361 CTTGAGAGGTGGTGTGAGTTCTCTGGTGTTCCTGGCCTCTGGAAGAAAATCC 420
Qy 421 ACTAGTACCCACCGATTTCTCAGCCTTCTTACTGTGGCAATTTGGGCAAC 480
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Db 841 ATATCTCCAACTTCAATTTCTGCGGCCTCACTGCTGCTGCTGCTGCTGCTGCT 900
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Db 1141 AGTGGGCTGCACTGTGCGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
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Db 1261 TCTGTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1320
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Db 1321 AAGCTATGCGAGTTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
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Db 1381 GATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Qy 1441 AGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
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Db 1441 AGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
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Qy 1561 CTTTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1620
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Qy 1681 AAGAGTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 1740
Db 1681 AAGAGTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 1740
Qy 1741 GCTTACAGCTGACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
Db 1741 GCTTACAGCTGACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800
Qy 1801 CAGAGCAGAGTGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
Db 1801 CAGAGCAGAGTGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
Qy 1861 AAGCATTTTAAAGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
Db 1861 AAGCATTTTAAAGCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
Qy 1921 AGGTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Db 1921 AGGTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Qy 1981 ATCATTTAGGCTCTC 1995
Db 1981 ATCATTTAGGCTCTC 1995

RESULT 2
US-09-816-494-1
Sequence 1, Application US/09816494
Patent No. 6664089
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
FILE REFERENCE: 10448-030002
CURRENT APPLICATION NUMBER: US/09/816,494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,858
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3544
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (589)...(2583)
US-09-816-494-1

Query Match 99.8%; Score 1991.8; DB 4; Length 3544;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGCCCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
Db 589 ATGGCCCATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 648
Qy 61 AGTGAACGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 61 AGTGAACGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
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ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (135)...(2012)
 US-09-920-668-3

Query Match 19.4%; Score 387.8; DB 4; Length 2377;
 Best Local Similarity 59.9%; Pred. No. 2,6e-119;
 Matches 716; Conservative 0; Mismatches 453; Indels 27; Gaps 3;

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QY 28 ATTGTTACTGAGAGTTGGTGGCTCTGCTGGAAGTGGACGAAAAAGTGGCTAAAT 87
DB 165 ATGATGTCGAAGAAAGCTGGCCAGCTCTGCGGGGCGGCTCGGGGGCGCTGGTGCATC 224
QY 88 GATAGCCGGCCATTGTTGGAATATACATATCCACATTTTGAAGCATTAATATCAAC 147
DB 225 GACAGCGGCTCTTCTGTGGAGTACACAGCTGGAGATGTCTCAGCTCTGTCACATCTGC 284
QY 148 TGTCTTCAAGCTTTAAGACCGAAGTTGCAACAGACAAAGTTTAATTAAGAGCTCATC 207
DB 285 TGTCTCAAGCTGTGGAAGCGCGGCTGCAAGGCAAGGTGACATTTGCGAGCTCATC 344
QY 208 CAGCATTCAGCGAAACATAAAGTTGATGATTTGACAGTGAAGTTGATTTGATTCAT 267
DB 345 CAGCGGCTGCGACGCAAGCTGGAGGCTACGAGCCACAGGACGTTGTGTCTATGAC 404
QY 268 CAAAGCTCCCAAGATGTGCTCTCTCTTCAAGACTGTTTCTCACTGATCTTGGGT 327
DB 405 CAGAGCGCGGGAAGCGCAAGTGTGCGCGGACAGAGCTTCTTCCATCTGCTGAGC 464
QY 328 AAAGTGAAGAAAGCTTCAACTCTGTTCACCTCTTGCAGAGTGGTGGTTGCTGATCTCT 387
DB 465 AAGCTGAGCGGCTGTGCAAGAGTGGCCATCTTCACTGGGGGCTTCGCCACCTTCTCC 524
QY 388 CGTTGTTTCCCTGGCTCTGTGAAGAAAAATCCACT---CTAGTCCCTACCTGCATTTCT 444
DB 525 TCTGCTTCCCGGCTCTGCGAGGCAAGCTGCTGCTGCTACCAATGAGCTCTTCC 584
QY 445 CAGCCTTGTCTACTCTGTGGCAACATTTGGGCCAACCCGAATCTTCCCATCTTATCTT 504
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QY 505 GGTGCGCAGAGATGTCTCTCAACAAAGAGCTGATACAGACAAATGGGATTTGTTATGTG 564
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QY 625 GTGCTGTGAATGACAGCTTTTGTGAGAAATTTTGGCTGTGGTGGACAAATCAGTATGAT 684
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QY 745 TCCGCTCCGCGCAACATGCTATGCTTACATCAATGAAGAGATGACATGTCTTTAGAT 804
DB 885 TCCGCTGTGCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 944
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DB 945 GACGCTTACAGATTTGTAAGAAAGAAAGAAAGCTTCAATGATCTTCAAACTTCAATTTCTG 1004
QY 865 GCGCAATCTCTGGAATAAGAGAAAGATTAAGAACGAGCTGGAGCATCAGGGCCAAAG 924
DB 1005 GCGCAGCTGTGAGTACGAGCGCAGCTGAGAGTGTGCGCGCGCTGCGAGGCGAGCCG 1064
QY 925 AGCAAACTCAAGCTGTGCACTGTGAGAAAGCAATCAATCACTGCTCTGTGCTGAGAG 984
DB 1065 GGCA-----CCCCCTCAGGAGCGCCGAGGCTTCCGCGCAGTCTGCGCGCGGG 1112

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QY 985 GGTGACAGAAAGCAAGCGCCCTCATGTCCACCTGTGGCACTGTCTACTACAGAG 1044
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QY 1045 GCAGCAGAGCAAAAGCCCGGTGCATCCGCGCAGCGTCCAGCGTCCGCGTGCAGCGG 1104
DB 1173 GC-----CAGGAGAGGCGGCTGTGAGCGCGGCGGAGGAGCCCGCGCGCCCGCC 1220
QY 1105 TGTCTGTTAAGAGACAGCGCCGCTGTGAGCGGCTGACGTGGGCTGACACTGTCCGAGAC 1164
DB 1221 AGCGCCCGCGGACCGAGCGCACTGTGACAGAGGCGCTGCGGCTGTGACCTTCTCTGAGC 1280
QY 1165 AGCTTGAAGACAGCAATTAAGCTCAAGCGTTCCTTCTCTGTGATTAATCAATCAG 1219
DB 1281 GCGCTGACAGACATAACCGCTCAAGGCTCTTCTTCTGTGACATCAATGCTG 1335

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RESULT 4
 US-09-949-016-3250
 Sequence 3250, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: C0.01307
 CURRENT APPLICATION NUMBER: US/09/949,016
 PRIOR FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ IDS NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 3250
 LENGTH: 2351
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-3250

Query Match 19.4%; Score 386.2; DB 4; Length 2351;
 Best Local Similarity 59.8%; Pred. No. 9.1e-119;
 Matches 715; Conservative 0; Mismatches 453; Indels 27; Gaps 3;

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QY 28 ATTGTTACTGAGAGTTGGTGGCTCTGCTGGAAGTGGACGAAAAAGTGGCTAAAT 87
DB 139 ATGATGTCGAAGAAAGCTGGCCAGCTCTGCGGGGCGGCTCGGGGGCGCTGGTGCATC 198
QY 88 GATAGCCGGCCATTGTTGGAATATACATATCCCATTTTGAAGCAATTAATATCAAC 147
DB 199 GATAGCCGGCTCTTGTGTGAGTACAAAGCTGGCATGTGCTCAGCTCGTCAACATCTGC 258
QY 148 TGTCTCAAGCTTATGAAGGAAAGTTGCAACAGACAAAGTGAATTAATTAAGAGCTCATC 207
DB 259 TGTCTCAAGCTGTGTAAGCGGCGCTGCGAGGCAAGTGAACATTTGCGAACTCATC 318
QY 208 CAGCATTCAGCGAAACATTAAGTTGATCAATTTGCACTGAGTGTGATTTAGAT 267
DB 319 CAGCGGCTGACGCGCAGCGCAGGTGAGGCTACGAGCCACAGACGATGTGTATGAC 378
QY 268 CAAAGCTCCAAAGATGTGCTCTCTCTTCAACATGTTTCTCACTGTATCTTGGGT 327
DB 379 CAGAGCAAGCGGAGCGCAGGCTGTGCGGCAAGCTTCTCTCATCTGCTGAGC 438
QY 388 AAAGTGAAGAAAGCTTCACTGTGTTCACTGTGCTTCAAGTGGGTTTGTGAGTGTCT 387
DB 439 AAGCTGAGCGGCTGCTTGAAGGAGGAGGATCTTCACTGTGGGCTTCCGCACTTCTCC 428
QY 388 CGTTGTTTCCCTGGCTCTGTGAAAGAAATCCACT---CTAGTCCCTACCTGCAATTTCT 444

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Db      499 TCCGCTTCCCGGCTCTGCGAGGGCAAGCCTGCTCCCTGCTACAGAGCCCTCC 558
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Db      559 CAGCCTGCTTCTGCTGCTGCGGCTGAGCCCGATCTGCTTCACTCTTACCTG 618
Qy      505 GGCCTGCGAGAGATGCTCTCAACAAGAGCTGATACAGCAGATGGATGGATTGATG 564
Db      619 GGCCTGCGAGAGAGATGCTCTCAACAAGAGATGATGAGCAAAATGATAGTACG 678
Qy      565 TTAATGCCAGTATACCTGCTCAAAAGCTGATCTTATCCCGAGTCTTATTTCTG 624
Db      679 CTCAAGCGCAGACATCTCCCGCAAGCTGATCTGAGAGCGCTTCAATGCGG 738
Qy      625 GTGCGTGAATGAGAGCTTTTGTGAGAAATTTTGGCTGGTGGAGCAATCAATAGT 684
Db      739 GTCCCATCAACGACATCACTGTGAAAACTGCTGCTGCTGAGACAGTCAATGAG 798
Qy      685 TTCAATTGAGAAAGCAAAAGCCTCAATGATGTTTCTAGTCACTGTTTACCTGGATC 744
Db      799 TTCAATGATTAAGCAAGCTCTCCAGCTGCCAAGTCAATGCTCACTGCTGCTGATC 858
Qy      745 TCCGCTCGCCCACTATGCTATGCTCTATCATCATGAGAGAGATGACATGCTTAA 804
Db      859 TCCCGCTCTGCGCAGTCCATCGCTTACATCATGAGAACCATGAGGATGCTCCG 918
Qy      805 GAAGCTTACAGATTGTGAAAGAAAAAGCCTACTATATCTTCCAACTTGAATTTTCT 864
Db      919 GACGCTCAGAGTTGTGTAAGAGAGCGCGCTCATCTGCGCCCACTTCAACTTCTG 978
Qy      865 GAGCAACTCTGGAATATAGAAAGATTAAGAACAGACTGAGACATCAAGGCGCAAG 924
Db      979 GAGCAAGCTGCTGATAGAGAGGAGAGCTGAAAGCTGAGCGCCCTGAGAGGCG 1038
Qy      925 AGCAAACTCAAGCTGCTGCACTGAGAGAGCCAAATGAACCTGCTGCTGCTCAG 984
Db      1039 GGCAC-----CCCCCTCAGAGAGCGCGAGAGCTCCGCGCCAGTCTCCCGCGG 1086
Qy      995 GGTGACAGAAAGGAGACCGCCCTCACTGCACTCTGCTGCTGCTGCTGCTCAAG 1044
Db      1087 GCGCGCTGCGCAGGCTGCAACACTTACCTTGAAGAGCGCTGCCACAGGAGATG 1146
Qy      1045 GCAGCAGAGCAAAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1104
Db      1147 GC-----CAGGAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1194
Qy      1105 TCGCTGTAAGAGACAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1164
Db      1195 AGCGCGCGCGGAGCAGGCACTGCAAGAGGCGCTGCGCGGCTGCACTCTCTG 1254
Qy      1165 AGGCTGGAAGACAGCAATTAAGTCAAGGCTTCTTCTCTGCTGCTGCTGCTG 1219
Db      1255 CGCCTGAGAGACATCAACCGCTCAAGCGCTCTCTCTCTGAGATCAAGTCTG 1309

RESULT 5
US-09-513-999C-2877
; Sequence 2877, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513, 999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent, pm
; SEQ ID NO 2877

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; LENGTH: 333
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 127..333
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 17
; OTHER INFORMATION: h-a or c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: y-c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 19
; OTHER INFORMATION: k-g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 36
; OTHER INFORMATION: n-a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 58
; OTHER INFORMATION: r-a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 237
; OTHER INFORMATION: w-a or t
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 37
; OTHER INFORMATION: Xaa=His or Glu
; US-09-513-999C-2877

Query Match      14.8%; Score 294.6; DB 4; Length 333;
Best Local Similarity 97.3%; Pred. No. 1,6e-88;
Matches 326; Conservative 5; Mismatches 0; Indels 4; Gaps 3;

Qy      34 ACTGAGAGTGGTGGCTCTGCTGGAAGGAAAGCG-AAAAAGTCTGCTAATGATG 92
Db      1 ACTGAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 58
Qy      93 CCGGCATTTTGGGAAAT-CAATACATCCCATTTTGAAGCCATTAAATCAACTGCT 151
Db      59 CCGGCATTTTGGGAAATCAATACATCCCATTTTGAAGCCATTAAATCAACTGCT 118
Qy      152 CCAAGCTTATGAGGAAAGTTGGCAAGAGCAAGAAAGTTAATTACAGAGCTATCCAGC 211
Db      119 CCAAGCTTATGAGGAAAGTTGGCAAGAGCAAGAAAGTTAATTACAGAGCTATCCAGC 178
Qy      212 ATTGAGCAAAATTAAGTTGACATTTGATTCAGTCAAGAGGTTGATTTACATCAA 271
Db      179 ATTGAGCAAAATTAAGTTGACATTTGATTTGACATTTGACATTTGATTTGACAT 238
Qy      272 GCTCCCAAGATGTTGCTCTCTCTTCAAGCTGTTTCTCACTGTAATCTTGGTTAAC 331
Db      239 GCTCCCAAGATGTTGCTCTCTCTTCAAGCTGTTTCTCACTGTAATCTTGGTTAAC 298
Qy      332 TGGAGAGAGCTTCAACTGTTCACTGTTCACTGTTCACTGTTCACTGTTCACTG 366
Db      299 TGGAGAGAGCTTCAACTGTTCACTGTTCACTGTTCACTGTTCACTGTTCACTG 333

RESULT 6
US-09-016-434-91
; Sequence 91, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Sellhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

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Query Match	9.4%	Score 187.8	DB 4	Length 378
Best Local Similarity	99.0%	Pred. No. 2,2e-57		
Matches 189	Conservative 0	Mismatches 2	Indels 0	Gaps 0
QY	44	TSGTGCTCTGTGGAAAGTGAACGAAAAAGCTGCTTAATTGATACCGGCCATTGG	103	
Db	378	TGTTGGCTCTGCTGAAAGTGAACGAAAAAGTGTGCTTAATTGATACCGGCCATTGG	319	
QY	104	TGGAATACAAATACATCCCACTTTTGGAGCCATTAAATCAACTGCTCCAAAGTTATTGA	163	
Db	318	TGAAATACAAATACATCCCACTTTTGGAGCCATTAAATCAACTGCTCCAAAGTTATTGA	259	
QY	164	ACCGAAGGTGCACACGACCAAAAGTGTAAATTCACAGAGTCATCCAGCATTCAGCGAAAC	223	
Db	258	ACCGAAGGTGCACACGACCAAAAGTGTAAATTCACAGAGTCATCCAGCATTCAGCGAAAC	199	
QY	224	ATAAGGTTCAC 234		
Db	198	ATAAGTAAAC 188		

Query March	6.2 %	Score 124.6	DB 4	Length 1830
Best Local Similarity	56.7 %	Pred. No. 1.7e-30		
Matches 251	Conservative 0	Mismatches 189	Indels 3	Gaps 1
QY	461	TTGCGAACATTTGGGGCCAAACCCGAATTTCTTCCCAATCTTATCTTGAGGCGACAGAGATG	520	
QY	1036	TCGAGAACCGTGAAGCTACACCCCACTTGCCCTTCTGTTCTTGGCAATGACGAGAGATG	1095	
QY	521	TCCTCAACAGAGAGCTGATACAGCAGAAATGGATTTGTTATGTTTAATGCCAGCTATA	580	
QY	1096	CTCAGAGCCTGGACACCAATGACGAGCGGTGAACAATCGGTAGCTATCAACGTACACATTC	1155	
QY	581	CCGTGTCCAAAGCGCTACTTT--ATCCCGAGTCTCATTTCTCGCGTGCCTGTGAATG	637	
QY	1156	ATCTTCCCTCTACACATATGAGAAAGGCGCTGTTCATCTACAAAGCGGCTCCAGGCACATG	1215	

Qy 638 ACAGCTTTTGAGAAAAATTTTGGCGGTGGAGCAAAATCAGTAGATTCAATTGAGAAAG 697
Db 1216 ACAGCAACAGAGAACTCGGCGCAGTACTTTGAGAGAGGCTTTGAGTTCATGAGGAAG 1275
Qy 698 CAAAAGCTTCCAAATGATGTGTCTAGTGCATCTTTAGCTGGGATCTCCGCTCCGCA 757
Db 1276 CTCACAGCTGGGAAAGGGGCTTCTCATCTCCAGGCTGGGGGTGTCCGCTCCGCA 1335
Qy 758 CCATGCTATGCGCTTACATCATGAGAGATGACATGCTTTAGATGAGCTTACAGAT 817
Db 1336 CCATGCTATGCTTACTTATGAGGACACTCGGATACATGACTATGCTTATTAAT 1395
Qy 818 TTGCAAAAAGAAAAAGACTTATATCTCCAAATTTCTGGGCCAATCTCTG 877
Db 1396 TTGCAAAAGGCAACGACCAATATATCTCCAACTTACTTCAATGGGCAAGTTGCTAG 1455
Qy 878 ACTATGAGAGAGATTAAGAAC 900
Db 1456 AGTTCAGAGAAAGACTTAACAAC 1478

RESULT 9

US-09-949-016-4617
; Sequence 4617, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4617
; LENGTH: 2283
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4617

Query Match 5.4%; Score 106.8; DB 4; Length 2283;
Best Local Similarity 55.3%; Pred. No. 2.1e-24;
Matches 229; Conservative 0; Mismatches 182; Indels 3; Gaps 1;

Qy 475 CCAACCCGAATTTTCCCAATCTTATTTGGCTGCCAGGAGATCTTCAACAAGAG 534
Db 723 CCTGTCCAGATCTGCCCCCACTCTATCTGGGAGTCCCGGAAATTTGGAG 782
Qy 535 CTGATPACGAGAAATGGGATGTGTTAATGTCAGCTATACCTGTCCAAA---G 591
Db 783 AGCTGGCCAAACCTGGGATCGCTACATCTCATGTGACCCCAACCTTCCAACTTC 842
Qy 592 CCGTACTTATCCCGAGTCTCATTTCTGCGTGTGCTGTGAATGACAGCTTTGTGAG 651
Db 843 TTGAGAGAAATGTGATCTTCACTACAGAGATCCCACTCCGACACTGGAGCCAG 902
Qy 652 AAAATTTTGGCGGTGGGAGCAAAATCAGTAGATTTCATTTGAGAAAGCAAAAGCTCCAA 711
Db 903 AACCTGTGCGGCTTCTTCCGAGGCCAATGATTCATGATGAGGCTTGTCCAGAAC 962
Qy 712 GGATGTGTTTATGACATGTTTATGCTGGAGATCTCCGCTCCGACACATGCTATGSCC 771
Db 963 TCGGGGTGCTGCTCCTGCTTGGCGGGGTCAAGCCCTTGTGACCCGTACGTGTGCC 1022
Qy 772 TACATCATGAGAGATGACATGTCTTTAGATGAGCTTACAGATTTGTGAAAAA 831
Db 1022 TACATCATGAGAGATGACATGTCTTTAGATGAGCTTACAGATTTGTGAAAAA 831

Db 1023 TACCTCATGAGAGATCTCCACTCTCTCTCAACAGATGCTTATGACTGTCAAGAGAG 1082
Qy 832 AGACCTACTATATCTCCAACTTCAATTTTGGGCCAATCTTGAATATGAG 885
Db 1083 AAGCTAACATCTCCCACTTCACTTCAATGGGAGGAGTTGCTGACTTTGAG 1136

RESULT 10

US-09-922-146-3
; Sequence 3, Application US/09922146
; Patent No. 6566133
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowseart
; APPLICANT: Brett P. Montia
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 9 EXPRESSION
; FILE REFERENCE: RUS-0252
; CURRENT APPLICATION NUMBER: US/09/922,146
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 3
; LENGTH: 2303
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (114)...(1268)
US-09-922-146-3

Query Match 5.4%; Score 106.8; DB 4; Length 2303;
Best Local Similarity 55.3%; Pred. No. 2.1e-24;
Matches 229; Conservative 0; Mismatches 182; Indels 3; Gaps 1;

Qy 475 CCAACCCGAATTTTCCCAATCTTATTTGGCTGCCAGGAGATCTTCAACAAGAG 534
Db 723 CCTGTCCAGATCTGCCCCCACTCTATCTGGGAGTCCCGGAAATTTGGAG 782
Qy 535 CTGATPACGAGAAATGGGATGTGTTAATGTCAGCTATACCTGTCCAAA---G 591
Db 783 AGCTGGCCAAACCTGGGATCGCTACATCTCATGTGACCCCAACCTTCCAACTTC 842
Qy 592 CCGTACTTATCCCGAGTCTCATTTCTGCGTGTGCTGTGAATGACAGCTTTGTGAG 651
Db 843 TTGAGAGAAATGTGATCTTCACTACAGAGATCCCACTCCGACACTGGAGCCAG 902
Qy 652 AAAATTTTGGCGGTGGGAGCAAAATCAGTAGATTTCATTTGAGAAAGCAAAAGCTCCAA 711
Db 903 AACCTGTGCGGCTTCTTCCGAGGCCAATGATTCATGATGAGGCTTGTCCAGAAC 962
Qy 712 GGATGTGTTTATGACATGTTTATGCTGGAGATCTCCGCTCCGACACATGCTATGSCC 771
Db 963 TCGGGGTGCTGCTCCTGCTTGGCGGGGTCAAGCCCTTGTGACCCGTACGTGTGCC 1022
Qy 772 TACATCATGAGAGATGACATGTCTTTAGATGAGCTTACAGATTTGTGAAAAA 831
Db 1023 TACCTCATGAGAGATCTCCACTCTCTCTCAACAGATGCTTATGACTGTCAAGAGAG 1082
Qy 832 AGACCTACTATATCTCCAACTTCAATTTTGGGCCAATCTTGAATATGAG 885
Db 1083 AAGCTAACATCTCCCACTTCACTTCAATGGGAGGAGTTGCTGACTTTGAG 1136

RESULT 11

US-09-016-434-1135
; Sequence 1135, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

```
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1135:
SEQUENCE CHARACTERISTICS:
LENGTH: 2109 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1418933
US-09-016-434-1135

Query Match
Best Local Similarity 4.8%; Score 96.2; DB 4; Length 2109;
Matches 222; Conservative 0; Mismatches 188; Indels 3; Gaps 1;

QY 484 ATTCTTCCCAATCTTTATCTTGTGCTGCAGCGAGATGTCCTCAACAAGAGCTGATACG 543
DB 979 ATCTTGCCCTTCTCTACTTGAGCTGTGTGCCAAGACTCCACCACCTTGACGTGTGGAG 1038
QY 544 CAGAAATGGAGTTGTTATGTGTTAAATGCCAGCTATACCTGTCCAAAGC---CTGACTTT 600
DB 1039 GAATTCGGCATCAAGTACATCTTGAACGTCAACCCCAATTTGCCGAATCTTTGAGAAC 1098
QY 601 ATCCCGAGTCTCATTTCTGCGTGTGCTGTGAATGACAGCTTTTGTGAGAAAATTTTG 660
DB 1099 GCAGAGAGTTTAAATACAGCAAAATCCCATCTCGATCACTGAGCCAAACCTGTCC 1158
QY 661 CCGTGTGAGCAAAATCAGTATGATTTCATTGAGAAAGCAAAAGCCTCCAAATGATGTGTT 720
DB 1159 CAGTTTTTCCGTGAGGCCATTTCTTCAATAGTAGAAGCCCGGGCAAGACTGTGTGTTC 1218
QY 721 CTATGCACTGTTTACTGCTGAGATCTCCGCTCCGCCCAACATCGTATCGCCTACATCATG 780
DB 1219 TTGTACATTTCTTGGCTGGCATTTAGCCGCTCACTGACTGTGACTGTGCTTACTTATG 1278
QY 781 AAGAGATGAGCAGTCTTTAGATGAGAGCTTACAGATTTGTGAGAAAAGAAAGCTACT 840
DB 1279 CAGAAAGCTCAATCTGTGATGAAGATGCCATATGTCAAATGAAAATCCAACTCCAAC 1338
QY 841 ATATCTCCAAATCTCAATTTTCTGGGCCAACTCCTGAGACTATGAGAGAAAGAT 893
DB 1339 ATATCCCTACTTCACTTCACTTATGATGATGCTGTGATGAGAGAGAGCT 1391
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```
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 946:
SEQUENCE CHARACTERISTICS:
LENGTH: 2109 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1418933
US-09-023-655-946

Query Match
Best Local Similarity 4.8%; Score 96.2; DB 4; Length 2109;
Matches 222; Conservative 0; Mismatches 188; Indels 3; Gaps 1;

QY 484 ATTCTTCCCAATCTTTATCTTGTGCTGCAGCGAGATGTCCTCAACAAGAGCTGATACG 543
DB 979 ATCTTGCCCTTCTCTACTTGAGCTGTGTGCCAAGACTCCACCACCTTGACGTGTGGAG 1038
QY 544 CAGAAATGGAGTTGTTATGTGTTAAATGCCAGCTATACCTGTCCAAAGC---CTGACTTT 600
DB 1039 GAATTCGGCATCAAGTACATCTTGAACGTCAACCCCAATTTGCCGAATCTTTGAGAAC 1098
QY 601 ATCCCGAGTCTCATTTCTGCGTGTGCTGTGAATGACAGCTTTTGTGAGAAAATTTTG 660
DB 1099 GCAGAGAGTTTAAATACAGCAAAATCCCATCTCGATCACTGAGCCAAACCTGTCC 1158
QY 661 CCGTGTGAGCAAAATCAGTATGATTTCATTGAGAAAGCAAAAGCCTCCAAATGATGTGTT 720
DB 1159 CAGTTTTTCCGTGAGGCCATTTCTTCAATAGTAGAAGCCCGGGCAAGACTGTGTGTTC 1218
QY 721 CTATGCACTGTTTACTGCTGAGATCTCCGCTCCGCCCAACATCGTATCGCCTACATCATG 780
DB 1219 TTGTACATTTCTTGGCTGGCATTTAGCCGCTCACTGACTGTGACTGTGCTTACTTATG 1278
QY 781 AAGAGATGAGCAGTCTTTAGATGAGAGCTTACAGATTTGTGAGAAAAGAAAGCTACT 840
DB 1279 CAGAAAGCTCAATCTGTGATGAAGATGCCATATGTCAAATGAAAATCCAACTCCAAC 1338
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Qy 841 ATATCTCCAACTTCAATTTCTGGGCAACTCTGAGCTATGAGAGAAGAT 893
Db 1339 ATATCCCTTAATCTCACTTATGGGTGAGCTGAGCTTGAGAGAGAGCT 1391

RESULT 13
US-09-949-016-2615

; Sequence 2615, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2615
; LENGTH: 2475
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2615

Query Match 4.8%; Score 96.2; DB 4; Length 2475;
Best Local Similarity 53.8%; Pred. No. 8.7e-21;
Matches 222; Conservative 0; Mismatches 188; Indels 3; Gaps 1;

Qy 484 ATCTTCCCAATCTTATCTTGGCTGCCAGAGATGCTTCAACAGAGCTGATACAG 543
Db 1068 ATCTTCCCTTCTCTACTTGGGCTGTGCCAAGACTCCACCACTTGAGCTGTGAG 1127
Qy 544 CAGAAATGGATGTTGTTATGTGTTAAATGCCAGCTTACTCTCCAAAC---CTGACTT 600
Db 1128 GAATTCGGCATCAAGTACATCTTGAAAGCTCAACCCCAATTTGCCCAATCTTTGAGAAC 1187
Qy 601 ATCCCGAGTCTCATTTCTCGTGTGCTGTAATGACAGCTTTTGAAGAAATTTTG 660
Db 1188 GCAGAGAGTTTAAATACAGCAATCCCATCTGAGTACTGAGACCAAACTGTGCC 1247
Qy 661 CCGTGTGGAACAATCAGTATGATTTCATTGAGAAAGCAAAAGCCTCCATGATGTGT 720
Db 1248 CAGTTTTCCTGAGAGCCATTTCTTCAATGATGAGCCGGGGCAGAACTGTGTGTC 1307
Qy 721 CTAGTGCACTGTTTACGTGGATCTCCGCTCCGACCACTGCTATGCTTACATCTG 780
Db 1308 TTGTGACATTCCTGGCTGGGATTAAGCCGCTACGACCTGAGCTGTGCTTACCTTATG 1367
Qy 781 AAGAGATGACATGCTTTTATGATGAGCTTACAGATTGGAAGAAAGAAAGACTTACT 840
Db 1368 CAGAGCTCAATCTGTCATGAGATGAGTCTTATGACATTTGCAAAATATAAATCCAAC 1427
Qy 841 ATATCTCCAACTTCAATTTCTGGGCAACTCTGAGCTATGAGAGAAGAT 893
Db 1428 ATATCCCTTAATCTCACTTATGGGTGAGCTGAGCTTGAGAGAGAGCT 1480

RESULT 14
US-09-023-655-347

; Sequence 347, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; EXPRESSION

; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 347:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1208 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; IMMEDIATE SOURCE:
; LIBRARY: THYNOT03
; CLONE: 1444245
US-09-023-655-347

Query Match 4.7%; Score 94.6; DB 4; Length 1208;
Best Local Similarity 64.3%; Pred. No. 1.7e-20;
Matches 142; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 680 TAGATTCATGAGAAAGCAAAAGCCTCCATGATGTTCTGAGCTGTTAGCTG 739
Db 4 TTGATTCATGAGAAAGCTCACCAGTGTGGAAGGGCTTCTATCCACTGCCAGGCTG 63
Qy 740 GGATCTCCGCTCCGCCACCATCGCTATCGCTACATCATGAGATGACATGTCTT 799
Db 64 GGGTGTCCGCTCCGCCACCATCGCTATCGCTTATGATGAGACACCTGGATGACCA 123
Qy 800 TAGATGAACTTACAGATTGTTGAAAGAAAGAAAGCACTACTATATCTCCAACTTCAATT 859
Db 124 TGACTGATGCTTATTAATTTGTCAAGGCAAAAGCAACCAATATCTCCCAACTTAAT 183
Qy 860 TTCTGGGCAACTCTGAGCTATGAGAAAGATTTAAGAC 900
Db 184 TCATGGGGCAGTGTCTAGAGTTGAGAGAAAGCTTAACAC 224

RESULT 15
US-09-702-705-801

; Sequence 801, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Ranger, Gary
; APPLICANT: Vedvik, Tom
; APPLICANT: Carter, Darlick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane

```
/ APPLICANT: Fan, Liqun
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.478C14
/ CURRENT APPLICATION NUMBER: US/09/702,705
/ NUMBER OF SEQ ID NOS: 1833
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 801
/ LENGTH: 1619
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-702-705-801
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Best Local Similarity 52.3%; Pred. No. 4.6e-20;
Matches 222; Conservative 0; Mismatches 209; Indels 3; Gaps 1;

QY 484 ATCTTCCCAATCTTATCTTGTGCTGCCAGAGATGTCCTCACAAGAGCTGATACAG 543
Db 320 ATCTTCCCTTCTCTACTCTCGCAGTGCCTACATGCTGCCGAGAGACATGCTGAGC 379
QY 544 CAGATGGATGGTTATGTATGTTAAATGCCACTATACCTGTCCAAAGCTGACTTTATC 603
Db 380 GCCCTGGGATACAGGCTCTGTGTAATGTCCTCGAAGCTGCCCAACC--ACTTTGAA 436
QY 604 CCCGAGTCATTTCTCGCTGCTGCTGATGAAGACAGCTTTGTGAGAAATTTTGGCG 663
Db 437 GGACACTATCACTACAGTGCATCCCAAGTGAAGATTAACACAGGCCGACATCAGCTCC 496
QY 664 TGGTTGACAAATCAGTAGATTTCATGTAGAAAGCAAAAGCCTCCATGATGTGTCTA 723
Db 497 TGGTTCATGGAAGCCATAGATGATCATGATGCGGTGAAGACTGCGGTGGGGCGTGTG 556
QY 724 GTGCACTGTTTGTGGGATTCCTCCGCTCCGCCACCATGCTATGCTTACATCATGAAG 783
Db 557 GTGCACTGCAAGCGGCGGATCTCGCGGTGCGGCACCATCTGCTGCTTACCTGATGATG 616
QY 784 AGGATGACATGTCTTTAGATGAAGCTTACAGATTGTGAAAGAAAAAGACCTACTATA 843
Db 617 AAGAAACGGGTGAGGCTGAGAGAGGCTTCGAGTTCTTTAAGCAGCGCCGACATTTATC 676
QY 844 TCTCCAAACTTCATTTTCTGGGCCAATCTCTGACTATGAGAAAGAGATTAAAGAACCA 903
Db 677 TCGCCCAACTTCAGCTTCATGGGGCAGCTGCTGAGTTCAGATCCAGAGTGTGGCCACG 736
QY 904 ACTGGAGATCAGGGGCCAAAGAGC 927
Db 737 TCTGTGCTGCGAGGCTGCTAGC 760
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GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

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Perfect score: 1995
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5378673 seqs, 2950229984 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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19: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1991.8	99.8	1998	17	US-10-377-072-27
3	1991.8	99.8	1998	18	US-10-377-072-27
4	1991.8	99.8	1059	17	US-10-257-026-1
5	1991.8	99.8	3496	9	US-09-964-277-1
6	1991.8	99.8	3521	18	US-10-370-7158-261
7	1991.8	99.8	3544	9	US-09-816-494-1
8	1991.8	99.8	3544	17	US-10-377-072-25
9	1991.8	99.8	3544	18	US-10-377-072-25
10	1991.8	99.8	3625	17	US-10-425-114-26234
11	1991.8	99.8	3766	17	US-10-343-357-17

12	1991.8	99.8	4790	18	US-10-648-593-115	Sequence 115, App
13	1991.8	99.8	5145	18	US-10-357-930-20824	Sequence 20824, A
14	1991.8	99.8	5145	18	US-10-357-930-20969	Sequence 20969, A
15	1991.8	99.8	5145	18	US-10-357-930-21071	Sequence 21071, A
16	1991.8	99.8	5145	18	US-10-357-930-21083	Sequence 21083, A
17	1991.8	99.8	5145	18	US-10-357-930-21303	Sequence 21303, A
18	1991.8	99.8	5145	18	US-10-357-930-21307	Sequence 21307, A
19	1991.8	99.8	5145	18	US-10-357-930-21307	Sequence 21307, A
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21	1991.8	99.8	5145	18	US-10-357-930-26685	Sequence 26685, A
22	1991.8	99.8	5145	18	US-10-357-930-26912	Sequence 26912, A
23	1991.8	99.8	5145	18	US-10-357-930-26923	Sequence 26923, A
24	1991.8	99.8	5145	18	US-10-357-930-27145	Sequence 27145, A
25	1991.8	99.8	5145	18	US-10-357-930-27149	Sequence 27149, A
26	1991.8	99.8	5145	18	US-10-357-930-28675	Sequence 28675, A
27	1990.2	99.8	2732	17	US-10-168-505-2	Sequence 2, Appl1
28	1988.6	99.7	2102	17	US-10-094-749-673	Sequence 673, App
29	1988.6	99.7	2966	17	US-10-296-115-520	Sequence 520, App
30	1986.2	98.4	2071	17	US-10-072-012-257	Sequence 257, App
31	1906.8	95.6	2200	17	US-10-072-012-255	Sequence 255, App
32	1653.8	82.9	3332	9	US-09-964-277-20	Sequence 20, Appl1
33	879.4	44.1	1916	17	US-10-108-260A-2429	Sequence 2429, App
34	417.2	20.9	425	18	US-10-357-930-10717	Sequence 10717, A
35	415.2	20.8	467	18	US-10-357-930-31909	Sequence 31909, A
36	415.2	20.8	467	18	US-10-357-930-40868	Sequence 40868, A
37	415.2	20.8	467	18	US-10-357-930-41017	Sequence 41017, A
38	411.2	20.6	461	18	US-10-357-930-11243	Sequence 11243, A
39	410.2	20.6	461	18	US-10-357-930-32416	Sequence 32416, A
40	410.2	20.6	461	18	US-10-357-930-41000	Sequence 41000, A
41	410.2	20.6	461	18	US-10-357-930-41346	Sequence 41346, A
42	401.2	20.1	408	18	US-10-357-930-10898	Sequence 10898, A
43	399.2	20.0	438	18	US-10-357-930-32077	Sequence 32077, A
44	395.4	19.8	427	18	US-10-357-930-10878	Sequence 10878, A
45	382	19.1	2453	13	US-10-005-858-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-816-494-3
; Sequence 3, Application US/09816494
; Patent No. US20020034807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-816-494-3

Query Match 99.8%; Score 1991.8; DB 9; Length 1998;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCCCATGAGATGATGGAATCTTACTGAGAGGTTGGCTCTGCTGGA 60
DB 1 ATGCCCATGAGATGATGGAATCTTACTGAGAGGTTGGCTCTGCTGGA 60
QY 61 AGTGAAGCGAAAGAGCTGCTATGATGAGCGGCAATTTGGGAATACATCATCC 120
DB 61 AGTGAAGCGAAAGAGCTGCTATGATGAGCGGCAATTTGGGAATACATCATCC 120
QY 121 CACATTTTGAAGCATTAATATCACTGCTCCAGGCTTATGAAGCGAAGTTGCAACAG 180

Db 121 CACATTTGGAAGCCATTATATCACTGCTCCAGGTTATGAGGCAAGGTTGCAACAG 180
Qy 181 GACAAAGGTTAATTAACAGAGCTATCCAGATTTACAGGAAACATAAGTTGACATTGAT 240
Db 181 GACAAAGGTTAATTAACAGAGCTATCCAGATTTACAGGAAACATAAGTTGACATTGAT 240
Qy 241 TGCAGTGAAGAGTTGATGATTGATCAAGAGCTCCCAAGATGTTGCTCTCTCTCA 300
Db 241 TGCAGTGAAGAGTTGATGATTGATCAAGAGCTCCCAAGATGTTGCTCTCTCTCA 300
Qy 301 GACTGTTTTCTCACTGTAATTTCTGGGTAACCTGAGAGAGCTTCAACTCTGTTACCTG 360
Db 301 GACTGTTTTCTCACTGTAATTTCTGGGTAACCTGAGAGAGCTTCAACTCTGTTACCTG 360
Qy 361 CTGGCAGAGGAGTTGCTGAGTTCTCTGCTGTTTCCCTGCTGCTGTAAGAGAAATCC 420
Db 361 CTGGCAGAGGAGTTGCTGAGTTCTCTGCTGTTTCCCTGCTGCTGTAAGAGAAATCC 420
Qy 421 ACTCTAGTCCCTACCTGATTTCTCAGCCCTTGCCTTACCTGTTGCAACATGGGCGCAAC 480
Db 421 ACTCTAGTCCCTACCTGATTTCTCAGCCCTTGCCTTACCTGTTGCAACATGGGCGCAAC 480
Qy 481 CGAATTTCTCCCATCTTTATCTTGGCTGCGAGAGATGCTCTCAACAGAGCTGAT 540
Db 481 CGAATTTCTCCCATCTTTATCTTGGCTGCGAGAGATGCTCTCAACAGAGCTGAT 540
Qy 541 CAGCAGAAATGGAGTTGATGTTAATGCGAGTATACCTGTCGAAGCTGACT 600
Db 541 CAGCAGAAATGGAGTTGATGTTAATGCGAGTATACCTGTCGAAGCTGACT 600
Qy 601 ATCCCGAGTCTCATTTCTGCGCTGCTGCTGATGACAGCTTTTGTGAGAAATTTTG 660
Db 601 ATCCCGAGTCTCATTTCTGCGCTGCTGCTGATGACAGCTTTTGTGAGAAATTTTG 660
Qy 661 CCGTGGTGGAGAAATCAGTATGATTTGATGAGAAAGCAAAAGCTTCAATGATGTTT 720
Db 661 CCGTGGTGGAGAAATCAGTATGATTTGATGAGAAAGCAAAAGCTTCAATGATGTTT 720
Qy 721 CTAGTGCATGTTTAGCTGGGATCTCCGCTCCGCAACCATGCTATGCGCTACATCAG 780
Db 721 CTAGTGCATGTTTAGCTGGGATCTCCGCTCCGCAACCATGCTATGCGCTACATCAG 780
Qy 781 AAGAGATGAGATGCTTTAGATGAAAGCTTACAGATTTGAGAAAGAAAGACTTACT 840
Db 781 AAGAGATGAGATGCTTTAGATGAAAGCTTACAGATTTGAGAAAGAAAGACTTACT 840
Qy 841 ATATCTCCAACTTCAATTTCTGGGCAACTCCCTGAGCTATGAGAGAAAGATTAGAAC 900
Db 841 ATATCTCCAACTTCAATTTCTGGGCAACTCCCTGAGCTATGAGAGAAAGATTAGAAC 900
Qy 901 CAGACTGAGATCAAGGCGCAAGAGCAAACTCAAGCTGCTGACCTTGAAGAGCAAT 960
Db 901 CAGACTGAGATCAAGGCGCAAGAGCAAACTCAAGCTGCTGACCTTGAAGAGCAAT 960
Qy 961 GAACTGTCCTGCTGCTGCTGCTGAGAGGTTGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 961 GAACTGTCCTGCTGCTGCTGCTGAGAGGTTGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Qy 1021 TGTGCGAATCTGCTAATCTCAGAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db 1021 TGTGCGAATCTGCTAATCTCAGAGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Qy 1081 CCCAGCGTGGCAG 1140
Db 1081 CCCAGCGTGGCAG 1140
Qy 1141 AGTGGGCGAG 1200
Db 1141 AGTGGGCGAG 1200
Qy 1201 TCTCTGATATCAATATGATTTCTATTTCAAGCCAGATGAGATGCTTCAATGAGTTTC 1260
Db 1201 TCTCTGATATCAATATGATTTCTATTTCAAGCCAGATGAGATGCTTCAATGAGTTTC 1260

Db 1201 TCTCTGATATCAATATGATTTCTATTTCAAGCCAGATGAGATGCTTCAATGAGTTTC 1260
Qy 1261 TCTCTGATGAGAGATGCTTTGGAATACTACAAACCTTCCATCTGATGAGAGAGAGAG 1320
Db 1261 TCTCTGATGAGAGATGCTTTGGAATACTACAAACCTTCCATCTGATGAGAGAGAGAG 1320
Qy 1321 AAGCTATGCGAGTTTCCCTGTTTCAAGAACTATGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 AAGCTATGCGAGTTTCCCTGTTTCAAGAACTATGAGAGAGAGAGAGAGAGAGAGAG 1380
Qy 1381 GATTAAG 1440
Db 1381 GATTAAG 1440
Qy 1441 AGCAAGGATTTGCAATTTGGGTGAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Db 1441 AGCAAGGATTTGCAATTTGGGTGAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Qy 1501 TCTCCATGATCGAATGGGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Db 1501 TCTCCATGATCGAATGGGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Qy 1561 CTTTCCAG 1620
Db 1561 CTTTCCAG 1620
Qy 1621 TCGATATCTTGGGCCCCCAG 1680
Db 1621 TCGATATCTTGGGCCCCCAG 1680
Qy 1681 ACAGAGTCTCCAGATCTTCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 ACAGAGTCTCCAGATCTTCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Qy 1741 GCTTACAGCTGAG 1800
Db 1741 GCTTACAGCTGAG 1800
Qy 1801 CAG 1860
Db 1801 CAG 1860
Qy 1861 AAGCAGTTTAAAGCAG 1920
Db 1861 AAGCAGTTTAAAGCAG 1920
Qy 1921 AGGTCAAGGAG 1980
Db 1921 AGGTCAAGGAG 1980
Qy 1981 ATCATTGAGAGTCTCC 1995
Db 1981 ATCATTGAGAGTCTCC 1995

RESULT 2
US-10-377-072-27
; Sequence 27, Application US/10377072
; Publication No. US2004009501A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Miyoung
; APPLICANT: Tsai, Fong-yang
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; FILE REFERENCE: MP103-0180NMIM

CURRENT APPLICATION NUMBER: US/10/377,072
CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US 09/895,860
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,370
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/723,806
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/187,455
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/843,297
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199,801
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: US 09/861,801
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205,508
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/816,494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/815,419
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1998)
US-10-377-072-27

Query Match 99.8%; Score 1991.8; DB 17; Length 1998;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGGCCATGAGTATTTGGAATTCGAGAGTGGTGGCTGCTGGA 60
1 ATGGCCATGAGTATTTGGAATTCGAGAGTGGTGGCTGCTGGA 60
61 AGTGAAGGAAAAGTCTGCTAATTTAGAGCCGATTTGGAATACATATCC 120
61 AGTGAAGGAAAAGTCTGCTAATTTAGAGCCGATTTGGAATACATATCC 120
121 CACATTTTGAAGCATTATATCACTGCTCAAGCTTATGAAAGGTTGCAACG 180
121 CACATTTTGAAGCATTATATCACTGCTCAAGCTTATGAAAGGTTGCAACG 180
181 GACAAAGTTTATATCAAGAGTCTATCCAGCATTCAGGAAACATTAAGTTGACATTGAT 240
181 GACAAAGTTTATATCAAGAGTCTATCCAGCATTCAGGAAACATTAAGTTGACATTGAT 240
241 TGCAGTCAAGAGTTTATGATTTAGATCAAAAGCTCCAAAGTTGGCTCTCTCTTCA 300
241 TGCAGTCAAGAGTTTATGATTTAGATCAAAAGCTCCAAAGTTGGCTCTCTCTTCA 300
301 GACTGTTTCTCACTGTACTTCTGGGTAACTGGAAGAGCTTCACTGTTCACTG 360
301 GACTGTTTCTCACTGTACTTCTGGGTAACTGGAAGAGCTTCACTGTTCACTG 360
361 CTGGAAGTGGGTGCTGAGTTCTCTGTGTTCCTGGCTCTGGAAGGAAATCC 420
361 CTGGAAGTGGGTGCTGAGTTCTCTGTGTTCCTGGCTCTGGAAGGAAATCC 420
421 ACTGAGTCCCTACCTGATTTCTAGCCTTACCTTACCTGTTGCAACATTTGGGCAAC 480
421 ACTGAGTCCCTACCTGATTTCTAGCCTTACCTTACCTGTTGCAACATTTGGGCAAC 480
481 CGAATTTCTCCCAATCTTATCTTGGCTGCAAGAGATGCTCAACAAGAGTGTATA 540
481 CGAATTTCTCCCAATCTTATCTTGGCTGCAAGAGATGCTCAACAAGAGTGTATA 540

541 CAGCAGATGGATTTGTTATGTTAAATCCAGCTATACCTGTCCAAAGCTGACTTT 600
541 CAGCAGATGGATTTGTTATGTTAAATCCAGCATACTGTCCAAAGCTGACTTT 600
601 ATCCCGAGTCTCATTTCTGGGTGCTGCTGAAATGACAGTTTGTGAGAAATTTTG 660
601 ATCCCGAGTCTCATTTCTGGGTGCTGCTGAAATGACAGTTTGTGAGAAATTTTG 660
661 CCGTGTGGAACAAATGATGATTTCAATTGAAAGCAAAAGCTCCAAATGAGATGTT 720
661 CCGTGTGGAACAAATGATGATTTCAATTGAAAGCAAAAGCTCCAAATGAGATGTT 720
721 CTAGTCACTGTTTATGCTGAGATCTCCGCTCCGCAATGCTGATGCTTACATCAG 780
721 CTAGTCACTGTTTATGCTGAGATCTCCGCTCCGCAATGCTGATGCTTACATCAG 780
781 AAGAGATGACATGCTTTTATGATGAACTTACAGATTTGTAAGAAAGAAAGCTACT 840
781 AAGAGATGACATGCTTTTATGATGAACTTACAGATTTGTAAGAAAGAAAGCTACT 840
841 ATATCTCCAACTTCAATTTTCTGGGCCAATCTCTGAGCTATGAGAAAGTTAAGAC 900
841 ATATCTCCAACTTCAATTTTCTGGGCCAATCTCTGAGCTATGAGAAAGTTAAGAC 900
901 CAGACTGAGATCAGAGGCAAGAGCAAAAGCTCAAGCTGCTGCACTGGAAGCAAT 960
901 CAGACTGAGATCAGAGGCAAGAGCAAAAGCTCAAGCTGCTGCACTGGAAGCAAT 960
961 GAACCTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
961 GAACCTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
1021 TGTGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
1021 TGTGCGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
1081 CCGAGCGTCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
1081 CCGAGCGTCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
1141 AGTGGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
1141 AGTGGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
1201 TCTCTGATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1260
1201 TCTCTGATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1260
1261 TCTCTGATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1320
1261 TCTCTGATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1320
1321 AAGCTATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
1321 AAGCTATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1380
1381 GATTAAGGAGAGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
1381 GATTAAGGAGAGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
1441 GATTAAGGAGAGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
1441 GATTAAGGAGAGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
1501 TCTCTCACTGATCAAGTGGAGGCTGGAAGCAATTAACAACAAGCTTCTTTTGGGC 1560
1501 TCTCTCACTGATCAAGTGGAGGCTGGAAGCAATTAACAACAAGCTTCTTTTGGGC 1560
1561 CTTTCCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1620
1561 CTTTCCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1620

QY	1621	TCGAGATATCTGGCCCCCCAGACCTCTACCCCTTCCCTGACCCAGACGCTGGATTTGGCC	1680
Db	1621	TCGGAATCTTGGCCCCCCAGACCTCTACCCCTTCCCTGACCCAGACGCTGGATTTGGCC	1680
QY	1681	ACAGAGTCCCTCACACTTCTACCTGSCCAGCCATCTAAGGAGGAGTGCAGATTACTCT	1740
Db	1681	ACAGAGTCCCTCACACTTCTACTCTGCTCCAGCCATCTAAGGAGGAGTGCAGATTACTCT	1740
QY	1741	GCTTACAGCTGCAGCCAGCTGCCCCATTGCGAGACCAAGTCTATTCTGTGCGAGGCGG	1800
Db	1741	GCTTACAGCTGCAGCCAGCTGCCCCATTGCGAGACCAAGTCTATTCTGTGCGAGGCGG	1800
QY	1801	CAGAAGCCAATGACAGAGCTGACTCTCGGCGCGAGCTGCACTAAGAGAGGCCCTTTGAA	1860
Db	1801	CAGAAGCCAATGACAGAGCTGACTCTCGGCGCGAGCTGCACTAAGAGAGGCCCTTTGAA	1860
QY	1861	AAGCAGTTTAAACGCAGAAAGCTGCGCAATGGAATTTGGAGAGACATCAAGTCAGAGAAC	1920
Db	1861	AAGCAGTTTAAACGCAGAAAGCTGCGCAATGGAATTTGGAGAGACATCAAGTCAGAGAAC	1920
QY	1921	AGGTCAACGGGAGAGAGCTGGGGGAAAGTGGGCACTCACTAGCTTTTCGGGCAAGATGAA	1980
Db	1921	AGGTCAACGGGAGAGAGCTGGGGGAAAGTGGGCACTCACTAGCTTTTCGGGCAAGATGAA	1980
QY	1981	ATCATTTGAGGTCTCC	1995
Db	1981	ATCATTTGAGGTCTCC	1995

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RESULT 3
US-10-377-072-27
Sequence 27, Application US/10377072
Publication No. US20040157221A9
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals Inc.
APPLICANT: Curtis, Rory A.J.
APPLICANT: Logan, Thomas Joseph
APPLICANT: Glucksmann, Maria A.
APPLICANT: Meyers, Rachel E.
APPLICANT: Williamson, Mark J.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Chun, Miyoung
APPLICANT: Tsai, Feng-Ying
TITLE OF INVENTION: NOVEL, 25869, 25934, 26335, 50365, 21117,
TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: MPI03-0180MINT
CURRENT APPLICATION NUMBER: US/10/377,072
CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US 09/895,860
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,370
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/723,806
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/187,455
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/843,297
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199,801
PRIOR FILING DATE: 2000-04-26
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PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205,508
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/816,494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/815,419
PRIOR FILING DATE: 2001-03-22
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27

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; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (1998)
;
US-10-377-072-27

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Query Match	99.8%	Score 1991.8;	DB 18;	Length 1998;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 1993; Conservative	0;	Mismatches	2;	Indels 0; Gaps 0;

QY	1	ATGGCCCATGAGATGATTTGAACTCAAAATTTGTTACTGAGAGGTTGATGCTCGTGGAA	60
Db	1	ATGGCCCATGAGATGATTTGAACTCAAAATTTGTTACTGAGAGGTTGATGCTCGTGGAA	60
QY	61	ACGTGAACGGAAAAAGTCTGCTAAATGATAGCCGGCAATTTGTGAAATACATACATCC	120
Db	61	ACGTGAACGGAAAAAGTCTGCTAAATGATAGCCGGCAATTTGTGAAATACATACATCC	120
QY	121	CACATTTTGGAAAGCCATTATATCAACGTCTCCAAAGCTTATGAAAGCAAGTTGCAACAG	180
Db	121	CACATTTTGGAAAGCCATTATATCAACGTCTCCAAAGCTTATGAAAGCAAGTTGCAACAG	180
QY	181	GACAAAGTGTATTAATACAGAGCTCACAGCAATTCAGCGAAACATTAAGTTGACATTGAT	240
Db	181	GACAAAGTGTATTAATACAGAGCTCACAGCAATTCAGCGAAACATTAAGTTGACATTGAT	240
QY	241	TGCAAGTCAGAAAGTGTATGATTAACATCAAAAGCTCCCAAGATGTGGCTCTCTCTTCA	300
Db	241	TGCAAGTCAGAAAGTGTATGATTAACATCAAAAGCTCCCAAGATGTGGCTCTCTCTTCA	300
QY	301	GACTGTTTCTCACTGATCTTCTGGGTAACTGAGAAAGACTTCAACTCTGTTCACTG	360
Db	301	GACTGTTTCTCACTGATCTTCTGGGTAACTGAGAAAGACTTCAACTCTGTTCACTG	360
QY	361	CTTGCAGGTGGGTTTGCTGAATTCCTCTGTTGTTCCCTGGCTCTGTGAAGAAAAATCC	420
Db	361	CTTGCAGGTGGGTTTGCTGAATTCCTCTGTTGTTCCCTGGCTCTGTGAAGAAAAATCC	420
QY	421	ACTAGATCCCTACCTGATCTTCAGGCTTGCTTACCTGTGGCAACATTTGGGCCAAC	480
Db	421	ACTAGATCCCTACCTGATCTTCAGGCTTGCTTACCTGTGGCAACATTTGGGCCAAC	480
QY	481	GGAATTTCTCCCAATCTTTATCTTGAGTGCACAGAGATGCTCTCAACAAGAGCTGATA	540
Db	481	GGAATTTCTCCCAATCTTTATCTTGAGTGCACAGAGATGCTCTCTCAACAAGAGCTGATA	540
QY	541	CAGCAGATGGGATTTGGTATATGTTTAAAGCCAGCTATCTGTGCCAAAGCTGACTTT	600
Db	541	CAGCAGATGGGATTTGGTATATGTTTAAAGCCAGCTATCTGTGCCAAAGCTGACTTT	600
QY	601	ATCCCGAGTCTATTTCTGCGTGTGCTGTGATGACAGCTTTTGTGAGAAAAATTTTG	660
Db	601	ATCCCGAGTCTATTTCTGCGTGTGCTGTGATGACAGCTTTTGTGAGAAAAATTTTG	660
QY	661	CCGTGTGTGACAAATCAGTAGATTTTATGAGAAAGCAAAAGCTTCCAAATGATGTGTT	720
Db	661	CCGTGTGTGACAAATCAGTAGATTTTATGAGAAAGCAAAAGCTTCCAAATGATGTGTT	720
QY	721	CTAGTGCAGTTTTAGCTGGGATCTCCCGCTCCGACACATGCGCTATGCGCTACATCAG	780
Db	721	CTAGTGCAGTTTTAGCTGGGATCTCCCGCTCCGACACATGCGCTATGCGCTACATCAG	780
QY	781	AAGAGATGACATGCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGACTTACT	840
Db	781	AAGAGATGACATGCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGACTTACT	840
QY	841	ATAATCTCAAACTTCAATTTTCTGGGCCCAACTCTGGAATATAGAGAAAGATTTAAGAC	900
Db	841	ATAATCTCAAACTTCAATTTTCTGGGCCCAACTCTGGAATATAGAGAAAGATTTAAGAC	900
QY	901	CAGACTGAGACATCAGGCGCAAAAGACAAACTCAAGCTGCTCAGCTGAGAAAGCCAAAT	960

Db 787 CCGTGGTGGCAATCAGTAGATTTCATTGAGAAAGCAAAAGCTCAATGATGTT 846
Qy 721 CTAAGGCACTGTTAGCTGGGATCTCCGCTCCGCCCACTCGCTATGCTTACATCAG 780
Db 847 CTAATGCACTGTTAGCTGGGATCTCCGCTCCGCCCACTCGCTATGCTTACATCAG 906
Qy 781 AAGAGATGACATGCTTATGATGAAGCTTACAGATTTGTGAAAAGAAAAGCACT 840
Db 907 AAGAGATGACATGCTTATGATGAAGCTTACAGATTTGTGAAAAGAAAAGCACT 966
Qy 841 ATATCTCAAACTTCAATTTTCTGGGCAACTCTGTGACTATGAGAAAGATTAAAG 900
Db 967 ATATCTCAAACTTCAATTTTCTGGGCAACTCTGTGACTATGAGAAAGATTAAAG 1026
Qy 901 CAGACTGAGACATCAGGGCCAAAGAGCAACTGAGCTGTGCACTGTGAGAAAGCA 960
Db 1027 CAGACTGAGACATCAGGGCCAAAGAGCAACTGAGCTGTGCACTGTGAGAAAGCA 1086
Qy 961 GAACCTGTCTCTGTCTGAGAGGGTGAACAGAAAAGCGAGAGCGCCCTCAGTCCACC 1020
Db 1087 GAACCTGTCTCTGTCTGAGAGGGTGAACAGAAAAGCGAGAGCGCCCTCAGTCCACC 1146
Qy 1021 TGAGCCGACTCTGCTACCTCAGAGGAGAGCAAGAGCCGCTGATCCCGCAGCGTG 1080
Db 1147 TGAGCCGACTCTGCTACCTCAGAGGAGAGCAAGAGCCGCTGATCCCGCAGCGTG 1206
Qy 1081 CCCAGGCTGCCAGCGTGAAGCGCTGCTGTTAGAGAGAGCGCGCTGATCAGGCGCTC 1140
Db 1207 CCCAGGCTGCCAGCGTGAAGCGCTGCTGTTAGAGAGAGCGCGCTGATCAGGCGCTC 1266
Qy 1141 AGTGGGCTCAGACTGTGCTCCGAGAGAGGCTGAAAGACAGCAATTAAGCTCAGCTTC 1200
Db 1267 AGTGGGCTCAGACTGTGCTCCGAGAGAGGCTGAAAGACAGCAATTAAGCTCAGCTTC 1326
Qy 1201 TCTCTGATATCAAAATCAGTTTCATATTCAGCCAGATGGAGCATCCCTTACATGCTTC 1260
Db 1327 TCTCTGATATCAAAATCAGTTTCATATTCAGCCAGATGGAGCATCCCTTACATGCTTC 1386
Qy 1261 TCTCTCATCAGAAAGATGCTTTGGAATTAACAACCTTCACTACTGATGGAGCAAC 1320
Db 1387 TCTCTCATCAGAAAGATGCTTTGGAATTAACAACCTTCACTACTGATGGAGCAAC 1446
Qy 1321 AAGCTATGCAAGTCTCCCTGTGAGAGCAATTAAGAGAGAGCTCCGAAACAGTCTCT 1380
Db 1447 AAGCTATGCAAGTCTCCCTGTGAGAGCAATTAAGAGAGAGCTCCGAAACAGTCTCT 1506
Qy 1381 GATAAGGAGAGAGCCAGCATCCCAAGAGCTGAGACCGCCAGGCTTTCAGAGCGCAG 1440
Db 1507 GATAAGGAGAGAGCCAGCATCCCAAGAGCTGAGACCGCCAGGCTTTCAGAGCGCAG 1566
Qy 1441 AGCAAGGATGCAATTCGCTGAGAAACGAGAGAGTGGACCGCCAGAGGCTCCCTTTTA 1500
Db 1567 AGCAAGGATGCAATTCGCTGAGAAACGAGAGAGTGGACCGCCAGAGGCTCCCTTTTA 1626
Qy 1501 TCTCTCATCAGAAAGATGCTTTGGAATTAACAACCACTTCTCTTTTGGGC 1560
Db 1627 TCTCTCATCAGAAAGATGCTTTGGAATTAACAACCACTTCTCTTTTGGGC 1686
Qy 1561 CTTTTCACAGCCAGAGAGCACTTCAAGAGTCTGCTGAGCGCTTAAAGGCTGGCAG 1620
Db 1687 CTTTTCACAGCCAGAGAGCACTTCAAGAGTCTGCTGAGCGCTTAAAGGCTGGCAG 1746
Qy 1621 TCGGATATCTTGGGCCCCGAGAGCTTAACCCCTTCTGACAGAGCTGTATTTTGGC 1680
Db 1747 TCGGATATCTTGGGCCCCGAGAGCTTAACCCCTTCTGACAGAGCTGTATTTTGGC 1806
Qy 1681 ACAGAGTCTTCAACTTCTACTCTGCTCAGAGCACTTACAGAGGAGAGTGCATTTACT 1740
Db 1807 ACAGAGTCTTCAACTTCTACTCTGCTCAGAGCACTTACAGAGGAGAGTGCATTTACT 1866
Qy 1741 GCGTACGCTGACAGCGCTGCCACTTGGAGAGCAAGCTTATTTCTGTGCGAGCGCG 1800

Db 1867 GCGTACAGCTGACGCGACCTGCCACTTGGAGAGCAAGCTTATTTCTGTGCGAGCGG 1926
Qy 1801 CAGAGCCAGATGACAGAGCTGACTCGCGGGAGAGTGGATGAAGAGAGCCCTTTGAA 1860
Db 1927 CAGAGCCAGATGACAGAGCTGACTCGCGGGAGAGTGGATGAAGAGAGCCCTTTGAA 1986
Qy 1861 AAGCATTTAAACGAGAGAGCTGCCAAATGGAATTTGAGAGAGCATCATGTCAGAGAC 1920
Db 1987 AAGCATTTAAACGAGAGAGCTGCCAAATGGAATTTGAGAGAGCATCATGTCAGAGAC 2046
Qy 1921 AGTTCACGGAGAGAGCTGGGAAAGTGGAGAGTCAAGCTTCTGGGAGAGAGTGA 1980
Db 2047 AGTTCACGGAGAGAGCTGGGAAAGTGGAGAGTCAAGCTTCTGGGAGAGAGTGA 2106
Qy 1981 ATCATTTAGTCTCC 1995
Db 2107 ATCATTTAGTCTCC 2121

RESULT 5
US-09-964-277-1
; Sequence 1, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 3496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-277-1

Query Match 99.8%; Score 1991.8; DB 9; Length 3496;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGCCCATGAGATGATGAACTCAATTTGTTACTGAGAGGTTGGTCTGCTGGAA 60
Db 562 ATGGCCCATGAGATGATGAACTCAATTTGTTACTGAGAGGTTGGTCTGCTGGAA 621
Qy 61 AGTGAACCGAAAGAGTCTGCTAAATGATAGCCGCGCAATTTGGAAATACATATCATCC 120
Db 622 AGTGAACCGAAAGAGTCTGCTAAATGATAGCCGCGCAATTTGGAAATACATATCATCC 681
Qy 121 CACATTTTGAAGCCATTAAATATCAACTGCTCAGCTTATGAGAGCGAAGTTGCAAG 180
Db 682 CACATTTTGAAGCCATTAAATATCAACTGCTCAGCTTATGAGAGCGAAGTTGCAAG 741
Qy 181 GACAAAGTGTAAATTAACAGAGCTATCCAGATTCAGGAAACATTAAGTTGACATTGAT 240
Db 742 GACAAAGTGTAAATTAACAGAGCTATCCAGATTCAGGAAACATTAAGTTGACATTGAT 801
Qy 241 TGCAGTCAAGAGGTGTGATTTACATCAAGAGTCCCAAGATGTTGCTCTCTCTTCA 300
Db 802 TGCAGTCAAGAGGTGTGATTTACATCAAGAGTCCCAAGATGTTGCTCTCTCTTCA 861
Qy 301 GACTGTTTCTCACTGTACTTCTGGGTAACTGAGAAAGAGCTTCAACTGTTCACCTG 360
Db 862 GACTGTTTCTCACTGTACTTCTGGGTAACTGAGAAAGAGCTTCAACTGTTCACCTG 921
Qy 361 CTGAGAGTGGGTTTGTGAGTTCTCTGCTGTTGTTTCCCTGGCTCTGTGAAGAAATCC 420
Db 922 CTGAGAGTGGGTTTGTGAGTTCTCTGCTGTTGTTTCCCTGGCTCTGTGAAGAAATCC 981
Qy 421 ACTTAAGTCCCTACCTGATTTCTCAGCTTGTCTTACTGTTGCAACATTTGGGCAAC 480
Db 982 ACTTAAGTCCCTACCTGATTTCTCAGCTTGTCTTACTGTTGCAACATTTGGGCAAC 1041

QY 481 CGAATTCCTCCCAATCTTATCTTGGCTGCGAGCGAGATGTCCTCAACAAGAGCTGTATA 540
 Db 1042 CGAATTCCTCCCAATCTTATCTTGGCTGCGAGCGAGATGTCCTCAACAAGAGCTGTATG 1101
 QY 541 CAGCAAGATGGGATTTGGTTATGTGTTAAATGCAAGCTATACCTGTCCAAAGCTGACTTT 600
 Db 1102 CAGCAAGATGGGATTTGGTTATGTGTTAAATGCAAGCTATACCTGTCCAAAGCTGACTTT 1161
 QY 601 ATCCCGAGTCATTTCTGGGTGTGCTGTGAATGACAGCTTTTGAGAAAATTTTG 660
 Db 1162 ATCCCGAGTCATTTCTGGGTGTGCTGTGAATGACAGCTTTTGAGAAAATTTTG 1221
 QY 661 CCGGTGTTGACAAATCAGTATGATTTCAATTGAGAAAGAAAAGCTCCATGATGATGTT 720
 Db 1222 CCGGTGTTGACAAATCAGTATGATTTCAATTGAGAAAGAAAAGCTCCATGATGATGTT 1281
 QY 721 CTAGTGCACTGTTTATAGTGGGATCTCCGCTCCGACCATGCTATGCTTACATCATG 780
 Db 1282 CTAGTGCACTGTTTATAGTGGGATCTCCGCTCCGACCATGCTATGCTTACATCATG 1341
 QY 781 AAGAGATGACATGCTCTTTAGATGACATTAAGATTTGTGAAGAAAAGACCTTACT 840
 Db 1342 AAGAGATGACATGCTCTTTAGATGACATTAAGATTTGTGAAGAAAAGACCTTACT 1401
 QY 841 ATATCTCCAACTTCAATTTTCTGGGCCCACTCTGACATATGAGAGAAAGATTAGAAC 900
 Db 1402 ATATCTCCAACTTCAATTTTCTGGGCCCACTCTGACATATGAGAGAAAGATTAGAAC 1461
 QY 901 CAGACTGAGCATCAGGGCCAAAGACAACTCAAGCTGTGACCTGAGAGAGCCAAAT 960
 Db 1462 CAGACTGAGCATCAGGGCCAAAGACAACTCAAGCTGTGACCTGAGAGAGCCAAAT 1521
 QY 961 GAACCTGTCTCTGCTGTCTCAGAGGGTGTGACAGAAAAGCGAGAGCCCTTCACTCAACC 1020
 Db 1522 GAACCTGTCTCTGCTGTCTCAGAGGGTGTGACAGAAAAGCGAGAGCCCTTCACTCAACC 1581
 QY 1021 TGTGCGCATGCTGCTACCTCAGAGGCGACAGGACAAAAGCCCGTGCATCCGCGCAGCGTG 1080
 Db 1582 TGTGCGCATGCTGCTACCTCAGAGGCGACAGGACAAAAGCCCGTGCATCCGCGCAGCGTG 1641
 QY 1081 CCGAGCGTCCAGCGTGCAGCGCTGCTGTTAGAGACAGCCCGCTGTACAGCGCTC 1140
 Db 1642 CCGAGCGTCCAGCGTGCAGCGCTGCTGTTAGAGACAGCCCGCTGTACAGCGCTC 1701
 QY 1141 AGTGGGCTGCACTGTCCGACAGACGGCTGGAAGACAGCAATAGCTCAAGGTTCTTTC 1200
 Db 1702 AGTGGGCTGCACTGTCCGACAGACGGCTGGAAGACAGCAATAGCTCAAGGTTCTTTC 1761
 QY 1201 TCTCTGATTAATCAATCAGTTTCAATTAATCAGCGAGCATGCGATCTCTTACATGCGCTTC 1260
 Db 1762 TCTCTGATTAATCAATCAGTTTCAATTAATCAGCGAGCATGCGATCTCTTACATGCGCTTC 1821
 QY 1261 TCTCTCATAGAAAGATGCTTTGGAATACTAACAACTTCCACTACTGTGATGAGACAAAC 1320
 Db 1822 TCTCTCATAGAAAGATGCTTTGGAATACTAACAACTTCCACTACTGTGATGAGACAAAC 1881
 QY 1321 AAGCTATGCAAGTTCTCCCTGTGTTACAGAACTATCGAGACAGACTCCGAAAACAGTCTT 1380
 Db 1882 AAGCTATGCAAGTTCTCCCTGTGTTACAGAACTATCGAGACAGACTCCGAAAACAGTCTT 1941
 QY 1381 GATTAAGGAGAAAGCAGACATCCCAAGAAAGCTGACAGCCGCGCTTCAAGACGACAG 1440
 Db 1942 GATTAAGGAGAAAGCAGACATCCCAAGAAAGCTGACAGCCGCGCTTCAAGACGACAG 2001
 QY 1441 AGCAAGCATGTCATTCGCTGAGAACAGACAGACATGAGCAACCGCCAGAGGTCCCTTTTA 1500
 Db 2002 AGCAAGCATGTCATTCGCTGAGAACAGACAGACATGAGCAACCGCCAGAGGTCCCTTTTA 2061
 QY 1501 TCTCCACTGTCATCGAAGTGGAGCGTGTGAGACAAATTAACAACAAGCTTCTCTTTGCGC 1560
 Db 2062 TCTCCACTGTCATCGAAGTGGAGCGTGTGAGACAAATTAACAACAAGCTTCTCTTTGCGC 2121

QY 1561 CTTTCCACAGCCAGACGACACCTTACAGAAATGTGTGCTGCGCTTAAAGGCTGGCAC 1620
 Db 2122 CTTTCCACAGCCAGACGACACCTTACAGAAATGTGTGCTGCGCTTAAAGGCTGGCAC 2181
 QY 1621 TCGGATATCTTGGGCCCCCAGACCTTACCCCTTCCCGACAGACGCTGTATTTTGGC 1680
 Db 2182 TCGGATATCTTGGGCCCCCAGACCTTACCCCTTCCCGACAGACGCTGTATTTTGGC 2241
 QY 1681 ACAGATCTCACAATTCTACTCTGCTCAGCCATCTACGAGAGGACGTCAGTACTCT 1740
 Db 2242 ACAGATCTCACAATTCTACTCTGCTCAGCCATCTACGAGAGGACGTCAGTACTCT 2301
 QY 1741 GCTTACAGCTGACAGCTGCTGCTGCGGAGAGCTGCGGACCAAGTCTATTCTGTCGCGAGCGG 1800
 Db 2302 GCTTACAGCTGACAGCTGCTGCTGCGGAGAGCTGCGGACCAAGTCTATTCTGTCGCGAGCGG 2361
 QY 1801 CAGAAAGCCAGTACAGAGCTGACTCGCGGCGGAGCTGCGGACATGAAAGAGAGCCCTTTGAA 1860
 Db 2362 CAGAAAGCCAGTACAGAGCTGACTCGCGGCGGAGCTGCGGACATGAAAGAGAGCCCTTTGAA 2421
 QY 1861 AAGCATTTAAACGACAGAGCTGCGCAATGGAATTTGAGAGAGCATGATGACAGAAAC 1920
 Db 2422 AAGCATTTAAACGACAGAGCTGCGCAATGGAATTTGAGAGAGCATGATGACAGAAAC 2481
 QY 1921 AGGTCAAGGAGAGAGCTGGGAGAAAGTGGGAGTCAAGTCACTTTTCGGGACATGGA 1980
 Db 2482 AGGTCAAGGAGAGAGCTGGGAGAAAGTGGGAGTCAAGTCACTTTTCGGGACATGGA 2541
 QY 1981 ATCATTTAGGTCTCC 1995
 Db 2542 ATCATTTAGGTCTCC 2556

RESULT 6

US-10-370-715B-261
 ; Sequence 261, Application US/10370715B
 ; Publication No. US20040258678A1

GENERAL INFORMATION:

; Patin Docket Preview
 ; APPLICANT: BODARY, SARAH C.
 ; APPLICANT: CLARK, HILARY
 ; APPLICANT: BRISDELL, HUNTER
 ; APPLICANT: JACKMAN, JANEY
 ; APPLICANT: SCHOENFELD, JILL R.
 ; APPLICANT: WILLIAMS, P. MICKEY
 ; APPLICANT: WOOD, WILIAM I.
 ; APPLICANT: WU, THOMAS D.
 ; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
 ; FILE REFERENCE: P1948P1-US
 ; CURRENT APPLICATION NUMBER: US/10/370,715B
 ; NUMBER OF SEQ ID NOS: 742
 ; SEQ ID NO 261
 ; LENGTH: 3521
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; US-10-370-715B-261

Query Match 99.8%; Score 1991.8; DB 18; Length 3521;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCCATGATGATGATGGAATCTCAAAATTTTACTGAGAGGTTGGTGTCTGTGTGAA 60
 Db 564 ATGGCCCATGATGATGATGGAATCTCAAAATTTTACTGAGAGGTTGGTGTCTGTGTGAA 623
 QY 61 AGTGAACGGAAGAAAGTGTGCTAATGATGCGCGCATTTGGAATTAACATCATCC 120
 Db 624 AGTGAACGGAAGAAAGTGTGCTAATGATGCGCGCATTTGGAATTAACATCATCC 683
 QY 121 CACATTTTGAAGGACATTAATATCAACTGCTCAAGCTTATGAAGCGAAGGTTGCAAG 180

Dh 684 CACATTTTGAAGCCATTAATATCACTGCTCAAGCTTATGAAGCGAAGGTTGCAACAG 743
Qy 181 GACAAAGTGAATTAACAGAGCTGATCCAGATTCACGAAACATTAAGGTTGACATTGAT 240
Dh 744 GACAAAGTGAATTAACAGAGCTGATCCAGATTCACGAAACATTAAGGTTGACATTGAT 803
Qy 241 TGCAGTCAGAAAGGTTGATGTTTACGATCAAAAGCTCCCAAGATGTTGCTCTCTCTTCA 300
Dh 804 TGCAGTCAGAAAGGTTGATGTTTACGATCAAAAGCTCCCAAGATGTTGCTCTCTCTTCA 863
Qy 301 GACGTTTCTCACTGATCTTCTGGGTTAACTGGAAGAGGCTTCAACTCTGTTCACTG 360
Dh 864 GACGTTTCTCACTGATCTTCTGGGTTAACTGGAAGAGGCTTCAACTCTGTTCACTG 923
Qy 361 CTTCAGAGTGGGTTGCTGAGTTCTCTGTTGTTTCCCTGGCCCTGTTGAAGGAAATCC 420
Dh 924 CTTCAGAGTGGGTTGCTGAGTTCTCTGTTGTTTCCCTGGCCCTGTTGAAGGAAATCC 983
Qy 421 ACTCTAGTCCCTTACCTGATCTTCTGAGCTTTTACCTGTTGCTTCAATGAGGCAAC 480
Dh 984 ACTCTAGTCCCTTACCTGATCTTCTGAGCTTTTACCTGTTGCTTCAATGAGGCAAC 1043
Qy 481 CGAATTCCTCCCAATCTTATCTTGGCTGCAAGAGATGCTCTCAACAGAGCTGATG 540
Dh 1044 CGAATTCCTCCCAATCTTATCTTGGCTGCAAGAGATGCTCTCAACAGAGCTGATG 1103
Qy 541 CAGCAGATGAGATGTTGTTATGTTTAAATGCGAGCTATACCTGTCGAAGCTGACTT 600
Dh 1104 CAGCAGATGAGATGTTGTTATGTTTAAATGCGAGCAATACCTGTCGAAGCTGACTT 1163
Qy 601 ATCCCGAGTCTCATTTTCTGCTGCTGCTGCTGATGACAGCTTTTGTGAAGAAATTTTG 660
Dh 1164 ATCCCGAGTCTCATTTTCTGCTGCTGCTGCTGATGACAGCTTTTGTGAAGAAATTTTG 1223
Qy 661 CCGTGTGTTGAGCAAAATCAGTATGATTCATTGAGAAAGCAAAAGCTCCAAAGGATGTT 720
Dh 1224 CCGTGTGTTGAGCAAAATCAGTATGATTCATTGAGAAAGCAAAAGCTCCAAAGGATGTT 1283
Qy 721 CTAGTCACTGTTTATGCTGGGATCTTCGCGCTCGCCACCATGCTATGCTTACATCATG 780
Dh 1284 CTAGTCACTGTTTATGCTGGGATCTTCGCGCTCGCCACCATGCTATGCTTACATCATG 1343
Qy 781 AAGAGATGAGATGCTTATGATGAGGTTACAGATTTGTGAAGAAAGAAAGACTTCT 840
Dh 1344 AAGAGATGAGATGCTTATGATGAGGTTACAGATTTGTGAAGAAAGAAAGAAAGACTTCT 1403
Qy 841 ATATCTCCAACTTCAATTTTCTGGGCCAACTCTGACCTATGAGAGAAAGATTAAAGAC 900
Dh 1404 ATATCTCCAACTTCAATTTTCTGGGCCAACTCTGACCTATGAGAGAAAGATTAAAGAC 1463
Qy 901 CAGACGTGAGATCAAGGGCCAAAGAGCAAACTCAAGCTGTGACCTTGAGAGACCAAT 960
Dh 1464 CAGACGTGAGATCAAGGGCCAAAGAGCAAACTCAAGCTGTGACCTTGAGAGACCAAT 1523
Qy 961 GAACCTGTCCCTGCTGCTCTCAGAGGGTGAAGAGAAAGAGAGAGAGAGAGAGAGAGAG 1020
Dh 1524 GAACCTGTCCCTGCTGCTCTCAGAGGGTGAAGAGAAAGAGAGAGAGAGAGAGAGAGAG 1583
Qy 1021 TGTGCGCATCTGCTGCTCTCAGAGGAGAGAGCAAAAGGCGCTGATCCCGCCAGAGGTG 1080
Dh 1584 TGTGCGCATCTGCTGCTCTCAGAGGAGAGAGCAAAAGGCGCTGATCCCGCCAGAGGTG 1643
Qy 1081 CCCAGCGGCGCAGAGGAG 1140
Dh 1644 CCCAGCGGCGCAGAGGAG 1703
Qy 1141 AGTGGGCTGCACTGTCCGAGAGAGAGGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Dh 1704 AGTGGGCTGCACTGTCCGAGAGAGAGGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1763
Qy 1201 TCTCTGATATCAATCAAGTTTCAATTTCAAGCAGAGATGCGAGATCTTACATGAGCTTC 1260
Dh 1764 TCTCTGATATCAATCAATCAAGTTTCAATTTCAAGCAGAGATGCGAGATCTTACATGAGCTTC 1823

Qy 1261 TCTCATCAAGAGATGCTTTGGAATATCAAAACCTTCCACTACTGATGAGAGCAAC 1320
Dh 1824 TCTCATCAAGAGATGCTTTGGAATATCAAAACCTTCCACTACTGATGAGAGCAAC 1883
Qy 1321 AAGCTATGCGAGTTTCTCCCTGTTTCAAGAACTATGAGAGAGAGAGAGAGAGAGAG 1380
Dh 1884 AAGCTATGCGAGTTTCTCCCTGTTTCAAGAACTATGAGAGAGAGAGAGAGAGAGAG 1943
Qy 1381 GATTAAG 1440
Dh 1944 GATTAAG 2003
Qy 1441 AGCAAGCGATGATGCTGCTGATGAGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Dh 2004 AGCAAGCGATGATGCTGCTGATGAGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2063
Qy 1501 TCTCCACTGATGCAAG 1560
Dh 2064 TCTCCACTGATGCAAG 2123
Qy 1561 CTTTCCACAG 1620
Dh 2124 CTTTCCACAG 2183
Qy 1621 TCGGATATCTTGGGCCCCAG 1680
Dh 2184 TCGGATATCTTGGGCCCCAG 2243
Qy 1681 ACAGAGTCTCAACATCTTCTACTGCTGCTCAGAGCATCTACAGAGAGAGAGAGAGAGAG 1740
Dh 2244 ACAGAGTCTCAACATCTTCTACTGCTGCTCAGAGCATCTACAGAGAGAGAGAGAGAGAG 2303
Qy 1741 GCTTACAGCTGACAG 1800
Dh 2304 GCTTACAGCTGACAG 2363
Qy 1801 CAG 1860
Dh 2364 CAG 2423
Qy 1861 AAGCAGTTTAAACAG 1920
Dh 2424 AAGCAGTTTAAACAG 2483
Qy 1921 AGGTCAAGGAG 1980
Dh 2484 AGGTCAAGGAG 2543
Qy 1981 ATCATTGAGGTCTCC 1995
Dh 2544 ATCATTGAGGTCTCC 2558

RESULT 7
US-09-816-494-1
Sequence 1, Application US/09816494
Patent No. US2002034807A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
FILE REFERENCE: 10448-030002
CURRENT APPLICATION NUMBER: US/09/816,494
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,858
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3544
TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
; NAME/KEY: CDS
; LOCATION: (589) ... (2583)
US-09-816-494-1

Query Match 99.8%; Score 1991.8; DB 9; Length 3544;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCCATGAGATTTGGAACCTAAATTGTACTGAGAGGTGTGGCTGTGTGAA 60
DB 569 ATGGCCCATGAGATTTGGAACCTAAATTGTACTGAGAGGTGTGGCTGTGTGAA 648
QY 61 AGTGGACGGAAGAAAGTGTCTGTAATGATAGCCGCAATTTGTGAAATACAAATCATCC 120
DB 649 AGTGGACGGAAGAAAGTGTCTGTAATGATAGCCGCAATTTGTGAAATACAAATCATCC 708
QY 121 CACATTTTGAAGCCATTAAATCACTGCTCCAAAGCTTATGAAAGCGAAGTTGCAACAG 180
DB 709 CACATTTTGAAGCCATTAAATCACTGCTCCAAAGCTTATGAAAGCGAAGTTGCAACAG 768
QY 181 GACAAAGTTTAATTAACAGAGCTCATCCAGCATTCAGGGAACATAAGTTGACATTGAT 240
DB 769 GACAAAGTTTAATTAACAGAGCTCATCCAGCATTCAGGGAACATAAGTTGACATTGAT 828
QY 241 TGCAGTCAGAAAGTTGTAGTTTACGATCAAAAGCTCCCAAGATGTGGCTCTCTCTTCA 300
DB 829 TGCAGTCAGAAAGTTGTAGTTTACGATCAAAAGCTCCCAAGATGTGGCTCTCTCTTCA 888
QY 301 GACTGTTTTCTCACTGTACTTCTGTGGTAACTGGAAGAGGCTTCAACTCTGTTCACCTG 360
DB 889 GACTGTTTTCTCACTGTACTTCTGTGGTAACTGGAAGAGGCTTCAACTCTGTTCACCTG 948
QY 361 CTGTGAGGTGGGTTTGTCTGAGTTCTCTGTGTTTCCCTGGCTCTGTGAAGAAATCC 420
DB 949 CTGTGAGGTGGGTTTGTCTGAGTTCTCTGTGTTTCCCTGGCTCTGTGAAGAAATCC 1008
QY 421 ACTGAGTCCCTACCTGCAATTTCTGAGCTTGCTTACCGTTGGCCAACTTGGGCAAC 480
DB 1009 ACTGAGTCCCTACCTGCAATTTCTGAGCTTGCTTACCGTTGGCCAACTTGGGCAAC 1068
QY 481 CGAATTTCTCCCAATCTTATCTTGGCTGCCAGCAGATGTCTTCAACAGAGCTGATA 540
DB 1069 CGAATTTCTCCCAATCTTATCTTGGCTGCCAGCAGATGTCTTCAACAGAGCTGATA 1128
QY 541 CAGCAGAAATGGGATTTGTATGTGTTAAATGCAAGCAATACCTGTCCAAAGCTGACTTT 1188
DB 1129 CAGCAGAAATGGGATTTGTATGTGTTAAATGCAAGCAATACCTGTCCAAAGCTGACTTT 1188
QY 601 ATCCCGAGTCAATTTCTGTGTGTGCTGTGAATGACAGTTTGTGAAGAAATTTTG 660
DB 1189 ATCCCGAGTCAATTTCTGTGTGTGCTGTGAATGACAGTTTGTGAAGAAATTTTG 1248
QY 661 CCGTGTGTGCAAAATCAGTATGATTTCAATTGGAAGAAAGAAAGCTCCCAATGATGTGT 720
DB 1249 CCGTGTGTGCAAAATCAGTATGATTTCAATTGGAAGAAAGAAAGCTCCCAATGATGTGT 1308
QY 721 CTAGTGCATGTTTGTGAGTGTCTCCGCTCCGCAATGCTTATGCTTACATCATG 780
DB 1309 CTAGTGCATGTTTGTGAGTGTCTCCGCTCCGCAATGCTTATGCTTACATCATG 1368
QY 781 AAGAGAGTGAACATGCTTTTGAATGAGCTTAACAAATTTGTGAAGAAAGAAAGCTTACT 840
DB 1369 AAGAGAGTGAACATGCTTTTGAATGAGCTTAACAAATTTGTGAAGAAAGAAAGCTTACT 1428
QY 841 ATATCTCCAAATTTCTGAGGCAACTCTCTGACTATGAGAAAGATTAAAGAC 900
DB 1429 ATATCTCCAAATTTCTGAGGCAACTCTCTGACTATGAGAAAGATTAAAGAC 1488
QY 901 CAGACTGAGCATCAGGCGCAAGCAAACTCAAGCTGTGCACTTGAAGAGCAAT 960
DB 1489 CAGACTGAGCATCAGGCGCAAGCAAACTCAAGCTGTGCACTTGAAGAGCAAT 1548

QY 961 GAACCTGTCTCTGCTGTCTAGAGGGTGAACAAAGACGAGACGCCCCCTCATGTCACACC 1020
DB 1549 GAACCTGTCTCTGCTGTCTAGAGGGTGAACAAAGACGAGACGCCCCCTCATGTCACACC 1608
QY 1021 TGTGCGCATCTGTCTACTCAGAGGCAACAGGACAAAGCCCTGTGATTCGCCGACGGTG 1080
DB 1609 TGTGCGCATCTGTCTACTCAGAGGCAACAGGACAAAGCCCTGTGATTCGCCGACGGTG 1668
QY 1081 CCCAGCGGCCAGGGTCAAGCCGTGTGATGAGGACAGCCGCTGTGACAGGCGCTC 1140
DB 1669 CCCAGCGGCCAGGGTCAAGCCGTGTGATGAGGACAGCCGCTGTGACAGGCGCTC 1728
QY 1141 AGTGGCTGCACTGTCTCGCAGACAGGCTGGAAGAACAATTAAGCTCAAGGCTTCTTC 1200
DB 1729 AGTGGCTGCACTGTCTCGCAGACAGGCTGGAAGAACAATTAAGCTCAAGGCTTCTTC 1788
QY 1201 TCTGTGATTAATCAATCAGTTTCAATTTCAAGCAGCATGAGCATCTTACATGGCTTC 1260
DB 1789 TCTGTGATTAATCAATCAGTTTCAATTTCAAGCAGCATGAGCATCTTACATGGCTTC 1848
QY 1261 TCTCATGAGAAAGATGCTTTGGAATATCAAAACCTTCACTACTCTGATGGGACAAAC 1320
DB 1849 TCTCATGAGAAAGATGCTTTGGAATATCAAAACCTTCACTACTCTGATGGGACAAAC 1908
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DB 1909 AAGCTATGCAAGTTCTCCCTGTTCAGGAACTATGAGAGACAGACTCCGAAACAGTCT 1968
QY 1381 GATTAAGAGAAAGCCAGCATCCCAAGAGCTGCAGACCGCCAGGCTTCAAGACAGCAG 1440
DB 1969 GATTAAGAGAAAGCCAGCATCCCAAGAGCTGCAGACCGCCAGGCTTCAAGACAGCAG 2028
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DB 2029 AGCAAGCAATGCAATGCGGTGAGAAACAGAGAGCTGACACCGCCAGAGGCTCTTTTA 2088
QY 1501 TCTCCACTGCAATGCAAGTGGAGCGGTGAGAGCAATTAACAACAAGCTTCTTTTGGGC 1560
DB 2089 TCTCCACTGCAATGCAAGTGGAGCGGTGAGAGCAATTAACAACAAGCTTCTTTTGGGC 2148
QY 1561 CTTTCCACGACGACGACGACCTTCAAGAGTCTGTGGCTCTTGAAGGGCTGGCAC 1620
DB 2149 CTTTCCACGACGACGACGACCTTCAAGAGTCTGTGGCTCTTGAAGGGCTGGCAC 2208
QY 1621 TCGAATATCTTGGCCCCCAGACCTTACCCCTTCCGACCAAGAGCTGTGATTTTGC 1680
DB 2209 TCGAATATCTTGGCCCCCAGACCTTACCCCTTCCGACCAAGAGCTGTGATTTTGC 2268
QY 1681 ACAGAGTCTCAACTTCTACTGTGCTCAGCAGCTTACGAGAGGAGGAGGCTTACTCT 1740
DB 2269 ACAGAGTCTCAACTTCTACTGTGCTCAGCAGCTTACGAGAGGAGGAGGCTTACTCT 2328
QY 1741 GCTTACAGCTTCAAGCAGCTTCCCACTTGGGAGACCAAGTCTATTTCTGTGGCAGGCG 1800
DB 2329 GCTTACAGCTTCAAGCAGCTTCCCACTTGGGAGACCAAGTCTATTTCTGTGGCAGGCG 2388
QY 1801 CAGAAAGCAATGACAGAGCTGATCTCGGCGGAGAGCTGTGATGAAGAGACCCCTTTGA 1860
DB 2389 CAGAAAGCAATGACAGAGCTGATCTCGGCGGAGAGCTGTGATGAAGAGACCCCTTTGA 2448
QY 1861 AAGAGTTTAAACGAGAGCTGCAAAATGGAATTTGAGAGAGCATGATGACAGAAC 1920
DB 2449 AAGAGTTTAAACGAGAGCTGCAAAATGGAATTTGAGAGAGCATGATGACAGAAC 2508
QY 1921 AGGTCAAGGAAAGAGCTGGGAAAGTGGGCAAGTCAAGTCTTTTCGGGACAGATGAA 1980
DB 2509 AGGTCAAGGAAAGAGCTGGGAAAGTGGGCAAGTCAAGTCTTTTCGGGACAGATGAA 2568
QY 1981 ATCAATTGAGTCTCC 1995
DB 2569 ATCAATTGAGTCTCC 2583

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RESULT 8
US-10-377-072-25
; Sequence 25, Application US/10377072
; Publication No. US2004009501A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Gluckmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Miyoung
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; TITLE OF INVENTION: AND US$ THEREFOR
; FILE REFERENCE: MEI03-0180NMIM
; CURRENT APPLICATION NUMBER: US/10/377,072
; PRIOR APPLICATION NUMBER: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895,860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/843,297
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)...(2586)
US-10-377-072-25

Query Match          99.8%; Score 1991.8; DB 17; Length 3544;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  ATGGCCCATGAGATGATGGAATCTCAATTTGTAATGAGAGGTTGTGCTCTCTGCGAA 60
DB      589  ATGGCCCATGAGATGATGGAATCTCAATTTGTAATGAGAGGTTGTGCTCTCTGCGAA 648
QY      61  AGTGAAGCGAAAGAGTGTCTGTAATGATGCGCGGCGCATTTTGTGGAATACATACATCC 120
DB      649  AGTGAAGCGAAAGAGTGTCTGTAATGATGCGCGGCGCATTTTGTGGAATACATACATCC 708
QY      121  CACATTTTGAAGCCATTATATCACTGCTCAAGCTTATGAAGCGAGTTGCAACAG 180
DB      709  CACATTTTGAAGCCATTATATCACTGCTCAAGCTTATGAAGCGAGTTGCAACAG 768
QY      181  GACAAAGTTAATTAACAGAGCTCATCCAGATTACAGGAAACATAAGTTGACATTGAT 240
DB      769  GACAAAGTTAATTAACAGAGCTCATCCAGATTACAGGAAACATAAGTTGACATTGAT 828
QY      241  TGCAATGCAAGAGTTGTAGTTTACATCAACAGCTCCAAAGATGTGCTCTCTCTTCA 300
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DB      829  TGCAGTCAGAAAGTTGTAGTTTACATCAACAGCTCCAAAGATGTGCTCTCTCTTCA 888
QY      301  GACTGTTTCTACATGTAATCTTGTGTAATCTGGAAGAAAGACTTCAATCTGTTCACCTG 360
DB      889  GACTGTTTCTACATGTAATCTTGTGTAATCTGGAAGAAAGACTTCAATCTGTTCACCTG 948
QY      361  CTTCAGAGTGGTTTGTGTAATCTTGTGTAATCTTGTGTAATCTTGTGTAATCTTGTGTA 420
DB      949  CTTCAGAGTGGTTTGTGTAATCTTGTGTAATCTTGTGTAATCTTGTGTAATCTTGTGTA 1008
QY      421  ACTTGAATGCTTACCTGATTTCTCAAGCTTCTTACTGTTGCAACATTGGGCAACC 480
DB      1009  ACTTGAATGCTTACCTGATTTCTCAAGCTTCTTACTGTTGCAACATTGGGCAACC 1068
QY      481  CGAATTTCTCCCAATCTTATCTTGGGCTCCAGAGAGATGCTCCCAAGAGACTGATA 540
DB      1069  CGAATTTCTCCCAATCTTATCTTGGGCTCCAGAGAGATGCTCCCAAGAGACTGATA 1128
QY      541  CAGCAAAATGGAAATGTTATGTTAAATGCCAGCTTATCTTCCAAAGCTGACTTT 600
DB      1129  CAGCAAAATGGAAATGTTATGTTAAATGCCAGCTTATCTTCCAAAGCTGACTTT 1188
QY      601  ATCCCGAGTCTCAATTTCCGCGCTGCTGCTGTAATGACAGCTTTTGTGAAATTTTG 660
DB      1189  ATCCCGAGTCTCAATTTCCGCGCTGCTGCTGTAATGACAGCTTTTGTGAAATTTTG 1248
QY      661  CCGTGTGTAACAATATGATGATTTTCAATGAGAAAGCAAAAGCTTCAATGATGTT 720
DB      1249  CCGTGTGTAACAATATGATGATTTTCAATGAGAAAGCAAAAGCTTCAATGATGTT 1308
QY      721  CTATGCACTGTTTAAAGTGGATCTCCGCTCCGCCAATGCTTATGCTTATCATCATG 780
DB      1309  CTATGCACTGTTTAAAGTGGATCTCCGCTCCGCCAATGCTTATGCTTATCATCATG 1368
QY      781  AAGAGATGACATGTTTAAATGAGCTTACAGATTTGTGAAGAAAGAAAGAAAGCTTACT 840
DB      1369  AAGAGATGACATGTTTAAATGAGCTTACAGATTTGTGAAGAAAGAAAGAAAGCTTACT 1428
QY      841  ATATCTCAAACTCAATTTTCTGGGCAACTCTGGAATGAGAAAGAAATTAAGAAC 900
DB      1429  ATATCTCAAACTCAATTTTCTGGGCAACTCTGGAATGAGAAAGAAATTAAGAAC 1488
QY      901  CAGACTGAGCACTACAGGCGCAAGAAAGCAAACTTAAGCTGTGCACTGGAAGAAAGCTTAA 960
DB      1489  CAGACTGAGCACTACAGGCGCAAGAAAGCAAACTTAAGCTGTGCACTGGAAGAAAGCTTAA 1548
QY      961  GAACTGTCTGCTGTCTCAGAGGCTGGAAGAAAGCAAGCGCCCTCACTGCAACCC 1020
DB      1549  GAACTGTCTGCTGTCTCAGAGGCTGGAAGAAAGCAAGCGCCCTCACTGCAACCC 1608
QY      1021  TGTGCGGATCTGCTTCAAGAGGCAAGCAAGAAAGGCGCTGATCCGCAAGCGTG 1080
DB      1609  TGTGCGGATCTGCTTCAAGAGGCAAGCAAGAAAGGCGCTGATCCGCAAGCGTG 1668
QY      1081  CCCAGGCTCCAGAGCTGAGCGCTGCTGTAAGAGGCAAGCGCGCTGTAAGCGCGTG 1140
DB      1669  CCCAGGCTCCAGAGCTGAGCGCTGCTGTAAGAGGCAAGCGCGCTGTAAGCGCGTG 1728
QY      1141  AGTGGCTGCACTGTGCGCAAGAGCTGGAAGCAAGCAATTAAGCTCAAGGCTTCTTC 1200
DB      1729  AGTGGCTGCACTGTGCGCAAGAGCTGGAAGCAAGCAATTAAGCTCAAGGCTTCTTC 1788
QY      1201  TCTCTGATATTAATTCAGATTTCATATTCAGCAGACTGAGCACTCTTATCATGCTTC 1260
DB      1789  TCTCTGATATTAATTCAGATTTCATATTCAGCAGACTGAGCACTCTTATCATGCTTC 1848
QY      1261  TCTCATCAGAAAGCTTGTGGAATATACAACTTCACTCACTCTGAGTGGAGCAAC 1320
DB      1849  TCTCATCAGAAAGCTTGTGGAATATACAACTTCACTCACTCTGAGTGGAGCAAC 1908
QY      1321  AAGCTATGCAAGTTTCTCCCTGTTCAAGAACTATGAGAGACTCCGGAACCAAGTCTT 1380
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Db	1909	AAGCATGCGACCTTCTCCCTGTCAGAAACTATCGAGAGACATCCCGAAACAGTCT	1968
Qy	1381	GATTAAGAGAGAGCCAGCATCCCGAAGAGCTGCAACCGCCAGGCTTTCAGACAGCCAG	1440
Db	1969	GATTAAGAGAGAGCCAGCATCCCGAAGAGCTGCAACCGCCAGGCTTTCAGACAGCCAG	2028
Qy	1441	AGCAAGCGATTGCTCATTCGCTCAGAAACACAGACAGTGGGACCGCCAGAGGTCCCTTTTA	1500
Db	2029	AGCAAGCGATTGCTCATTCGCTCAGAAACACAGACAGTGGGACCGCCAGAGGTCCCTTTTA	2088
Qy	1501	TCTCCACTGTCATCGAAGTGGGAGCGTGGAGGACAAATTACACACAGCTTCTTTTCGCG	1560
Db	2089	TCTCCACTGTCATCGAAGTGGGAGCGTGGAGGACAAATTACACACAGCTTCTTTTCGCG	2148
Qy	1561	CTTTCCACCAGCCAGACAGCACTCAGAAAGTGTGCTGGCCCTTAAAGGCTGGCAC	1620
Db	2149	CTTTCCACCAGCCAGACAGCACTCAGAAAGTGTGCTGGCCCTTAAAGGCTGGCAC	2208
Qy	1621	TGGATATCTTGGCCCCCGACACTCTACCCCTTCCCTACACAGACAGCTGTATTTTGGC	1680
Db	2209	TGGATATCTTGGCCCCCGACACTCTCTACCCCTTCCCTACACAGACAGCTGTATTTTGGC	2268
Qy	1681	ACAGAGTCTCTACACTTCTACTCTGCTCAGCCATCTACGAGGACGTCAGATTACTCT	1740
Db	2269	ACAGAGTCTCTACACTTCTACTCTGCTCAGCCATCTACGAGGACGTCAGATTACTCT	2328
Qy	1741	GCTTACAGCTGACGCGACGCTGCGCACTTGGCGAGAACCAAGTCTATTCTGTGCGCAGCG	1800
Db	2329	GCTTACAGCTGACGCGACGCTGCGCACTTGGCGAGAACCAAGTCTATTCTGTGCGCAGCG	2388
Qy	1801	CAGAACCCAGAGTGAACAGACTGACTGCGCGCGAGCTGGCATGAAAGAGCCCTTTGAA	1860
Db	2389	CAGAACCCAGAGTGAACAGACTGACTGCGCGCGAGCTGGCATGAAAGAGCCCTTTGAA	2448
Qy	1861	AAGCAGTTTAAACGCGAAGCTGCCAAATGAAATTGGAGAGCATCATGTCAGAGAAC	1920
Db	2449	AAGCAGTTTAAACGCGAAGCTGCCAAATGAAATTGGAGAGCATCATGTCAGAGAAC	2508
Qy	1921	AGGTCACGCGAAGAGCTGGGGAAGTGGGCACTGACTTGTTCGGGACAGCATGAA	1980
Db	2509	AGGTCACGCGAAGAGCTGGGGAAGTGGGCACTGACTTGTTCGGGACAGCATGAA	2568
Qy	1981	ATCATTTAGGCTCTCC	1995
Db	2569	ATCATTTAGGCTCTCC	2583
RESULT 9			
US-10-377-072-25			
Sequence 25, Application US/10377072			
Publication No. US20040157221A9			
GENERAL INFORMATION:			
APPLICANT: Millennium Pharmaceuticals Inc.			
APPLICANT: Curtis, Rory A.J.			
APPLICANT: Logan, Thomas Joseph			
APPLICANT: Glucksmann, Maria A.			
APPLICANT: Meyers, Rachel E.			
APPLICANT: Williamson, Mark J.			
APPLICANT: Rudolph-Owen, Laura A.			
APPLICANT: Chun, Miyoung			
APPLICANT: Tsai, Fong-Ying			
TITLE OF INVENTION: NOVEL 25669, 25934, 26335, 50365, 21117,			
TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES			
FILE REFERENCE: MP103-0180M1M			
CURRENT APPLICATION NUMBER: US/10/377, 072			
CURRENT FILING DATE: 2003-02-27			
PRIOR APPLICATION NUMBER: US 09/895, 860			
PRIOR FILING DATE: 2001-06-29			
PRIOR APPLICATION NUMBER: US 60/215, 370			
PRIOR FILING DATE: 2000-06-29			
PRIOR APPLICATION NUMBER: US 09/723, 806			
PRIOR FILING DATE: 2000-11-28			

	Query Match	99.8%;	Score 1991.8;	DB 18;	Length 3544;	
	Best Local Similarity	99.9%;	Pred. No. 0;			
	Matches 1993;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;	
QY	1 ATGGCCCATGAGATGATTGGAACTCAAAATTGTACTGAGAGGTTGGTGGCTCTGCTGGA	60				
DB	589 ATGGCCCATGAGATGATTGGAACTCAAAATTGTACTGAGAGGTTGGTGGCTCTGCTGGA	648				
QY	61 AGTGAACGGAAAAAGGCTGCTTAATTGATAGCGGCAATTTGGGAATACATATCATCC	120				
DB	649 AGTGAACGGAAAAAGGCTGCTTAATTGATAGCGGCAATTTGGGAATACATATCATCC	708				
QY	121 CACATTTTGGAGCCATTAATATCACTGCTCCAAAGCTTATGAAAGCAAGTTGCCAAG	180				
DB	709 CACATTTTGGAGCCATTAATATCACTGCTCCAAAGCTTATGAAAGCAAGTTGCCAAG	768				
QY	181 GACAAAGTGTAAATTACAGAGCTCATCCAGCATTCAGCGAAACATTAAGTTGACATTGAT	240				
DB	769 GACAAAGTGTAAATTACAGAGCTCATCCAGCATTCAGCGAAACATTAAGTTGACATTGAT	828				
QY	241 TGGAGTCAGAAAGGTGTAGTTTACGATCAAAAGTCCCAAGATGTGCTCTCTCTTCA	300				
DB	829 TGGAGTCAGAAAGGTGTAGTTTACGATCAAAAGTCCCAAGATGTGCTCTCTCTTCA	888				
QY	301 GACGTGTTTCTCACTGACTTCTGGGTAACCTGAGAAAGAGCTTCAACTGTTCACCTG	360				
DB	889 GACGTGTTTCTCACTGACTTCTGGGTAACCTGAGAAAGAGCTTCAACTGTTCACCTG	948				
QY	361 CTTGCAAGTGGGTTTGTGAGTTCCTCGTTGTTTCCCTGGCCTCTGTGAAGAAATCC	420				
DB	949 CTTGCAAGTGGGTTTGTGAGTTCCTCGTTGTTTCCCTGGCCTCTGTGAAGAAATCC	1008				
QY	421 ACTCTAGTCCCTTACCTGCAATTTCTCAGCCTTGCTTACTGTGGCAACATTGGGCCAAC	480				
DB	1009 ACTCTAGTCCCTTACCTGCAATTTCTCAGCCTTGCTTACTGTGGCAACATTGGGCCAAC	1068				
QY	481 CGAATTCCTCCCAATCTTTATCTTGGCTGCGACGGAATGCTTCAACAAGAGCTGATA	540				
DB	1069 CGAATTCCTCCCAATCTTTATCTTGGCTGCGACGGAATGCTTCAACAAGAGCTGATA	1128				
QY	541 CAGCAGAAATGGATTGGTTATGTGTAAATGCCAGCTATACCTGTCCAAAGCCTGACTTT	600				
DB	1129 CAGCAGAAATGGATTGGTTATGTGTAAATGCCAGCTATACCTGTCCAAAGCCTGACTTT	1188				
QY	601 ATCCCGGAGCTCATTTTCTCGCGTGGCCCTGTGAATGACAGCTTTTGTGAAGAAATTTTG	660				
DB	1189 ATCCCGGAGCTCATTTTCTCGCGTGGCCCTGTGAATGACAGCTTTTGTGAAGAAATTTTG	1248				

QY 661 CCGTGGTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGGCTCCAAATGANTGTGTT 720
DB 1249 CCGTGGTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGGCTCCAAATGANTGTGTT 1308
QY 721 CTAGTGCATCTGTTAGCTGGAGATCTCCGCTCCGCCACATCGCTATCGCTCATCATGAT 780
DB 1309 CTAGTGCATCTGTTAGCTGGAGATCTCCGCTCCGCCACATCGCTATCGCTCATCATGAT 1368
QY 781 AAGAGATGACATGTCTTTAGATGAGCTTACAGATTTTGTGAAAGAAAAGAAAGCTACT 840
DB 1369 AAGAGATGACATGTCTTTAGATGAGCTTACAGATTTTGTGAAAGAAAAGAAAGCTACT 1428
QY 841 ATATCTCCAACTTCAATTTTCTGGGCCAACTCCTGAGCTATAGAGAAAGATTAAAGAC 900
DB 1429 ATATCTCCAACTTCAATTTTCTGGGCCAACTCCTGAGCTATAGAGAAAGATTAAAGAC 1488
QY 901 CAGAGCTGAGCATCAGGGGCCAAAGAGCAAACTCAGCTGTGACCTTGAGAAAGCCAAAT 960
DB 1489 CAGAGCTGAGCATCAGGGGCCAAAGAGCAAACTCAGCTGTGACCTTGAGAAAGCCAAAT 1548
QY 961 GAACTGTCTCTGTCTCTCAGAGGGTGAAGAAAAGAGAGCGCCCTCAGTCCACCC 1020
DB 1549 GAACTGTCTCTGTCTCTCAGAGGGTGAAGAAAAGAGAGCGCCCTCAGTCCACCC 1608
QY 1021 TGTGCGGACTCTGTCTCTCAGAGGGTGAAGAAAAGAGAGCGCCCTCAGTCCACCC 1080
DB 1609 TGTGCGGACTCTGTCTCTCAGAGGGTGAAGAAAAGAGAGCGCCCTCAGTCCACCC 1668
QY 1081 CCCAGGCTGCGCGAGCGGTGAGCGGTGTGAGAGACAGCCCGTGTGATCAGGCGCTC 1140
DB 1669 CCCAGGCTGCGCGAGCGGTGAGCGGTGTGAGAGACAGCCCGTGTGATCAGGCGCTC 1728
QY 1141 AGTGGCTGACCTGTCTCAGAGAGCTGAGAGACAGCAATTAAGTCAAGGCTTCTTC 1200
DB 1729 AGTGGCTGACCTGTCTCAGAGAGCTGAGAGACAGCAATTAAGTCAAGGCTTCTTC 1788
QY 1201 TCTCTGAGATTCAAATCAGTTTCTATTTTCAAGCAGAGTGGACATCTCTTACATGCTTC 1260
DB 1789 TCTCTGAGATTCAAATCAGTTTCTATTTTCAAGCAGAGTGGACATCTCTTACATGCTTC 1848
QY 1261 TCTCTCAGAGAGATCTTGGAAATCTTCAAACTTCCACTCAGTGTGAGAGCCAC 1320
DB 1849 TCTCTCAGAGAGATCTTGGAAATCTTCAAACTTCCACTCAGTGTGAGAGCCAC 1908
QY 1321 AAGCTATGCGAGTTCTCCCTGTGTGAGAACTATCGAGAGCACTCCGAAACAGTCTCT 1380
DB 1909 AAGCTATGCGAGTTCTCCCTGTGTGAGAACTATCGAGAGCACTCCGAAACAGTCTCT 1968
QY 1381 GATTAAGAGAGAGCAGAGATCCCAAGAGCTGCGAGACCGCCAGGCTTCAAGAGCCAG 1440
DB 1969 GATTAAGAGAGAGCAGAGATCCCAAGAGCTGCGAGACCGCCAGGCTTCAAGAGCCAG 2028
QY 1441 AGCAAGCAGATTGCTTGGTGTGAGAACTGAGAGCTGAGACCGCCAGAGGCTCCCTTTTA 1500
DB 2029 AGCAAGCAGATTGCTTGGTGTGAGAACTGAGAGCTGAGACCGCCAGAGGCTCCCTTTTA 2088
QY 1501 TCTCAGCTGATCGAAGTGGAGGGTGGAGCAATTACACACAGCTTCTTTTGGGC 1560
DB 2089 TCTCAGCTGATCGAAGTGGAGGGTGGAGCAATTACACACAGCTTCTTTTGGGC 2148
QY 1561 CTTTTCACAGCAGCAGAGCAGCTTCAAGAGCTGCTGGCTTGGGCTTTAAGGCTGGAC 1620
DB 2149 CTTTTCACAGCAGCAGAGCAGCTTCAAGAGCTGCTGGCTTGGGCTTTAAGGCTGGAC 2208
QY 1621 TCGGATATCTTGGCTCCCGACAGCTTACCCCTTCCCTGACAGCAGCTGTATTTTGGC 1680
DB 2209 TCGGATATCTTGGCTCCCGACAGCTTACCCCTTCCCTGACAGCAGCTGTATTTTGGC 2268
QY 1681 ACAGAGTCTCAGACTTCTATCTGCTCAGCAGCTTACAGAGGAGGCTGCAAGTTACTCT 1740
DB 2269 ACAGAGTCTCAGACTTCTATCTGCTCAGCAGCTTACAGAGGAGGCTGCAAGTTACTCT 2328

QY 1741 GCTTACAGCTGAGCAGCAGCTGCCCATTGCGAGAGCAAGTCTATTTCTGTGCGAGGCGG 1800
DB 2329 GCTTACAGCTGAGCAGCAGCTGCCCATTGCGAGAGCAAGTCTATTTCTGTGCGAGGCGG 2388
QY 1801 CAGAAAGCAGAGTGAAGAGCTGATCTCGCGCGAGAGCTGAGCTGAAAGAGAGCCCTTTGAA 1860
DB 2389 CAGAAAGCAGAGTGAAGAGCTGATCTCGCGCGAGAGCTGAGCTGAAAGAGAGCCCTTTGAA 2448
QY 1861 AAGCAGTTTAAACGAGAGCTGCGCAATGGAATTTGAGAGAGCATCATCTCAGAGAC 1920
DB 2449 AAGCAGTTTAAACGAGAGCTGCGCAATGGAATTTGAGAGAGCATCATCTCAGAGAC 2508
QY 1921 AGTCAAGGAGAGAGCTGAGAGAGTGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1980
DB 2509 AGTCAAGGAGAGAGCTGAGAGAGTGGAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 2568
QY 1981 ATCATTTGAGTCTCC 1995
DB 2569 ATCATTTGAGTCTCC 2583

RESULT 10
US-10-425-114-26234

Sequence 26234, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yinua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OR INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OR INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5313)B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 26234
LENGTH: 3625
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
OTHER INFORMATION: Clone ID: LIB4119-028-H6_FLI
US-10-425-114-26234

Query Match 99.8%; Score 1991.8; DB 17; Length 3625;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCATGAGATGTTGGAATCTCAATTTGTACTGAGAGGTTGGTGGCTTGTCTGGA 60
DB 692 ATGGCCATGAGATGTTGGAATCTCAATTTGTACTGAGAGGTTGGTGGCTTGTCTGGA 751
QY 61 AGTGAACGGAAGAGTGTCTGTAATGATAGCCGACATTTGTGGAATCAATCATCC 120
DB 752 AGTGAACGGAAGAGTGTGTGTAATGATAGCCGACATTTGTGGAATCAATCATCC 811
QY 121 CACATTTTGAAGCCATTAATTAATCACTGCTCAAGCTTAATGAAGCGAAGGTTCAACAG 180
DB 812 CACATTTTGAAGCCATTAATTAATCACTGCTCAAGCTTAATGAAGCGAAGGTTCAACAG 871
QY 181 GACAAAGTGTATTAACAGAGCTATCAGAGCTTCAAGGAAACATAAGGTTGACATGAT 240
DB 872 GACAAAGTGTATTAACAGAGCTATCAGAGCTTCAAGGAAACATAAGGTTGACATGAT 931
QY 241 TGCAGTCAAGAGTTGATGATTAAGATCAAGCTCCCAAGATGTGCTCTCTTCA 300
DB 932 TGCAGTCAAGAGTTGATGATTAAGATCAAGCTCCCAAGATGTGCTCTCTTCA 991
QY 301 GACTGTTTTCACATGATCTTGTGATTAATGAGAGAGCTTCAACTGTGTACCTG 360
DB 992 GACTGTTTTCACATGATCTTGTGATTAATGAGAGAGCTTCAACTGTGTACCTG 1051


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; PRIOR APPLICATION NUMBER: US 60/231,366
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 3766
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040058341A1 7480570CBI
US-10-343-357-17
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Query Match      99.8%; Score 1991.8; DB 17; Length 3766;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      1 ATGGCCCATNGATNGATGGAATCTCAATTTGTTACTGAGAGGTTGGTGGCTGTGCGAA 60
Db      538 ATGGCCCATNGATNGATGGAATCTCAATTTGTTACTGAGAGGTTGGTGGCTGTGCGAA 597
QY      61 AGTGAACGGAAGAGTGTCTAATTTAGTGGCCGCAATTTGGAAATACATACATCC 120
Db      598 AGTGAACGGAAGAGTGTCTAATTTAGTGGCCGCAATTTGGAAATACATACATCC 657
QY      121 CACATTTTGAAGCCATTAATATCAATCTGCTCCAGCTTATGAGGAGTTGGAACAG 180
Db      658 CACATTTTGAAGCCATTAATATCAATCTGCTCCAGCTTATGAGGAGTTGGAACAG 717
QY      181 GACAAAGTGTATTTACAGAGCTCATCCGAAATTCAGCGCAACATTAAGTTGACTTGAT 240
Db      718 GACAAAGTGTATTTACAGAGCTCATCCGAAATTCAGCGCAACATTAAGTTGACTTGAT 777
QY      241 TGCAGTCAGAGGTTGTAGTTTACATCAAGCTCCAGAGTGGTGGCTCTCTCTTCA 300
Db      778 TGCAGTCAGAGGTTGTAGTTTACATCAAGCTCCAGAGTGGTGGCTCTCTCTTCA 837
QY      301 GACTGTTTCTCACTGACTTCTGGGTTAACTGAGAGAGCTTCAACTGTGTACCTG 360
Db      838 GACTGTTTCTCACTGACTTCTGGGTTAACTGAGAGAGCTTCAACTGTGTACCTG 897
QY      361 CTGTGAGGTGGTGTGCTGAGTCTCTGTTGTTCCCGGCTGCTGGGAGGAAATCC 420
Db      898 CTGTGAGGTGGTGTGCTGAGTCTCTGTTGTTCCCGGCTGCTGGGAGGAAATCC 957
QY      421 ACTTAGTCCCTACCTGCAATTTCTCAGCTTGTCTTACCTGTTGCCAATTTGGGCAACC 480
Db      958 ACTTAGTCCCTACCTGCAATTTCTCAGCTTGTCTTACCTGTTGCCAATTTGGGCAACC 1017
QY      481 GCAATTTCTCCCAATCTTATCTTGGCTGCCAGCGAGATGTCCTCAACAAGAGCTGATA 540
Db      1018 GCAATTTCTCCCAATCTTATCTTGGCTGCCAGCGAGATGTCCTCAACAAGAGCTGATA 1077
QY      541 CAGCAGAAATGGAGATTTGTTATGTGTTAAATGCCAGCTATACCTGTCCAAAGCTGACTT 600
Db      1078 CAGCAGAAATGGAGATTTGTTATGTGTTAAATGCCAGCTATACCTGTCCAAAGCTGACTT 1137
QY      601 ATCCCCGAGTCTCATTTTCTGCTGCTGCTGCTGTAATGACAGCTTTTGTGAGAAATTTTG 660
Db      1138 ATCCCCGAGTCTCATTTTCTGCTGCTGCTGCTGTAATGACAGCTTTTGTGAGAAATTTTG 1197
QY      661 CCGTGTGTGGAACAATCAGTAGATTTTCAATGAGAAAGGAAAGGCTCAATGATGTGTT 720
Db      1198 CCGTGTGTGGAACAATCAGTAGATTTTCAATGAGAAAGGAAAGGCTCAATGATGTGTT 1257
QY      721 CTATGCACTGTATTAGTGGATCTCCGCTCCGCAACATCGCTATCGCTACATCATG 780
Db      1258 CTATGCACTGTATTAGTGGATCTCCGCTCCGCAACATCGCTATCGCTACATCATG 1317
QY      781 AAGAGATGACAGTCTTTTATGATGAAGCTTACAGATTTGTGAAAGGAAAGGCTTACT 840
Db      1318 AAGAGATGACAGTCTTTTATGATGAAGCTTACAGATTTGTGAAAGGAAAGGCTTACT 1377
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QY      841 AATATCTCCAAACTTCAATTTTCTGGGCCCACTCTCTGACATATGAGAGAAATTAAGAC 900
Db      1378 AATATCTCCAAACTTCAATTTTCTGGGCCCACTCTCTGACATATGAGAGAAATTAAGAC 1437
QY      901 CAGACTGAGACATCAGGSCCAAAAGACAACTCAAGCTGTGCACTGTGAGAAAGCCAAAT 960
Db      1438 CAGACTGAGACATCAGGSCCAAAAGACAACTCAAGCTGTGCACTGTGAGAAAGCCAAAT 1497
QY      961 GAACCTGTCCCTGCTGTCTACAGAGGTGAGCAGAAAACGAGAGCCCTTCAAGTCCACC 1020
Db      1498 GAACCTGTCCCTGCTGTCTACAGAGGTGAGCAGAAAACGAGAGCCCTTCAAGTCCACC 1557
QY      1021 TGTGCGCATCTGCTGCTACTCTGAGAGGACAGAGGAAAGGCCCCGTGATCCCGCAGGCTG 1080
Db      1558 TGTGCGCATCTGCTGCTACTCTGAGAGGACAGAGGAAAGGCCCCGTGATCCCGCAGGCTG 1617
QY      1081 CCCAGCGTCCCAAGCGTGCAGCCGCTGCTGTTAGAGACAGCCCGCTGTATCAGAGCGCTC 1140
Db      1618 CCCAGCGTCCCAAGCGTGCAGCCGCTGCTGTTAGAGACAGCCCGCTGTATCAGAGCGCTC 1677
QY      1141 AGTGGCTGCACTGTCTCCGAGACAGGCTGGAACAGCAATAGCTCAAGCTTCTTC 1200
Db      1678 AGTGGCTGCACTGTCTCCGAGACAGGCTGGAACAGCAATAGCTCAAGCTTCTTC 1737
QY      1201 TCTGTGATATCAATCAGTTTCAATTTAGCCAGCATGAGCAGATCTTCAATGCTTC 1260
Db      1738 TCTGTGATATCAATCAGTTTCAATTTAGCCAGCATGAGCAGATCTTCAATGCTTC 1797
QY      1261 TCTCATCAGAAAGTCTTTGAAATCTACAAACCTTCCACTACTGTGATGGAACAAC 1320
Db      1798 TCTCATCAGAAAGTCTTTGAAATCTACAAACCTTCCACTACTGTGATGGAACAAC 1857
QY      1321 AAGCTATGCAAGTCTCCCTGTTTCAAGAACTATGGAAGAGCTCCCGAAACAGTCTCT 1380
Db      1858 AAGCTATGCAAGTCTCCCTGTTTCAAGAACTATGGAAGAGCTCCCGAAACAGTCTCT 1917
QY      1381 GATTAAGAGAGAACCCAGATCCCAAGAAAGCTCAGAACCCGAGGCTTTCAGACAGCAG 1440
Db      1918 GATTAAGAGAGAACCCAGATCCCAAGAAAGCTCAGAACCCGAGGCTTTCAGACAGCAG 1977
QY      1441 AGCAAGGATTTGATTTGGTTCAGAACCAAGAGTGGCAACGCGCCAGAGGTCCTTTTAA 1500
Db      1978 AGCAAGGATTTGATTTGGTTCAGAACCAAGAGTGGCAACGCGCCAGAGGTCCTTTTAA 2037
QY      1501 TCTCACTGATGAAGTGGGAGCGTGGAGCAATTAACAACAAGCTTCTTTTGGCG 1560
Db      2038 TCTCACTGATGAAGTGGGAGCGTGGAGCAATTAACAACAAGCTTCTTTTGGCG 2097
QY      1561 CTTTCCACAGCCAGCAGACCTCAAGAAATGTGCTGGCTGAGGCTTAAAGGCTGGCAC 1620
Db      2098 CTTTCCACAGCCAGCAGACCTCAAGAAATGTGCTGGCTGAGGCTTAAAGGCTGGCAC 2157
QY      1621 TCGGATATCTTGGCCCCCCAGACCTTACCCCTTCCCTGACCAAGAGCTGTATTTTGGC 1680
Db      2158 TCGGATATCTTGGCCCCCCAGACCTTACCCCTTCCCTGACCAAGAGCTGTATTTTGGC 2217
QY      1681 ACAGAGTCTCACTACTCTGCTCAGGCACTTACGAGGAGAGGAGGCAAGTACTACT 1740
Db      2218 ACAGAGTCTCACTACTCTGCTCAGGCACTTACGAGGAGAGGAGGCAAGTACTACT 2277
QY      1741 GCTTACAGCTGACGCACTGCTGCCACTTGGCGAGACCAAGTCTATTTGTGTGCGAGCGG 1800
Db      2278 GCTTACAGCTGACGCACTGCTGCCACTTGGCGAGACCAAGTCTATTTGTGTGCGAGCGG 2337
QY      1801 CAGAAGCCAAAGTGAAGAGCTGACTCGGCGGAGAGCTGGCATGAAGAGCCCTTTGAA 1860
Db      2338 CAGAAGCCAAAGTGAAGAGCTGACTCGGCGGAGAGCTGGCATGAAGAGCCCTTTGAA 2397
QY      1861 AAGCAGTTTAAACGAGAGAGCTGCAATGGAATTTTGGAGAGAGCATATGTCAGAGAAC 1920
Db      2398 AAGCAGTTTAAACGAGAGAGCTGCAATGGAATTTTGGAGAGAGCATATGTCAGAGAAC 2457
QY      1921 AGGTCAAGGAGAAAGCTGGGAGAAAGTGGGCAGTCAAGTCTTATCTTTTGGGAGCATGGA 1980
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Db      2458 AGGTACCGGAGAGAGCTGGGGAGAAAGTGGGACAGTCTAGCTTTCCGGGACAGCATGAA 2517
Qy      1981 ATCATTTAGAGTCTCC 1995
Db      2518 ATCATTTAGAGTCTCC 2532

RESULT 12
US-10-648-593-115
; Sequence 115, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 115
; LENGTH: 4790
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-648-593-115

Query Match      99.8%; Score 1991.8; DB 18; Length 4790;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ATGCCCATGAGATGATTGAACTCAAAATTGTTACTGAGAGGTGTGTGCTCTGTGAA 60
Db      184 ATGGCCCATGAGATGATTGAACTCAAAATTGTTACTGAGAGGTGTGTGCTCTGTGAA 243
Qy      61 AGTGAAGGAAAGTCTGTCTAATTGATGACCGGCAATTTGTGAAATACATATCC 120
Db      244 AGTGAAGGAAAGTCTGTCTAATTGATGACCGGCAATTTGTGAAATACATATCC 303
Qy      121 CACATTTTGAAGCATTAATATCACTGCTCCAGCTTATGAGCGAAGTTGCAACG 180
Db      304 CACATTTTGAAGCATTAATATCACTGCTCCAGCTTATGAGCGAAGTTGCAACG 363
Qy      181 GACAAAGTGTATTAACAGAGCTCATCCAGCATTCAGCGAAACATPAAGTTGACATTGAT 240
Db      364 GACAAAGTGTATTAACAGAGCTCATCCAGCATTCAGCGAAACATPAAGTTGACATTGAT 423
Qy      241 TGCAGTCGAAAGTGTATGTTAAGATCAAAAGCTCCCAAGATGTGCTCTCTCTTCA 300
Db      424 TGCAGTCGAAAGTGTATGTTAAGATCAAAAGCTCCCAAGATGTGCTCTCTCTTCA 483
Qy      301 GACTGTTTCTCACTGTACTTCTGGGTAACCTGAGAAAGAGCTTCAACTCTGTACCGT 360
Db      484 GACTGTTTCTCACTGTACTTCTGGGTAACCTGAGAAAGAGCTTCAACTCTGTACCGT 543
Qy      361 CTTCGAGGTGGGTTTGTCTGAGTTCTCTGTTGTTTCCCTGGGCTCTGTGAAGAAATCC 420
Db      544 CTTCGAGGTGGGTTTGTCTGAGTTCTCTGTTGTTTCCCTGGGCTCTGTGAAGAAATCC 603
Qy      421 ACTCTAGTCCCTCACTGCTGATTTCTAGGCTTGCTTAAGCTTTGGCAACATTGGGCAAC 480
Db      604 ACTCTAGTCCCTCACTGCTGATTTCTAGGCTTGCTTAAGCTTTGGCAACATTGGGCAAC 663
Qy      481 GCAATTTCTCCCAATCTTATCTTGGCTGGCCAGAGATGCTCAACAGAGAGCTGATA 540
Db      664 GCAATTTCTCCCAATCTTATCTTGGCTGGCCAGAGATGCTCAACAGAGAGCTGATA 723
Qy      541 CAGCAGAAATGGGATTTGTTATGTGTTAAATGCGACGTAACCTGTCCAAAGCTGACTTT 600
Db      724 CAGCAGAAATGGGATTTGTTATGTGTTAAATGCGACGTAACCTGTCCAAAGCTGACTTT 783

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Qy      601 ATCCCGAGTCTCATTTCTGCGTGTGCTGTGAATGACAGCTTTTGTGAGAAAATTTTG 660
Db      784 ATCCCGAGTCTCATTTCTGCGTGTGCTGTGAATGACAGCTTTTGTGAGAAAATTTTG 843
Qy      661 CCGTGGTTGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCTCCATGAGATGTGT 720
Db      844 CCGTGGTTGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCTCCATGAGATGTGT 903
Qy      721 CTAGTGCATGTTTGTAGCTGGGATCTCCCGCTCCGACCATGCGTATGCGCTACATCAG 780
Db      904 CTAGTGCATGTTTGTAGCTGGGATCTCCCGCTCCGACCATGCGTATGCGCTACATCAG 963
Qy      781 AAGAGATGACATGCTTTTATAGATAGAGCTTACAGATTGTGTAAGAAAAGAAAGCTACT 840
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Db      1024 ATATCTCCAAATCTTCAATTTTCTGGGCCAACTCTGACTATGAGAGAAAGATTAAAG 1083
Qy      901 CAGACTGAGCATTCAGGGCCAAAGCAAACTCAAGCTGCTGACCTGAGAGAGCCAAAT 960
Db      1084 CAGACTGAGCATTCAGGGCCAAAGCAAACTCAAGCTGCTGACCTGAGAGAGCCAAAT 1143
Qy      961 GAACCTGTCCCTGCTGTCAAGAGGTGGAAGAAAGAGAGACGCGCTCAGTCCAGCC 1020
Db      1144 GAACCTGTCCCTGCTGTGTCTCAAGAGGTGGAAGAAAGAGAGACGCGCTCAGTCCAGCC 1203
Qy      1021 TGTGCGAATCTGTACTCTCAGAGGACAGAGCAAAAGCCCGTCAATCCCGCAGCGTG 1080
Db      1204 TGTGCGAATCTGTACTCTCAGAGGACAGAGCAAAAGCCCGTCAATCCCGCAGCGTG 1263
Qy      1081 CCCAGCTGCGCCAGGCTGACGCGTGTGTTAAGAGACAGCCGCTGTGTAAGGCGCTC 1140
Db      1264 CCCAGCTGCGCCAGGCTGACGCGTGTGTTAAGAGACAGCCGCTGTGTAAGGCGCTC 1323
Qy      1141 AGTGGGCTGCACCTGTCCGAGAGACAGGCTGGAAGACAGAAATPAAGCTCAAGGCTTCTTC 1200
Db      1324 AGTGGGCTGCACCTGTCCGAGAGACAGGCTGGAAGACAGAAATPAAGCTCAAGGCTTCTTC 1383
Qy      1201 TCTCTGATATCAATCAATGTTTCATATTCAGCCAGCATGCGCATCTTACATGAGCTTC 1260
Db      1384 TCTCTGATATCAATCAATGTTTCATATTCAGCCAGCATGCGCATCTTACATGAGCTTC 1443
Qy      1261 TCTCTCATGAAAGATGCTTTGGAATATTAACAACTTCCATCTCTGTGATGGACCAAC 1320
Db      1444 TCTCTCATGAAAGATGCTTTGGAATATTAACAACTTCCATCTCTGTGATGGACCAAC 1503
Qy      1321 AAGCTATGCCAGTCTCCCTGTTCAAGAACTATGCGAGACGATCCCGAAACCAAGTCTCT 1380
Db      1504 AAGCTATGCCAGTCTCCCTGTTCAAGAACTATGCGAGACGATCCCGAAACCAAGTCTCT 1563
Qy      1381 GATAAGAGAGAAAGCAGCATCCCGAAGAGCTGACAGCCGCAAGGCTTTCAGACAGCCAG 1440
Db      1564 GATAAGAGAGAAAGCAGCATCCCGAAGAGCTGACAGCCGCAAGGCTTTCAGACAGCCAG 1623
Qy      1441 AGCAAGCATGTTGATTTGGTCAAGAACAGAGCAAGTGCACCGCCAGAGTCCCTTTT 1500
Db      1624 AGCAAGCATGTTGATTTGGTCAAGAACAGAGCAAGTGCACCGCCAGAGTCCCTTTT 1683
Qy      1501 TCTCTCATGCAATCCAGAGTGGAGAGCTGAGAGCAATTAACCAACAGCTTCTTTTGGCC 1560
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Qy      1561 CTTTTCAACACAGCAGACACCTCAAGAAATCTGTGCTGAGCTTGAAGGCTGGGAC 1620
Db      1744 CTTTTCAACACAGCAGACACCTCAAGAAATCTGTGCTGAGCTTGAAGGCTGGGAC 1803
Qy      1621 TCGAATATCTTGGCCCGCCAGACCTTACCCCTTCTGACCAAGACGTGATTTTGGC 1680
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QY	1681	ACAGAGTCTTCA CACTTCTACTCTCTCCCTCAGCATCTTACGAGAGGACATGCTTCACTCT	1740
Db	1684	ACAGAGTCTTCA CACTTCTACTCTCTCTCCTCAGCATCTTACGAGAGGACATGCTTCACTCT	1923
QY	1741	GCTTACAGCTGACGCAAGCTGCGCACTTTCGCGAGACCAAGTCTATTCTGTGTCGCGAGCGG	1800
Db	1924	GCTTACAGCTGACGCAAGCTGCGCACTTTCGCGAGACCAAGTCTATTCTGTGTCGCGAGCGG	1983
QY	1801	CAGAAAGCAAGTGA CAGAGCTGACCTCGGCGGGGAGCTGGCATTTGAGAGAGAGCCCTTTGAA	1860
Db	1984	CAGAAAGCAAGTGA CAGAGCTGACCTCGGCGGGAGCTGGCATTTGAGAGAGAGCCCTTTGAA	2043
QY	1861	AAGCAGTTTAAACGCAGAAAGCTGCCAAATGGAATTTGGAGAGCATCATGTCCAGAGAAC	1920
Db	2044	AAGCAGTTTAAACGCAGAAAGCTGCCAAATGGAATTTGGAGAGCATCATGTCCAGAGAAC	2103
QY	1921	AGGTCAACGGGAAGAGCTGGGGAAGATGGGGCAGTCAAGTCTAGCTTTTGGGGCAGCATGGA	1980
Db	2104	AGGTCAACGGGAAGAGCTGGGGAAGATGGGGCAGTCAAGTCTAGCTTTTGGGGCAGCATGGA	2163
QY	1981	ATCATTTAGAGTCTCC	1995
Db	2164	ATCATTTAGAGTCTCC	2178

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RESULT 13
US-10-357-930-20824
; Sequence 20824; Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
PRIOR FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20824
LENGTH: 5145
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc feature
LOCATION: 1, 5144, 5145
OTHER INFORMATION: n = A,T,C or G
US-10-357-930-20824

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Query Match	99.8%	Score 1991.8;	DB 18;	Length 5145;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 1993; Conservative	0;	Mismatches	2;	Indels 0; Gaps 0.

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Db 589 ATGGCCCATGAGATGATTGGAACTCAAAATTTGTTACTGAAGGGTGGTGGCTCTGCTGGA 648

QY	61	AGTGGAAACGAAAAAGTCGTCAATTGTAATGACCGGCATTTTGTGAAATTCATATACATCC	120
Db	649	AGTGGAAACGAAAAAGTCGTCAATTGTAATGACCGGCATTTTGTGAAATTCATATACATCC	708
QY	121	CACATTTTGGAGCCATTATATATCAATGTCTCCAGACTTATGAAGCGAAGTTGCAACAG	180
Db	709	CACATTTTGGAGCCATTATATATCAATGTCTCCAGACTTATGAAGCGAAGTTGCAACAG	768
QY	181	GACAAGTGTATTTACAGAGCTATCCAGCATTCAGCGAAACATAAGTTGACATTGAT	240
Db	769	GACAAGTGTATTTACAGAGCTATCCAGCATTCAGCGAAACATAAGTTGACATTGAT	828
QY	241	TGCAGTCAGAAGGTTTATGTTTACATCAAAAGTCCCAAGATGTTGCTCTCTCTTCA	300
Db	829	TGCAGTCAGAAGGTTTATGTTTACATCAAAAGTCCCAAGATGTTGCTCTCTCTTCA	888
QY	301	GACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAAGCTTCAACTGTTCACCTG	360
Db	889	GACTGTTTTCTCACTGTACTTCTGGGTAAACTGGAGAAAGCTTCAACTGTTCACCTG	948
QY	361	CTTGCAGAGTGGGTTTGTAGTTTCTCGTGTCTTCCGTGGCTCTGTGAAAGAAATCC	420
Db	949	CTTGCAGAGTGGGTTTGTAGTTTCTCGTGTCTTCCGTGGCTCTGTGAAAGAAATCC	1008
QY	421	ACTTAGTCCCTACCTGCATTTTCTCAGCCTTGCTTACCTGTGTCCAACTATTTGGCCAAAC	480
Db	1009	ACTTAGTCCCTACCTGCATTTTCTCAGCCTTGCTTACCTGTGTCCAACTATTTGGCCAAAC	1068
QY	481	CGAATTTCTCCCAATCTTTATCTTGTGGCTGCAGCGAGATGTCTCAACAGAGCTGATTA	540
Db	1069	CGAATTTCTCCCAATCTTTATCTTGTGGCTGCAGCGAGATGTCTCAACAGAGCTGATTA	1128
QY	541	CAGCAGAAATGGAGTGGTATGTATGTAAATGTCAGACTATACCTGTCCAAAGCTGACATT	600
Db	1129	CAGCAGAAATGGAGTGGTATGTATGTAAATGTCAGACTATACCTGTCCAAAGCTGACATT	1188
QY	601	ATCCCCGAGTCTCATTTTCTCGTGCTGCTGTGAATGACAGCTTTTGTGAGAAATTTTG	660
Db	1189	ATCCCCGAGTCTCATTTTCTCGTGCTGCTGTGAATGACAGCTTTTGTGAGAAATTTTG	1248
QY	661	CCGTGGTGGACAATTCAGTGAATTCATTTAGAGAAAGCAAAAGCTCCAAATGATGTCT	720
Db	1249	CCGTGGTGGACAATTCAGTGAATTCATTTAGAGAAAGCAAAAGCTCCAAATGATGTCT	1308
QY	721	CTAGTGCACTGTTAGCTGGAGTCTCCGCTCCGCGCACATTCGCTATCGCTTACATCATG	780
Db	1309	CTAGTGCACTGTTAGCTGGAGTCTCCGCTCCGCGCACATTCGCTATCGCTTACATCATG	1368
QY	781	AAGAGGAATGACAATGCTTTTGAATGAAGCTTACAGATTTTGTGAAGAAAGAAAGCTTACT	840
Db	1369	AAGAGGAATGACAATGCTTTTGAATGAAGCTTACAGATTTTGTGAAGAAAGAAAGCTTACT	1428
QY	841	ATATCTCCAACTCAATTTTCTGGGCAACTCTCGACATATGAGAGAAATTAAGAAC	900
Db	1429	ATATCTCCAACTCAATTTTCTGGGCAACTCTCGACATATGAGAGAAATTAAGAAC	1488
QY	901	CAGACTGAGGATCAGGGCCAAAGACGAACTCAAGCTGTGCACCTGAGAAAGCCAAAT	960
Db	1489	CAGACTGAGGATCAGGGCCAAAGACGAACTCAAGCTGTGCACCTGAGAAAGCCAAAT	1548
QY	961	GAACTGTGCCCTGTGCTCAGAGGGGTGGAACAGAAAGCGAGACGCCCTCAGTCCACC	1020
Db	1549	GAACTGTGCCCTGTGCTCAGAGGGGTGGAACAGAAAGCGAGACGCCCTCAGTCCACC	1080
QY	1021	TGTGCGCACTTGTCTACCTCAGAGGCGACAGCAAAAGCCCGTGCATCCCGCAGCGTG	1080
Db	1609	TGTGCGCACTTGTCTACCTCAGAGGCGACAGCAAAAGCCCGTGCATCCCGCAGCGTG	1668
QY	1081	CCAGAGCGTGCAGCGGTGACGCGCTGCTGTATGAGAGCAGCCCGCTGTGATCAGGCGCTC	1140
Db	1669	CCAGAGCGTGCAGCGGTGACGCGCTGCTGTATGAGAGCAGCCCGCTGTGATCAGGCGCTC	1728
QY	1141	AGTGGGTGACCTGTTCGACAGAGGCTGGAAGACAGCAATTAAGCTCAAGCGTTCCTTG	1200

QY	1081	1669	Db	QY
CCAGCGCTGCGCCGACGCTGACCGCTGCTGTATGAGGACAGACCGCGCTGATACAGGGCGTC	CCAGCGCTGCGCCGACGCTGACCGCTGCTGTATGAGGACAGACCGCGCTGATACAGGGCGTC	CCAGCGCTGCGCCGACGCTGACCGCTGCTGTATGAGGACAGACCGCGCTGATACAGGGCGTC	CCAGCGCTGCGCCGACGCTGACCGCTGCTGTATGAGGACAGACCGCGCTGATACAGGGCGTC	1140
AGTGGGCTGACCTGTCCTCGCAGACAGGGCTGGAGACAGCAATAAGCTCMAAGCGCTTCCTTC	AGTGGGCTGACCTGTCCTCGCAGACAGGGCTGGAGACAGCAATAAGCTCMAAGCGCTTCCTTC	AGTGGGCTGACCTGTCCTCGCAGACAGGGCTGGAGACAGCAATAAGCTCMAAGCGCTTCCTTC	AGTGGGCTGACCTGTCCTCGCAGACAGGGCTGGAGACAGCAATAAGCTCMAAGCGCTTCCTTC	1200

Db	1729	AGTGGGCTGCACCTGTCCGCGACAGAGGCTGGAAAGACAGCAATACCTCAAGCTTCTTC	1788
Qy	1201	TCTCTGATATCAAAATCAAGTTTCATATTCAGCCAGCATGGCAGCATCTTACATGAGCTTC	1266
Db	1789	TCTCTGATATCAAAATCAAGTTTCATATTCAGCCAGCATGGCAGCATCTTACATGAGCTTC	1848
Qy	1281	TCCTCATCAGAAAGATGCTTTGGAAATCTAACAACTTCCACTACTCTGTGGATGGACCAAC	1322
Db	1849	TCCTCATCAGAAAGATGCTTTGGAAATCTAACAACTTCCACTACTCTGTGGATGGACCAAC	1908
Qy	1321	AAGCATGACAGTTCTCCCTCTTTCAGGAATCATGAGACAGACTCCGGAACCAAGCTCT	1380
Db	1909	AAGCATGACAGTTCTCCCTCTTTCAGGAATCATGAGACAGACTCCGGAACCAAGCTCT	1968
Qy	1391	GATTAAGAGAAAGCCAGCATCCCAAGAAAGCTGACAGCCGCGAGCTTTCAGACAGCAG	1440
Db	1969	GATTAAGAGAAAGCCAGCATCCCAAGAAAGCTGACAGCCGCGAGCTTTCAGACAGCAG	2028
Qy	1441	AGCAAGCATTTGCAATTCGCTCAGAACCAAGCAGAGTGGACCGCCCAAGATCCCTTTTA	1500
Db	2029	AGCAAGCATTTGCAATTCGCTCAGAACCAAGCAGAGTGGACCGCCCAAGATCCCTTTTA	2088
Qy	1501	TCTCCACTGCATCGAAGTGGGAGGCTGGAGGACATTTACACACAGCTTCCTTTTCGGC	1566
Db	2089	TCTCCACTGCATCGAAGTGGGAGGCTGGAGGACATTTACACACAGCTTCCTTTTCGGC	2148
Qy	1561	CTTTCACACAGCCAGCAGCAGCACCCTCAGAAAGTCTGCTGGCCTTGAAGGCTGGAGC	1620
Db	2149	CTTTCACACAGCCAGCAGCAGCACCCTCAGAAAGTCTGCTGGCCTTGAAGGCTGGAGC	2208
Qy	1621	TCCGATATCTTTGGCCCCCAGACTCTACCCCTTCCCTGACCAAGCATGTGATTTTGGCC	1680
Db	2209	TCCGATATCTTTGGCCCCCAGACTCTACCCCTTCCCTGACCAAGCATGTGATTTTGGCC	2268
Qy	1681	ACAGAGTCTCTACACTTCTACCTGTCGCTCAGCCTCAGCAATCGAGGAGTGCAGATTACTCT	1748
Db	2269	ACAGAGTCTCTACACTTCTACCTGTCGCTCAGCCTCAGCAATCGAGGAGTGCAGATTACTCT	2328
Qy	1741	GCTTACAGCTGACAGCCAGCTGCCACTTTCGCGAGACCAAGTCTATTTCTGTGCGAGCGG	1800
Db	2329	GCTTACAGCTGACAGCCAGCTGCCACTTTCGCGAGACCAAGTCTATTTCTGTGCGAGCGG	2388
Qy	1801	CAGAAAGCCAAAGTACAGAGCTGACTCGCGCGAGCTGGCATGAAGAGCCCTTTGAA	1866
Db	2389	CAGAAAGCCAAAGTACAGAGCTGACTCGCGCGAGCTGGCATGAAGAGCCCTTTGAA	2448
Qy	1861	AAGCAGTTTAAACGCAAGAGCTGCGCAATTTGGAATTTGAGAGAGATCATGTCAAGAAC	1920
Db	2449	AAGCAGTTTAAACGCAAGAGCTGCGCAATTTGGAATTTGAGAGAGATCATGTCAAGAAC	2508
Qy	1921	AGGTCAACGGGAAGAGCTGGGGAAGATGGGAGTCAAGCTTTTCGGGAGCATGGAA	1980
Db	2509	AGGTCAACGGGAAGAGCTGGGGAAGATGGGAGTCAAGCTTTTCGGGAGCATGGAA	2568
Qy	1981	ATCATTTGAGGTCTCC 1995	
Db	2569	ATCATTTGAGGTCTCC 2583	
RESULT 14			
US-10-357-930-20969			
; Sequence 20969, Application US/10357930			
; Publication No. US20040259086A1			
; GENERAL INFORMATION:			
; APPLICANT: Schlegel, Robert			
; APPLICANT: Endege, Wilson			
; APPLICANT: Monahan, John			
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR			
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF			
; TITLE OF INVENTION: HUMAN PROSTATE CANCER			
; FILE REFERENCE: MRI-007BCN			
; CURRENT APPLICATION NUMBER: US/10/357,930			

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: CURRENT FILING DATE: 2003-02-04
: PRIOR APPLICATION NUMBER: 09/785,276
: PRIOR FILING DATE: 2003-02-16
: PRIOR APPLICATION NUMBER: 60/183,319
: PRIOR FILING DATE: 2000-02-17
: PRIOR APPLICATION NUMBER: 60/189,862
: PRIOR FILING DATE: 2000-03-16
: PRIOR APPLICATION NUMBER: 60/207,454
: PRIOR FILING DATE: 2000-05-25
: PRIOR APPLICATION NUMBER: 60/211,314
: PRIOR FILING DATE: 2000-06-09
: PRIOR APPLICATION NUMBER: 60/219,007
: PRIOR FILING DATE: 2000-07-18
: PRIOR APPLICATION NUMBER: 60/255,281
: PRIOR FILING DATE: 2000-12-13
: NUMBER OF SEQ ID NOS: 62232
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 20969
: LENGTH: 5145
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: 1, 5144, 5145
: OTHER INFORMATION: n = A,T,C or G
US-10-357-930-20969

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Query Match	99.8%	Score 1991.8	DB 18	Length 5145
Best Local Similarity	99.9%	Fred. No. 0		
Matches 1993	Conservative	0	Mismatches 2	Indels 0
				Gaps 0
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DB	589	ATGGCCCATGAGATGATTGAACCTCAATTTGTTACTGAGAGGTTGATGGCTCTGCTGNA	648	
QY	61	AGTGAACGGA AAAAGTGCTGCTAATTGATAGCCGGCATTTGTGAAATACATACATCC	120	
DB	649	AGTGAACGGA AAAAGTGCTGCTAATTGATAGCCGGCATTTGTGAAATACATACATCC	708	
QY	121	CACATTTTGGAGGCATTAATATACACATGCTCCACGCTTATGAAACCGAAGTTTGGACAG	180	
DB	709	CACATTTTGGAGGCATTAATATACACATGCTCCACGCTTATGAAACCGAAGTTTGGACAG	768	
QY	181	GACAAAGTGAATTAACAGAGCTCATCCAGCATTCAGCGAAACATPAAGTTGACATTTGAT	240	
DB	769	GACAAAGTGAATTAACAGAGCTCATCCAGCATTCAGCGAAACATPAAGTTGACATTTGAT	828	
QY	241	TGCAGTCGAAGGTTTGATTTACGATCAAAAGCTCCAAAGATGTTGCCCTCTCTCTTCA	300	
DB	829	TGCAGTCGAAGGTTTGATTTACGATCAAAAGCTCCAAAGATGTTGCCCTCTCTCTTCA	888	
QY	301	GACGTTTTCACATGATCTCTGGGTAACTGGAAGAGAGCTTCACTCTTTCACCTG	360	
DB	889	GACGTTTTCACATGATCTCTGGGTAACTGGAAGAGAGCTTCACTCTTTCACCTG	948	
QY	361	CTTCAGAGTGGGTTGCTGAGTTCTCTGCTGTTTCCCTGGCCTCTGTAAGAGAAATCC	420	
DB	949	CTTCAGAGTGGGTTGCTGAGTTCTCTGCTGTTTCCCTGGCCTCTGTAAGAGAAATCC	1008	
QY	421	ACTCTAGTCCCTACCTGATTTCTTCAGCTTTGCTTACCTGTTGCGCAACATTTGGGCCAAC	480	
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QY	481	CGAATTCCTCCACATCTTATCTTGGGCGCGACAGAGATATGTCCTCAACAAGAGCTGATG	540	
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QY	541	CAGCAGATGGATGTTATGTGTAAATCCAGCTATACCTGTCCAAAGCCTGACTTT	600	
DB	1129	CAGCAGATGGATGTTATGTGTAAATCCAGCATACTCTGTCCAAAGCCTGACTTT	1188	
QY	601	ATCCCGAGTCTCATTTCTCGCGGTGCTGTGAATGACAGCTTTTGTGAGAAATTTTG	660	

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Db 1249 CCGTGTGTGGAACAATAGTAGATTTTGAAGAAAGCAAAAGCTTCAATGTGATGT 1308
QY 721 CTAGTGCATGTTTTAGTGGGATCTCCGCTCCGCCACATCGCTATCGCTCATCATG 780
Db 1309 CTAGTGCATGTTTTAGTGGGATCTCCGCTCCGCCACATCGCTATCGCTCATCATG 1368
QY 781 AAGAGATGACATGCTTTTGAATGAGCTTACAGATTTTGTGAAAAAAGAACTTACT 840
Db 1369 AAGAGATGACATGCTTTTGAATGAGCTTACAGATTTTGTGAAAAAAGAACTTACT 1428
QY 841 ATATCTCCAAATCTTCAATTTTCTGGGCCAACTCTGTGACTATAGAAAGATTAAAGC 900
Db 1429 ATATCTCCAAATCTTCAATTTTCTGGGCCAACTCTGTGACTATAGAAAGATTAAAGC 1488
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Db 1489 CAGACTGAGACATCAGGGCCAAAGAGCAAACTCAAGCTGTGACCTTGAGAGCCCAAT 1548
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Db 1669 CCCAGGTCGCCAGCGCTGACAGCGCTGTGTGAGAGACAGCCCGCTGTACAGCGCTC 1728
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Db 1849 TCCCTATCAGAAAGATGCTTTGAAATATTAACAACCTTCACTACTGTGATGGAGCAAC 1908
QY 1321 AAGCTATGCAAGTTTCTCCCTGTGTCAGAACTATGAGAGAGACTCCCGAAACAGATGCT 1380
Db 1909 AAGCTATGCAAGTTTCTCCCTGTGTCAGAACTATGAGAGAGACTCCCGAAACAGATGCT 1968
QY 1381 GATTAGAGAGAAAGCAGACATCCCAAGAACTGACAGCCGACAGGCTTTCAGACAGCCAG 1440
Db 1969 GATTAGAGAGAAAGCAGACATCCCAAGAACTGACAGCCGACAGGCTTTCAGACAGCCAG 2028
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Db 2029 AGCAAGCATGTCATTCGATGAGAAACAGAGAGTGGCAACCGCCAGAGAGTCCCTTTTA 2088
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QY 1981 ATCATTGAGTCTCC 1995
Db 2569 ATCATTGAGTCTCC 2583
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; Sequence 21071, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-0078CN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21071
; LENGTH: 5145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..5145
; OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 2089 TCTCCAGTGCATCCGAAGTGGAGCGGTGAGAGCAATTAACAACAGGCTTCTTTTGGC 2148
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QY 1861 AAGCATTTAAACGAGAAAGCTGCCAAATTTGAGAGAGAGATCATGTCAAGAAAC 1920
Db 2449 AAGCATTTAAACGAGAAAGCTGCCAAATTTGAGAGAGAGATCATGTCAAGAAAC 2508
QY 1921 AGGTCAAGGAAAGAGCTGGGAAAGTGGCAGTCACTAGCTTTTGGGCGAGATGGA 1980
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Db 2569 ATCATTTGAGTCTCC 2583

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Job time : 1221.22 secs

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GenCore version 5.1.6
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OW nucleic - nucleic search, using SW model

Run on: February 15, 2005, 02:21:00 / Search time 163.961 Seconds
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Perfect score: 906
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

- 1: Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	902.8	99.6	3544	4	US-09-816-494-1
3	365.8	40.4	2377	4	US-09-920-668-3
4	364.2	40.2	2351	4	US-09-949-016-3250
5	294.6	32.5	333	4	US-09-513-999C-2877
6	223	24.6	279	4	US-09-016-434-91
7	187.8	20.7	380	4	US-09-513-999C-3684
8	124.6	13.8	1830	4	US-09-557-921-1
9	106.8	11.8	2283	4	US-09-949-016-4617
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11	96.2	10.6	2109	4	US-09-016-434-1135
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14	94.6	10.4	1208	4	US-09-023-655-347
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43	90	9.9	2109	4	US-09-671-325-826	Sequence 826, App
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ALIGNMENTS

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Sequence 3, Application US/09816494									
Patent No. 6664089									
GENERAL INFORMATION:									
APPLICANT: Meyers, Rachel A.									
TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY									
FILE REFERENCE: 10448-030002									
CURRENT APPLICATION NUMBER: US/09/816,494									
CURRENT FILING DATE: 2001-03-23									
PRIOR APPLICATION NUMBER: US 60/191,858									
PRIOR FILING DATE: 2000-03-24									
NUMBER OF SEQ ID NOS: 10									
SOFTWARE: FASTSEQ for Windows Version 4.0									
SEQ ID NO 3									
LENGTH: 1998									
TYPE: DNA									
ORGANISM: Homo sapiens									
US-09-816-494-3									
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Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
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RESULT 2
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; Sequence 1, Application US/09816494
; Patent No. 6664089
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)...(2583)
US-09-816-494-1

Query Match 99.6%; Score 902.8; DB 4; Length 3544;
Best Local Similarity 99.8%; Pred. No. 7.7e-308;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCCATGATGATTTGCAATCAATTTGTACTAGAGAGTTGGCTTCTGCTGAA 60
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QY 901 CAGACT 906
Db 1489 CAGACT 1494

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; Sequence 3, Application US/09920668
; Patent No. 6482644
; GENERAL INFORMATION:
; APPLICANT: Lex M. Coweert
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 8 EXPRESSION
; FILE REFERENCE: RTS-0246
; CURRENT APPLICATION NUMBER: US/09/920,668
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 3

LENGTH: 2377
 TYPE: DNA
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 LOCATION: (135)...(2012)
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Query Match 40.4% Score 365.8; DB 4; Length 2377;
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 88 GATAGCCGGCCATTGTTGGAATACATATCATCCCATTTTGGAAAGCCATTAAATCAAC 147
 225 GACAGCCGCTCTTCTGTGAGTACAAACAGCTGCGATGTCTCAGCTCCGTCACATCTGC 284
 148 TGCTCCAAAGCTTAAAGCAAGAGTTGGACAGACAAAGTTAAATTAACAGAGTCATC 207
 285 TGCTCCAAAGCTGTAAGCGCGGCTGACAGAGGCAAGGTGACCATTTGCGAGCTATC 344
 208 CAGCATTGAGGAAACATAAGTTGACATTTGACAGTCAAGAGTTGATTTACGAT 267
 345 CAGCCGCTGACAGCAGCAGCTGAGGCTACGAGCAGACAGACGTGTGTCTATAC 404
 268 CAAGCTCCCAAGATGTTGCTCTCTCTTCAAGCTGTTTCTCATCTGATCTTGGGT 327
 405 CAGAGCAGCGGAGCGCAGCGTGTGGCGCAGACAGCTTCTCTCCATCTGTGAGC 464
 328 AAATGGAAGAAAGCTTCAATCTGTGTACCTGTGTGAGGTGGTTGTGAGTTCTCT 387
 465 AAGCTGACGGCTCTTCTGACAGCGTGCATCTCATCTGAGGGCTTGCACCTCTTCC 524
 388 CGTGTGTTCCCTGCTCTGTGAGAAATTCACATCTCTAGTCCCTACCTGATTTCT 444
 525 TCTCTCTTCCCGGCTCTGTGAGAGGCAAGCTGTGCTGTCTGCTACCATAGCTCTCC 584
 445 CAGCTTGTCTTACCTGTGCAAGATTTGGGCAACCCGAAATCTTCCCATCTTATCTT 504
 585 CAGCCCTGCTGCTGTGAGCGAGGTGGCTGACCGGCATCTGCTCACTCACTGAGC 644
 505 GCGTCCAGAGATGTCTCAACAGAGCTGATACAGCAAGTGGATGGTTGTTATG 564
 645 GCGTCCAGAGAGCTCTTAAACAGAGATCTGATGACGAAAAATGAAATAGCTACGTC 704
 565 TTAAATGCAAGCTTACCTGTGCAAGCTGATCTTATCCCGAGTCTCATTTCTGTGCT 624
 705 CTCAAGCCAGCACTCTGCCCCAGCTGATCTTCACTGTGAGAGCCGCTTATGCGG 764
 625 GTGCTGTGATGACAGCTTTTGTGAGAAATTTTGGCGTGTGACAAATTCAGATAGT 684
 765 GTCCCATCAACGACACTAATGTGAAAACTGTGCGCTGTGCGACAAATTCATGAG 824
 685 TTCAATGGAAGAAAGCAAGCTCCATGATGTGTTCTAGTCACTGTTTACGCTGGATC 744
 825 TTCAATGGAAGAAAGCAAGCTCTCCAGCTGCCAAGTCTGATCTGCTGCTGGCATC 884
 745 TCCGCTCCGCAATGCTGATGCGCTATGCGCTATGATGAAAGAGATGAGATGCTTTGAT 804
 885 TCCGCTCTGCAACATGCGCTATGCTATCAATGAAAGCAATGAGGATGCTCTCCGAC 944
 805 GAACTTACAGATTTGTGAAAGAAAGAAAGCACTATATCTCCAAATTTCAATTTCTG 864
 945 GAGCGCTACAGATTTGTGAAAGAAAGAGAGCGCGCTGCTCAATCTGCCCACTTACCTCTG 1004
 865 GCGCACTCTGTAATGAGATGAGAAAGATTAAAG 897
 1005 GCGCAGCTGTGAGTACGAGCGCAGCTGAAG 1037

RESULT 4

US-09-949-016-3250

Sequence 3250, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 3250

LENGTH: 2351

TYPE: DNA

ORGANISM: Human

US-09-949-016-3250

Query Match 40.2% Score 364.2; DB 4; Length 2351;
 Best Local Similarity 64.4%; Pred. No. 2.2e-117;
 Matches 562; Conservative 0; Mismatches 308; Indels 3; Gaps 1;

28 ATTGTTACTGAGAGTTGGTGGCTCTGCTGGAAGTGAACGAAAAAGTCTGTAATT 87
 139 ATGATGCGAAGAGCTGGCCAGCTGTGGGGGGGGGGCTGGGGGGGGCGCTGTATC 198
 88 GATAGCCGGCCATTGTTGGAATACATATCATCCCATTTTGGAAAGCCATTAAATCAAC 147
 199 GACAGCCGCTCTTCTGTGAGTACAAACAGCTGCGATGTCTCAGCTCCGTCACATCTGC 258
 148 TGCTCCAAAGCTTAAAGCAAGAGTTGGACAGACAAAGTTAAATTAACAGAGTCATC 207
 259 TGCTCCAAAGCTGTAAGCGCGGCTGACAGAGGCAAGGTGACCATTTGCGAGCTATC 318
 208 CAGCATTGAGGAAACATAAGTTGACATTTGACAGTCAAGAGTTGATTTACGAT 267
 319 CAGCCGCTGACAGCAGCAGCTGAGGCTACGAGCAGACAGACGTGTGTCTATAC 378
 268 CAAGCTCCCAAGATGTTGCTCTCTCTTCAAGCTGTTTCTCATCTGATCTTGGGT 327
 379 CAGAGCAGCGGAGCGCAGCGTGTGGCGCAGACAGCTTCTCTCCATCTGTGAGC 438
 328 AAATGGAAGAAAGCTTCAATCTGTGTACCTGTGTGAGGTGGTTGTGAGTTCTCT 387
 439 AAGCTGACGGCTCTTCTGACAGCGTGCATCTCATCTGAGGGCTTGCACCTTCTCC 498
 388 CGTGTGTTCCCTGCTCTGTGAGAAATTCACATCTCTAGTCCCTACCTGATTTCT 444
 499 TCTCTCTTCCCGGCTCTGTGAGAGGCAAGCTGTGCTGTCTACCATAGCTCTCC 558
 445 CAGCTTGTCTTACCTGTGCAAGATTTGGGCAACCCGAAATCTTCCCATCTTATCTT 504
 559 CAGCCCTGCTGCTGTGAGCGAGGTGGCTGACCGGCATCTGCTCACTCACTGAGC 618
 505 GCGTCCAGAGATGTCTCAACAGAGCTGATACAGCAAGTGGATGGATGTTATG 564
 619 GCGTCCAGAGAGCTCTTAAACAGAGATCTGATGACGAAAAATGAAATAGCTACGTC 678
 565 TTAAATGCAAGCTTACCTGTGCAAGCTGATCTTATCCCGAGTCTCATTTCTGTGCT 624
 679 CTCAAGCCAGCAACTCTGTGCCCAAGCTGATCTTCACTGTGAGAGCGGCTTATGCGG 738
 625 GTGCTGTGATGACAGCTTTTGTGAGAAATTTTGGCGTGTGACAAATTCAGATAGT 684
 739 GTCCCATCAACGACACTAATGTGAAAACTGTGCGCTGTGAGCAAGTCTCATGAG 798

QY 685 TTCAATGAGAAAGCAAAAGCCTCCATGATGATGTCTAGTGCACGTGTTAGTGGATC 744
Db 799 TTCAATGAGTAAAGCCAAAGCTCTCCAGCTGCAAGTCAATCGTCTGCTGGCATC 858
QY 745 TCCGCTCCGACCACTGCTATGCTCTACATCATGAGAGATGACATGCTTTAGAT 804
Db 859 TCCGCTCCGACCACTGCTATGCTCTACATCATGAGAGATGACATGCTTTAGAT 804
QY 805 GAACTTACAGATTTGTAAGAAAGAAAGCCTATCTATCTCCAACTTCAATTTCTG 864
Db 919 GAGCCCTACAGGTTCTGTAAGAGACAGCGCCCTCTCTGCGCAACTTCACTTCTG 978
QY 865 GGCCTACTCTGACCTTGAAGAGAGATTTAG 897
Db 979 GGCCTACTCTGACCTTGAAGAGAGATTTAG 1011

RESULT 5
US-09-513-999C-2877

/ Sequence 2877, Application US/09513999C
/ Patent No. 6783961
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Duclert, A.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
/ Patent No. 6783961
/ FILE REFERENCE: 59.US2.REG
/ CURRENT APPLICATION NUMBER: US/09/513,999C
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/122,487
/ PRIOR FILING DATE: 1999-02-26
/ NUMBER OF SEQ ID NOS: 36681
/ SOFTWARE: Patent.pm
/ SEQ ID NO 2877
/ LENGTH: 333
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 127..333
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 17
/ OTHER INFORMATION: h=a or c or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 18
/ OTHER INFORMATION: y=c or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 19
/ OTHER INFORMATION: k=g or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 36
/ OTHER INFORMATION: n=a, g, c or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 58
/ OTHER INFORMATION: r=a or g
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 237
/ OTHER INFORMATION: w=a or t
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: 37
/ OTHER INFORMATION: Xaa=His or Gln
/ US-09-513-999C-2877

Query Match 32.5%; Score 294.6; DB 4; Length 333;
Best Local Similarity 97.3%; Pred. No. 2.2e-93;

Matches 326; Conservative 5; Mismatches 0; Indels 4; Gaps 3;
QY 34 ACTGAGAGGTGGTGGCTCTGCTGGAAGAGTGAACG-AAAAGGCTGCTTAATTGATG 92
Db 1 ACTGAGAGGTGGTGGH--KCTGAAAGTGAACGAAAGAGTGGCTTAATTGATG 58
QY 93 CCGGCTATTTGGTAAT-CAATACATCCCAATTTGGAAGCCATTAAATACATGCT 151
Db 59 CCGGCTATTTGGTAATCAATACATCCCAATTTGGAAGCCATTAAATACATGCT 118
QY 152 CCAAGCTTATGAAGGAAGTTGCAACAGACAAAGTTTAATACAGAGCTCATCCAGC 211
Db 119 CCAAGCTTATGAAGGAAGTTGCAACAGACAAAGTTTAATACAGAGCTCATCCAGC 178
QY 212 ATTACGCAAAATPAAGTTGACATTTGATTCAGTCAAGAGTTGTATTAGATCAAA 271
Db 179 ATTACGCAAAATPAAGTTGACATTTGATTCAGTCAAGAGTTGTATTAGATCAAA 238
QY 272 GCTCCCAAGATGTCCTCTCTCTTCAAGCTGTTTCTGACTGTACTTGGGTAAC 331
Db 239 GCTCCCAAGATGTCCTCTCTCTTCAAGCTGTTTCTGACTGTACTTGGGTAAC 298
QY 332 TGAAGAGAGCTTCAACTGTTTCACTGTTCA 366
Db 299 TGAAGAGAGCTTCAACTGTTTCACTGTTCA 333

RESULT 6
US-09-016-434-91

/ Sequence 91, Application US/09016434
/ Patent No. 6500938
/ GENERAL INFORMATION:
/ APPLICANT: Janice Au-Young
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
/ TITLE OF INVENTION: PATHWAY GENE EXPRESSION
/ NUMBER OF SEQUENCES: 1490
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/016,434
/ FILING DATE: HERewith
/ CLASSIFICATION:
/ Prior Application DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Zeller, Karen J.
/ REGISTRATION NUMBER: 37,071
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 845-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 91:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 279 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: LUNGPE103
/ CLONE: 1234795

US-09-016-434-91

Query Match 24.6%; Score 223; DB 4; Length 279;
Best Local Similarity 100.0%; Pred. No. 4.1e-68;
Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCCCATGATGATGATGAACTCAATTTGTTACTGAGAGGTTGTGCTCTGTGAA 60
DB 25 ATGCCCATGATGATGATGAACTCAATTTGTTACTGAGAGGTTGTGCTCTGTGAA 84
QY 61 AGTGAACGAAAAAGTGTCTTAATTTGATAGCCGCCCATTTTGTGAATACATCATCC 120
DB 85 AGTGAACGAAAAAGTGTCTTAATTTGATAGCCGCCCATTTTGTGAATACATCATCC 144
QY 121 CACATTTTGAAGCATTATATATCACTGCTCCAGCTTATGAGCGAAGTTGCAACAG 180
DB 145 CACATTTTGAAGCATTATATATCACTGCTCCAGCTTATGAGCGAAGTTGCAACAG 204
QY 181 GACAAAGTGTATATATACAGAGCTCATCCAGCATTCAGCGAAAC 223
DB 205 GACAAAGTGTATATATACAGAGCTCATCCAGCATTCAGCGAAAC 247

RESULT 7

US-09-513-999C-3684/C

; Sequence 3684, Application US/09513999C

; Patent No. 6783961

; GENERAL INFORMATION:

; APPLICANT: Dumas Mline Edwards, J.B.

; APPLICANT: Ducleit, A.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6783961

; FILE REFERENCE: 59 US2, REG

; CURRENT APPLICATION NUMBER: US/09/513, 999C

; CURRENT FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 3684

; LENGTH: 378

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 216..377

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 164

; OTHER INFORMATION: k=g or t

US-09-513-999C-3684

Query Match 20.7%; Score 187.8; DB 4; Length 378;
Best Local Similarity 99.0%; Pred. No. 1.5e-55;
Matches 189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 44 TGTGGCTCTGTGGAAGTGAACGAAAAAGTCTCTAATTGATAGCCGCCATTG 103
DB 378 TGTGGCTCTGTGGAAGTGAACGAAAAAGTCTCTAATTGATAGCCGCCATTG 319
QY 104 TGAATACATATCAATCCCAATTTTGAAGCATTATATCAACGCTCCAAAGTTATGA 163
DB 318 TGAATACATATCAATCCCAATTTTGAAGCATTATATCAACGCTCCAAAGTTATGA 259
QY 164 AGCGAAGTTGCAACAGCAAAAGTGTATATACAGAGCTCATCCAGATTCAAGGAAC 223
DB 258 AGCGAAGTTGCAACAGCAAAAGTGTATATACAGAGCTCATCCAGATTCAAGGAAC 199
QY 224 ATAAAGTTGAC 234
DB 198 ATAAAGTTAAC 188

RESULT 8

US-09-557-921-1

; Sequence 1, Application US/09557921

; Patent No. 6551810

; GENERAL INFORMATION:

; APPLICANT: Lucie, Ralf M.

; APPLICANT: Wei, Bo

; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE

; FILE REFERENCE: 200125.416

; CURRENT APPLICATION NUMBER: US/09/557,921

; CURRENT FILING DATE: 2000-04-20

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1830

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-557-921-1

Query Match 13.8%; Score 124.6; DB 4; Length 1830;
Best Local Similarity 56.7%; Pred. No. 1.1e-32;
Matches 251; Conservative 0; Mismatches 189; Indels 3; Gaps 1;

QY 461 TTGCCAATGAGGCAACCCGAATCTTCCCAATCTTATCTTGGCTGCCAGGAGATG 520
DB 1036 TTGGAAGCTGAGCTGACCCCACTTCTCTCTTCTTCTTGGCAATGAGAGATG 1095
QY 521 TCTTCAACAGAGCTGATACAGCAAAATGGATTTGTATGTGTTAAATGCCACTATA 580
DB 1096 CTGAGACCTGAGACCAATGACAGCGGCTGAAACATGCGCTACATCAACGTCACACTC 1155
QY 581 CCTGCAACACCTGACTT---ATCCCGAGTCTCATTTCTGCTGCTGCTGAGATG 637
DB 1156 ATCTTCCCTTACCATATAGAAAGCTGTTCACATACAGCGCTGAGCACTG 1215
QY 638 ACAGCTTTGTGAGAAATTTGCGGTGTGGAACAAATCAGATGATTTCAATTGAGAAG 697
DB 1216 ACAGCAACAGCAAGCACTGCGGAGTACTTTGAAGAGCTTTGATGATGAGGAAG 1275
QY 698 CAAAGCTCCATGATGATGTGTTTCTAGTCACTGTTTACTGAGATCTCCGCTCGCA 757
DB 1276 CTACACAGTGTGGAAGGGGCTTCTCATCTGCACTGCGAGGCTGCGCGCA 1335
QY 758 CCATGCTATGCGCTCATCATATGAAGAGATGACATCTTTAGATGAAGTTACAT 817
DB 1336 CCATGCTATGCGCTCATCATATGAAGAGCACTGCGATGACATGATGATGATTAAT 1395
QY 818 TTGTGAAGAAAGAAAGCACTATATCTCCAACTTCAATTTTCTGCGCAACTCTGG 877
DB 1396 TTGTGAAGAAAGAAAGCACTATATCTCCAACTTCAATTTTCTGCGCAACTCTGG 1455
QY 878 ACTATGAGAGAGATTAAGAC 900
DB 1456 AGTTGAGAGAGACTTAAGAC 1478

RESULT 9

US-09-949-016-4617

; Sequence 4617, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: C1001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 4617
;; LENGTH: 2283
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-4617

Query Match 11.8%; Score 106.8; DB 4; Length 2283;
Best Local Similarity 55.3%; Pred. No. 2,7e-26;
Matches 229; Conservative 0; Mismatches 182; Indels 3; Gaps 1;

Qy 475 CCAACCCGAATTCCTTCCCAATCTTTATCTTGGCTGCCAGAGAGATGCTCAACAAGAG 534
Db CCGTCCAGATCTCTGCCCACTCTATCTGGGAGAGGCCGGGATTCGCCCAATTTGGAG 782
Qy 535 CTGATACAGAGATGGAGATGGTGTATGTCTTAATGCCAGCTATACCTGTCCAA--G 591
Db AGCCTGCCCAACTGGGCGATCCGCTACATCTCAATGTCAACCCCAACTCCCAACTTC 842
Qy 592 CCGACTTTATCCCGAGCTCATTTCCGCGTGCAGTGAATGACAGCTTTGTGAG 651
Db TTGAGAGAGATGTGATCTTCACTACAGAGATCCCATCTCCGACCACTGGAGCCAG 902
Qy 652 AAAATTTTGGCGTGTGACAAATCATGATTTTCATTGAGAAAGCAAAAGCTTCCAT 711
Db AACCTGTCCGGGCTCTTTCGAGGCGCATTTAGTTGATGAGGCTGTCTCCAGAAC 962
Qy 712 GGATGTCTTAGTGACATGTTAGTGGAGATCTCCGCTCCGCCACATGCTATGCGC 771
Db TGGGGGTGTCTGTCCACTGCTGTGGGGGTGACGGCGTGTGTACCTGTGCTGAGCC 1022
Qy 772 TACATCATGAAGAGATGACATGTCTTTAGATGAAGCTTACAGATTGTGAAAGAAA 831
Db TACCTCATGCAAGAGCTCCACCTCTCTCAACGAGTCTATGACTGTGCAAGAGAG 1082
Qy 832 AGACCTACTATATCTTCCAACTTCAATTTTCTGGGCAACTCTTGACTATGAG 885
Db AAGCTAACATCTCCCCCACTTCAACTTCATGAGGGGAGTGTGCTGACTTTGAG 1136

RESULT 10
US-09-922-146-3
; Sequence 3, Application US/09922146
; Patent No. 6566133
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowbert
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 9 EXPRESSION
; FILE REFERENCE: RTS-0252
; CURRENT APPLICATION NUMBER: US/09/922.146
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 3
; LENGTH: 2303
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (114) ... (1268)
US-09-922-146-3

Query Match 11.8%; Score 106.8; DB 4; Length 2303;
Best Local Similarity 55.3%; Pred. No. 2,7e-26;
Matches 229; Conservative 0; Mismatches 182; Indels 3; Gaps 1;

Qy 475 CCAACCCGAATTCCTTCCCAATCTTTATCTTGGCTGCCAGAGAGATGCTCAACAAGAG 534
Db CCGTCCAGATCTCTGCCCACTCTATCTGGGAGAGGCCGGGATTCGCCCAATTTGGAG 782
Qy 535 CTGATACAGAGATGGAGATGGTGTATGTCTTAATGCCAGCTATACCTGTCCAA--G 591

Db 783 AGCCTGCCCAACTGGGCGATCCGCTACATCTCTCAATGTCAACCCCAACTCCCAACTTC 842
Qy 592 CCGACTTTATCCCGAGCTCATTTCCGCGTGCAGTGAATGACAGCTTTGTGAG 651
Db TTGAGAGAGATGTGATCTTCACTACAGAGATCCCATCTCCGACCACTGGAGCCAG 902
Qy 652 AAAATTTTGGCGTGTGACAAATCATGATTTTCATTGAGAAAGCAAAAGCTTCCAT 711
Db AACCTGTCCGGGCTCTTTCGAGGCGCATTTAGTTGATGAGGCTGTGTCCAGAAC 962
Qy 712 GGATGTCTTAGTGACATGTTAGTGGAGATCTCCGCTCCGCCACATGCTATGCGC 771
Db TGGGGGTGTCTGTCCACTGCTGTGGGGGTGACGGGTTGTGTACCGTCACTGTGCGC 1022
Qy 772 TACATCATGAAGAGATGACATGTCTTTAGATGAAGCTTACAGATTGTGAAAGAAA 831
Db TACCTCATGCAAGAGCTCCACCTCTCTCAAGATCTCTATGACCTGTGCAAGAGAG 1082
Qy 832 AGACCTACTATATCTCCAACTTCAATTTTCTGGGCAACTCTTGACTATGAG 885
Db AAGCTAACATCTCCCCCACTTCAACTTCATGAGGGGAGTGTGCTGACTTTGAG 1136

RESULT 11
US-09-016-434-1135
; Sequence 1135, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Sellhammer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1135:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2109 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1418933
US-09-016-434-1135

Query Match 10.6%; Score 96.2; DB 4; Length 2109;
Best Local Similarity 53.8%; Pred. No. 1,4e-22;

	Matches	222;	Conservative	0;	Mismatches	188;	Indels	3;	Gaps	1.
Qy	484	ATTCTTCCCAATCTTTATCTTGSGCTGCCAGCGAGATGCTCTTCAACAGAGAGCTGATACG	543							
Db	979	ATCTTGCCCTTCCTTACTTGGGGCTGTGGCAAAAGACTCACCAACTTGGAGCGTGTGGAG	1038							
Qy	544	CAGAAATGGAGATTGGTTATGTGTTAAATGCGACGCTATACCTGTGCCAAAGC--CTGACTTT	600							
Db	1039	GAAATTCGGCATCAAGTACATCTTGAACGACCCCAATTTGSCGAATCTCTTTGAGAAC	1098							
Qy	601	ATCCCGGAGTCTCATTTCTCGGSGTGCTGTGAATGACAGCTTTTGTGAGAAAATTTTG	660							
Db	1099	GCAGAGAGGTTTAAATACAGCAAAATCCCACTCTCGGATCACTGAGGCCAAAACCTGTCC	1158							
Qy	661	CCGTGGTTGGACAATTCAGTAGATTTCATTGAGAAAGCAAAAGCTCCAGTAGATGTGT	720							
Db	1159	CAGTTTTTCCCTGAGGCCATTTCTTTCATAGATGAAGCCCGGGGCAAGAACTGTGCTGC	1218							
Qy	721	CTAGTGCACTGTTTATGCTGGGATCTCCGGCTCCGCAACATGCGATGCGCCATCATATG	780							
Db	1219	TTGGTACATTCGTTGGCTGGGCACTTAAGCCGCTCAAGTCACTGTGACTGTGGCTTAACCTTAATG	1278							
Qy	781	AAGAGGATGAGCATCTCTTTAGATGATGAAGCTTACAGATTGTGTGAAGAAAAAAGACCTACT	840							
Db	1279	CAGAACTCAATCTGTGCATGAGCGATGCTATGACATTTGTCAAAATGAAAAATTCACAC	1338							
Qy	841	ATATCTCAAACTTCAATTTTCTGGGGCAACCTCGGACTATGAGAAAGAAAT	893							
Db	1339	ATATCTCCCTTAATTCACTTCAATGAGGTCAAGCTGTGAGACTTTCGAGAGAGCGCT	1391							

```

1 RESULT 12
2 US-09-023-655--946
3 : Sequence 946, Application US/09023655
4 : Patent No. 6607879
5 :
6 : GENERAL INFORMATION:
7 :
8 : APPLICANT: Cocks, Benjamin G.
9 : APPLICANT: Susan G. Stuart
10 : APPLICANT: Jeffrey J. Sellhammer
11 : TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENES
12 : TITLE OF INVENTION: EXPRESSION
13 : NUMBER OF SEQUENCES: 1508
14 :
15 : CORRESPONDENCE ADDRESS:
16 : ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
17 : STREET: 3174 PORTER DRIVE
18 : CITY: PALO ALTO
19 : STATE: CALIFORNIA
20 : COUNTRY: USA
21 : ZIP: 94304
22 :
23 : COMPUTER READABLE FORM:
24 : MEDIUM TYPE: FLOPPY disk
25 : COMPUTER: IBM PC compatible
26 : OPERATING SYSTEM: PC-DOS/MS-DOS
27 : SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
28 : CURRENT APPLICATION DATA:
29 : APPLICATION NUMBER: US/09/023.655
30 : FILING DATE: HERewith
31 : CLASSIFICATION:
32 : PRIOR APPLICATION DATA:
33 : APPLICATION NUMBER:
34 : FILING DATE:
35 : CLASSIFICATION:
36 : ATTORNEY/AGENT INFORMATION:
37 : NAME: Zeller, Karen J.
38 : REGISTRATION NUMBER: 37,071
39 : REFERENCE/DOCKET NUMBER: PA-0001 US
40 : TELECOMMUNICATION INFORMATION:
41 : TELEPHONE: (650) 855-0555
42 : TELEFAX: (650) 845-4166
43 : INFORMATION FOR SEQ ID NO: 946:
44 : SEQUENCE CHARACTERISTICS:
45 : LENGTH: 2109 base pairs
46 : TYPE: nucleic acid
47 :

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; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1418933
;
US-09-023-655-946

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Query Match	10.6%	Score 96.2	DB 4	Length 2109
Best Local Similarity	53.8%	Pred. No. 1.4e-22		
Matches 222; Conservative	0	Mismatches 188	Indels 3	Gaps 1

Qy	484	ATTCTCCCAATCTTTAACTTGGCTGGCCAGGAGATGCTTCACAAGAAGCTGTATACG	543
Db	979	ATCTTGCCCTTCTCTACTTGGGCTGTGSCCAAAAGCTCACCACTTGGACGTGTGGAG	1033
Qy	544	CAGATGGGATTTGTTATGTAAATGCCAGCTATATACCTGTCCAAAGC--CTGACTTT	600
Db	1039	GAATTCGGCATCAAGTACACTTGAAGGTCAACCCCAATTGGCCGAATCTTTTAGAAC	1099
Qy	601	ATCCCCGAGTCTCATTTCTTCGCTGTGCTGTGAATGACAGTTTGTGAGAAATTTTG	660
Db	1099	GCAGAGAGTGTAAATACAMACAAATCCCACTTCGATCACTGAGGCCAAACCTGTCC	1156
Qy	661	CCGTGGTTGACAATCAGTAGATTTCACTTAGAGAAAGAAAAGCTCCAAATGATGTGTT	720
Db	1159	CAGTTTTTCCCTGAGGCCATTTCTTTCAATAGATGAAGCCGGGGCAAGATCTGTGTGTC	1211
Qy	721	CTAGTGCACGTGTTAGCTGGGATCTCCGCTCCGCACATCTCGCTATCGCTTACATATG	780
Db	1219	TTGGTACATTTGCTTGGCTGGCATTAAGCGCTCAGTCACTGTGACCTGTGGCTTACTTATG	1276
Qy	781	AAGAGATGACATGCTCTTTAGATGAAGCTTACAGATTTGTGAAGAAAAGAAAGACTTACT	840
Db	1279	CAGAGGCTCAATCTGTGCATGAAGAGATCCTATGACATGTGCAAAATGAAAAAATCCAAC	1338
Qy	841	ATATCTCCAACTTCAATTTCTTGGGCCAATCTCGTGCATATGAGAAAGAT	893
Db	1339	ATATCTCCCACTTCACTTATAGGTCAGTCTGTGACCTTCGAGAGGACGCT	1391

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RESULT 13
US-09-949-016-2615
; Sequence 2615, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CITE REFERENCE: C001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2615
; LENGTH: 2475
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2615

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	Query Match	Best Local Similarity	Matches	Score	Pred.	No.	Mismatches	Indels	Gaps	Length
	10.6%	53.8%	222	96.2	1.66	22	188	3	1	2475
Oy	484	ATTCTTCCCAATCTTTATCTTGGCTGCCAGCATGTCTCTCAACAGGAGCTGATACG	543							
Db	1068	ATCTTGCCCTTCTCTCTACTGGGCGCTGGGCCAAGATCTCAACATCTGGAAGCTGTGGAG	1127							

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QY 544 CAGATGGGATTGGTAAATGTTAAATGCCAGCTATACCTGTCACAAAGC---CTGACTTT 600
Db 1128 GAATTCGGCATCAATGATTCATTTGACGTACACCCCAATTTGCCAATCTCTTGTGGAAC 1187
QY 601 ATCCCGAGTCTCATTTCTGCGTGGTGGCTGTGTAAGTACAGCTTTTGTGAAAATTTTG 660
Db 1188 GCAGAGAGTTTAAATACAGCAAAATCCCATCTCGATCATCTGAGACAAAACCTGTGC 1247
QY 661 CCGTGTGTGACAAATCAGTATGATTTGATGAAAGCAAAAGCTTCACATGATGTGT 720
Db 1248 CAGTTTTTCCCTGAGGCAATTTCTTTATAGATGAAAGCCCGGAGCAAGACTGTGTGTC 1307
QY 721 CTAGTGCAGTGTGTTAGCTGGAGATCTCCGCTCCGCCACCATCCCTATCCGCTACATG 780
Db 1308 TTGTTACATTTGCTGTGGCTGAGCATTAAGCCGCTCAGTCACTGTGACTGTGCTTACCTTA 1367
QY 781 AAGAGATGACATGCTTTAGATGAAAGCTTACAGATTTGTGAAAAGAAAAGACCTTACT 840
Db 1368 CAGAGCTCATCTGCTGATGAACGATGCTATGACATGTCAAATGAAAATATCAAC 1427
QY 841 ATATCTCCAACTCAATTTTCTGGCCAACTCCTGGAATGAGAAAGAT 893
Db 1428 ATATCCCTTAATCTCAATCTGAGGTCACTGTGACTTGGAGAGACGCT 1480

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RESULT 14
US-09-023-655-347
; Sequence 347, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhammer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSER: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; CLASSIFICATION:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 347:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1208 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THYROT03
; CLONE: 1444245
US-09-023-655-347

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Query Match 10.4%; Score 94.6; DB 4; Length 1208;
Best Local Similarity 64.3%; Pred. No. 3,4e-22;
Matches 142; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
QY 680 TAGATTTCATGAGAAACAAAGCTTCATGATGTGTTCTAGTGCACTGTTAGCTG 739
Db 4 TTGAGTTCAATGAGAAAGCACTCAGCAGTGTGGAAAGGGCTTCTATCCACTGCCAGGCTG 63
QY 740 GGATCTCCGCTCCGCCACCATCTATCCGCTTACATCATGAAAGAGATGACATGTCTT 799
Db 64 GGGTGTCCGCTCCGCCACCATCTATCCGCTTACATCATGAAAGAGCACTCGATGACCA 123
QY 800 TAGATGAGCTTACAGATTTGTGAAAAGAAAAGACCTTACTATATCTCCAACTTCAAT 859
Db 124 TGACTGATGCTTAAATTTGTCAAAGGCAAAACAGCAATATATCTCCCAACTTAAT 183
QY 860 TTCTGGGCCAACTCCTGGAATGAGAAAGATTAAGAAC 900
Db 184 TCATGGGCACTTCTAGAGTTTGAGGAGAGACCTTAACCAAC 224

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RESULT 15
US-09-702-705-801
; Sequence 801, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Derrick
; APPLICANT: Reiter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121,478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; NUMBER OF SEQ ID NOS: 2000-10-30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 801
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-801

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Query Match 10.1%; Score 91.6; DB 4; Length 1619;
Best Local Similarity 53.2%; Pred. No. 4,9e-21;
Matches 218; Conservative 0; Mismatches 189; Indels 3; Gaps 1;
QY 484 ATTTCTCCCAATCTTATCTTGGCTGCCAGAGATGTCCTCAACAGAGCTGATACG 543
Db 320 ATCTCTCCCTTCTTACTCTCGCAGTGCTTCAATGCTGCGGAGAGACATGTGAC 379
QY 544 CAGATGAGATTTGTATGTTAATGCCAGCTTATCTGTCCAAAGCTGACTTATC 603
Db 380 GCCCTGGGATCAGGCGCTGTGTAATGTCTCTGAGCTGCCAACC---ACTTTGAA 436
QY 604 CCGAGTCTATTTCTCGTGGTGGCTGTGAATGACACCTTTTGTGAAAATTTTGGCG 663
Db 437 GGACACTATCAGTACAGATGATCCCATGTGAAGATTAACCAAGGCCGATCAGCTCC 496
QY 664 TGGTTGACAAATTCATGATTTCACTTGAAGAAAGCAAGCTCCAAATGATGTGTTCTA 723
Db 497 TGGTTCAAGAGCCATCAGATCATGATGCCGTGAAGAGACTGCCGTGGCGGTGCTG 556
QY 724 GTGACGTGTTAGCTGGAGATCTCCGCTCCGCCACCATCGCTATCTGCTACATATGAG 783
Db 557 GTGCACTCCAGGCGGAGATCTCGGCTGGGCCACCATCTGCTGCTTACTGATGATG 616

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QY 784 AGATGACATGCTTTAGATGAAGCTTACAGATTGTGAAGAAAAAGACTTACTATA 843
Db 617 AAGAAACGGGTGAGGCTGAGAGAGGCTTCGAGTTGTTAAGCAGCGCCGAGCATATAC 676
QY 844 TCTCAAACTTCAATTTCTGGGCCCACTCCTGGACTATGAGAAAGAT 893
Db 677 TCGCCCAACTTCAGCTTCATGAGGCGAGCTGCGAGTTCGAGTCCAGAT 726

Search completed: February 15, 2005, 11:51:07
Job time : 164.961 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	902.8	99.6	1998	9	US-09-616-494-3	Sequence 3, Appli
2	902.8	99.6	1998	17	US-10-377-072-27	Sequence 27, Appli
3	902.8	99.6	1998	18	US-10-377-072-27	Sequence 27, Appli
4	902.8	99.6	2071	17	US-10-072-012-57	Sequence 257, Appli
5	902.8	99.6	2732	17	US-10-168-506-2	Sequence 2, Appli
6	902.8	99.6	3059	17	US-10-257-026-1	Sequence 1, Appli
7	902.8	99.6	3466	9	US-09-964-277-1	Sequence 1, Appli
8	902.8	99.6	3521	18	US-10-370-7158-.261	Sequence 261, Appli
9	902.8	99.6	3544	9	US-09-616-494-1	Sequence 1, Appli
10	902.8	99.6	3544	17	US-10-377-072-25	Sequence 25, Appli
11	902.8	99.6	3544	18	US-10-377-072-25	Sequence 25, Appli

12	902.8	99.6	3625	17	US-10-425-114-26234	Sequence 26234, A
13	902.8	99.6	3766	17	US-10-433-357-17	Sequence 17, A
14	902.8	99.6	4790	18	US-10-648-593-115	Sequence 115, App
15	902.8	99.6	5145	18	US-10-357-930-20824	Sequence 20824, A
16	902.8	99.6	5145	18	US-10-357-930-20969	Sequence 20969, A
17	902.8	99.6	5145	18	US-10-357-930-21071	Sequence 21071, A
18	902.8	99.6	5145	18	US-10-357-930-21083	Sequence 21083, A
19	902.8	99.6	5145	18	US-10-357-930-21303	Sequence 21303, A
20	902.8	99.6	5145	18	US-10-357-930-21307	Sequence 21307, A
21	902.8	99.6	5145	18	US-10-357-930-22820	Sequence 22820, A
22	902.8	99.6	5145	18	US-10-357-930-26669	Sequence 26669, A
23	902.8	99.6	5145	18	US-10-357-930-26815	Sequence 26815, A
24	902.8	99.6	5145	18	US-10-357-930-26912	Sequence 26912, A
25	902.8	99.6	5145	18	US-10-357-930-26923	Sequence 26923, A
26	902.8	99.6	5145	18	US-10-357-930-27145	Sequence 27145, A
27	902.8	99.6	5145	18	US-10-357-930-27149	Sequence 27149, A
28	902.8	99.6	5145	18	US-10-357-930-27149	Sequence 28155, A
29	901.2	99.5	2102	17	US-10-094-749-673	Sequence 673, App
30	899.6	99.3	2966	17	US-10-826-115-520	Sequence 520, App
31	817.8	90.3	2200	17	US-10-072-012-255	Sequence 255, App
32	554.8	62.3	3332	9	US-09-964-277-20	Sequence 20, App
33	411.2	45.4	418	18	US-10-357-930-11243	Sequence 11243, A
34	410.2	45.3	461	18	US-10-357-930-32416	Sequence 32416, A
35	410.2	45.3	461	18	US-10-357-930-41000	Sequence 41000, A
36	410.2	45.3	461	18	US-10-357-930-41346	Sequence 41346, A
37	395.4	43.6	427	18	US-10-357-930-10878	Sequence 10878, A
38	363.6	40.1	2453	13	US-10-005-858-1	Sequence 1, App
39	359.8	39.7	419	18	US-10-357-930-32060	Sequence 32060, A
40	349	38.5	422	18	US-10-357-930-2074	Sequence 2074, App
41	340.8	37.6	346	18	US-10-357-930-11236	Sequence 11236, A
42	339.8	37.5	345	18	US-10-357-930-2067	Sequence 2067, App
43	338.8	37.4	377	18	US-10-357-930-32409	Sequence 32409, A
44	338.8	37.4	377	18	US-10-357-930-41339	Sequence 41339, A
45	335.8	37.1	2476	17	US-10-220-120-28	Sequence 28, App

ALIGNMENTS

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US-09-816-494-3
RESULT 1
Sequence 3, Application US/09816494
Patent No. US20020034807A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 38692 AND 21117, NOVEL
FILE OF INVENTION: PROSPATHISE MOLECULE
TITLE REFERENCE: 10448 -030002
CURRENT APPLICATION NUMBER: US/09/816,494
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,858
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows
VERSION 4.0.
SEQ ID NO 3
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens
US-09-816-494-3

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	Query Match	99.6%	Score 902.8	DB 9	Length 1998
	Best Local Similarity	99.8%	Pred. No. 3.4e-280		
	Matches 904	Conservative 0	Mismatches 2	Indels 0	Gaps 0
Qy	1	ATGGCCCATGAGATGATTTGGAACCTCAATTCTTACTGAGAGTTGGTGGCTCGCTGGAA	60		
Db	1	ATGGCCCATGAGATGATTTGGAACCTCAATTCTTACTGAGAGTTGGTGGCTCGCTGGAA	60		
Qy	61	AGTGAACGGAAAAAGTGTCTTAATTGATAGCGGCCCATTTGTGGAATACATCATCC	120		
Db	61	AGTGAACGGAAAAAGTGTCTTAATTGATAGCGGCCCATTTGTGGAATACATCATCC	120		
Qy	121	CACATTTTGGAGCCATTATATATCACTGCTCCAGCTTATGAAAGCAAGTTGCACAG	180		

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: FILE REFERENCE: MP103-0180NM1M
: CURRENT APPLICATION NUMBER: US/10/377,072
: CURRENT FILING DATE: 2003-02-27
: PRIOR APPLICATION NUMBER: US 09/895,860
: PRIOR FILING DATE: 2001-06-29
: PRIOR APPLICATION NUMBER: US 60/215,370
: PRIOR FILING DATE: 2000-06-29
: PRIOR APPLICATION NUMBER: US 09/723,806
: PRIOR FILING DATE: 2000-11-28
: PRIOR APPLICATION NUMBER: US 60/187,455
: PRIOR FILING DATE: 2000-03-07
: PRIOR APPLICATION NUMBER: US 09/643,297
: PRIOR FILING DATE: 2001-04-25
: PRIOR APPLICATION NUMBER: US 60/199,801
: PRIOR FILING DATE: 2000-04-26
: PRIOR APPLICATION NUMBER: US 09/861,801
: PRIOR FILING DATE: 2001-05-21
: PRIOR APPLICATION NUMBER: US 60/205,508
: PRIOR FILING DATE: 2000-05-19
: PRIOR APPLICATION NUMBER: US 09/816,494
: PRIOR FILING DATE: 2001-03-23
: PRIOR APPLICATION NUMBER: US 09/815,419
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 114
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 27
: LENGTH: 1998
: TYPE: DNA
: ORGANISM: Homo Sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1) ... (1998)
US-10-377-072-27

Query Match          99.6%; Score 902.8; DB 17; Length 1998;
Best Local Similarity 99.8%; Pred. No. 3.4e-280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY      1 ATGGCCATGATGATATTGGAACCTAAATTGTTACTGAGAGTTGCTGCTGGA 60
DB      1 ATGGCCATGAGATGATTTGGAACCTAAATTGTTACTGAGAGTTGCTGCTGGA 60
QY      61 AGTGAACGAAAAAAGTCTGCTAATTATGATGACCGGCCATTGTTGGAATACAATCATCC 120
DB      61 AGTGAACGAAAAAAGTCTGCTAATTATGATGACCGGCCATTGTTGGAATACAATCATCC 120
QY      121 CACATTTGGAAGCCATTATATCATCACTGCTCCAGCTTATGAACGAAGTTGCACAG 180
DB      121 CACATTTGGAAGCCATTATATCATCACTGCTCCAGCTTATGAACGAAGTTGCACAG 180
QY      181 GACAAAGGTTAATTAACGAGCTCATCAGATTCAGGAAACATPAAGTTGACATTGAT 240
DB      181 GACAAAGGTTAATTAACGAGCTCATCAGATTCAGGAAACATPAAGTTGACATTGAT 240
QY      241 TGCAGTCAGAAAGTTGATGTTTACGATCAAAAGTCCCAAGATGTGCTCTCTTCA 300
DB      241 TGCAGTCAGAAAGTTGATGTTTACGATCAAAAGTCCCAAGATGTGCTCTCTTCA 300
QY      301 GACGTGTTTCTCATCTGTACTTTGAGGTTAACTGGAAGAAAGCTTCAACTCTGTTCACCTG 360
DB      301 GACGTGTTTCTCATCTGTACTTTGAGGTTAACTGGAAGAAAGCTTCAACTCTGTTCACCTG 360
QY      361 CTTGACAGTGGGTTTGCTGAGTTCTCTCGATGTGTTTCCCTGGCCCTGTGGAAGAAATTC 420
DB      361 CTTGACAGTGGGTTTGCTGAGTTCTCTCGATGTGTTTCCCTGGCCCTGTGGAAGAAATTC 420
QY      421 ACTCTAGTCCCTACCTGSCATTTTTCGAGCTTGTCTTACCTGTGGCAACATTTGGGCAAC 480
DB      421 ACTCTAGTCCCTACCTGSCATTTTTCGAGCTTGTCTTACCTGTGGCAACATTTGGGCAAC 480
QY      481 CGAATTCCTCCCAATCTTTATCTTGGTGTGCAAGAAATGCTTCAACAGAGCTGATA 540

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Db      481  GGAATCTTCCCAACTTATCTT66CTGCGACGAGATGTCOTCAAGAGGCTGATG 540
Qy      541  CAGCAGAAATGGGATGGTTATGTGTTAAATGCCAGCTATACCTGTCCAAAGCCTGACTTT 600
Db      541  CAGCAGAAATGGGATGGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTGACTTT 600
Qy      601  ATCCCGGAGTCATTTCTCGGCTGCGCTGGAATGAACAGCTTTTGTGAGAAATTTTG 660
Db      601  ATCCCGGAGTCATTTCTCGGCTGCGCTGGAATGAACAGCTTTTGTGAGAAATTTTG 660
Qy      661  CCGTGGTTGAGCAAAATCAGTAGATTTTCATTGAGAAAAGCAAAAGCCTCAATGATGTGTT 720
Db      661  CCGTGGTTGAGCAAAATCAGTAGATTTTCATTGAGAAAAGCAAAAGCCTCAATGATGTGTT 720
Qy      721  CTAGTGCACTGTTTAGTGGGATCTCCGCTCCGCCACCATGCTATGCTTACATCATG 780
Db      721  CTAGTGCACTGTTTAGTGGGATCTCCGCTCCGCCACCATGCTATGCTTACATCATG 780
Qy      781  AAGAGGATGACATCTCTTTAGATGAAGTTACAGATTTGTGTAAGAAAAAGACCTACT 840
Db      841  ATATCTCCAAACTTCAATTTTCTGGGCCCACTCTGACATATGAGAAAGATTAAGAAC 900
Qy      901  CAGACT 906
Db      901  CAGACT 906

RESULT 3
US-10-377-072-27
: Sequence 27, Application US/10377072
: Publication No. US20040157221A9
GENERAL INFORMATION:
: APPLICANT: Millennium Pharmaceuticals Inc.
: APPLICANT: Cutlis, Rory A.J.
: APPLICANT: Logan, Thomas Joseph
: APPLICANT: Glucksmann, Maria A.
: APPLICANT: Meyers, Rachel E.
: APPLICANT: Williamson, Mark J.
: APPLICANT: Rudolph-Owen, Laura A.
: APPLICANT: Tsai, Fong-Ying
: TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117.
: TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
: TITLE OF INVENTION: AND USES THEREFOR
: FILE REFERENCE: MPI03-0180MNIM
: CURRENT APPLICATION NUMBER: US/10/377,072
: CURRENT FILING DATE: 2003-02-27
: PRIOR APPLICATION NUMBER: US 09/895,860
: PRIOR FILING DATE: 2001-06-29
: PRIOR APPLICATION NUMBER: US 60/215,370
: PRIOR FILING DATE: 2000-06-29
: PRIOR APPLICATION NUMBER: US 09/723,806
: PRIOR FILING DATE: 2000-11-28
: PRIOR APPLICATION NUMBER: US 60/187,455
: PRIOR FILING DATE: 2000-03-07
: PRIOR APPLICATION NUMBER: US 09/843,297
: PRIOR FILING DATE: 2001-04-25
: PRIOR APPLICATION NUMBER: US 60/199,801
: PRIOR FILING DATE: 2000-04-26
: PRIOR APPLICATION NUMBER: US 09/861,801
: PRIOR FILING DATE: 2001-05-21
: PRIOR APPLICATION NUMBER: US 60/205,508
: PRIOR FILING DATE: 2000-05-19
: PRIOR APPLICATION NUMBER: US 09/816,494
: PRIOR FILING DATE: 2001-03-23
: PRIOR APPLICATION NUMBER: US 09/815,419
: PRIOR FILING DATE: 2001-03-22
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 114

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; SOFTWARE:FastSeq for Windows Version 4.0
; SEQ ID NO: 27
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (1998)
; US-10-377-072-27

Query Match      99.6%; Score 902.8; DB 18; Length 1998;
Best Local Similarity 99.8%; Pred. No. 3.4e-280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY      1 ATGCCCCATGAGATGATGTTGAACTCAATTGTTACTGAGAGGTGGTGGCTTGCTGGAA 60
DB      1 ATGCCCCCATGAGATGATGTTGAACTCAATTGTTACTGAGAGGTGGTGGCTTGCTGGAA 60
QY      61 AGTGAACCGGAAAAAAGTGCCTCTAATTGATGCGCGCAATTGTGTGAATAACAATCATCC 120
DB      61 AGTGAACCGGAAAAAAGTGCCTCTAATTGATGCGCGCAATTGTGTGAATAACAATCATCC 120
QY      121 CACATTTTGAAGCCATTAATATCAACTGCTCCACAGCTTATGACGAAAGTTGCAACAG 180
DB      121 CACATTTTGAAGCCATTAATATCAACTGCTCCACAGCTTATGACGAAAGTTGCAACAG 180
QY      181 GACAAAGTGTAAATTAACAAGCTCATCCAGCAATTGACGGAAACATPAAGTTGACATGAT 240
DB      181 GACAAAGTGTAAATTAACAAGCTCATCCAGCAATTGACGGAAACATPAAGTTGACATGAT 240
QY      241 TGCAGTCAAGAGTTTGTAGTTTACGATCAAAAGCTCCCAAGATGTGCTCTCTCTTCA 300
DB      241 TGCAGTCAAGAGTTTGTAGTTTACGATCAAAAGCTCCCAAGATGTGCTCTCTCTTCA 300
QY      301 GACGTTTTCTCACTGTACTCTGGGTAACTGGAAGAGCTTCACTCTGTACCTG 360
DB      301 GACGTTTTCTCACTGTACTCTGGGTAACTGGAAGAGCTTCACTCTGTACCTG 360
QY      361 CTTCAGGTGGGTGTGCTGAGTTCTCTGTTGTTCCCTGGCTCTGTGAAGAAAAATCC 420
DB      361 CTTCAGGTGGGTGTGCTGAGTTCTCTGTTGTTCCCTGGCTCTGTGAAGAAAAATCC 420
QY      421 ACTCTAGTCCCTACCTGCAATTTCTGACCTTGCTTACCTGTGTGCAACATTGGGCCAAC 480
DB      421 ACTCTAGTCCCTACCTGCAATTTCTGACCTTGCTTACCTGTGTGCAACATTGGGCCAAC 480
QY      481 CGAATTCCTCCCAATCTTTAATCTTGGCGCGACGAGATGTCCTCAACAAGAGCTGAT 540
DB      481 CGAATTCCTCCCAATCTTTAATCTTGGCGCGACGAGATGTCCTCAACAAGAGCTGAT 540
QY      541 CAGCAGAAATGGGAATGGTATGTGTAAATGCGACAGTAACTGTCACAAAGCTGACTTT 600
DB      541 CAGCAGAAATGGGAATGGTATGTGTAAATGCGACAGTAACTGTCACAAAGCTGACTTT 600
QY      601 ATCCCGAGTCTCAATTTCTGCGGTGCTGTAATGACAGCTTTGTGAGAAAAATTTTG 660
DB      601 ATCCCGAGTCTCAATTTCTGCGGTGCTGTAATGACAGCTTTGTGAGAAAAATTTTG 660
QY      661 CCGTGTGTGGAACAATCAGTGAATTTCAATTGAGAAAGCAAAAGCTCCCAATGAGTGT 720
DB      661 CCGTGTGTGGAACAATCAGTGAATTTCAATTGAGAAAGCAAAAGCTCCCAATGAGTGT 720
QY      721 CTAGTGCACGTATTAGCTGGAGATCTCCCGCTCCGCAACATGCGTATGCGCTTACATC 780
DB      721 CTAGTGCACGTATTAGCTGGAGATCTCCCGCTCCGCAACATGCGTATGCGCTTACATC 780
QY      781 AAGAGATGACATGCTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGACTTACT 840
DB      781 AAGAGATGACATGCTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAAAGACTTACT 840
QY      841 ATATCTCCAAACTTCAATTTCTGGGCCCACTCTCGACATGAGAAAGATTAAAGAC 900
DB      841 ATATCTCCAAACTTCAATTTCTGGGCCCACTCTCGACATGAGAAAGATTAAAGAC 900

```


APPLICANT: HILL, RON
APPLICANT: FLANAGAN, PETER
TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
FILE REFERENCE: 038602/1351
CURRENT APPLICATION NUMBER: US/10/168,506
CURRENT FILING DATE: 2002-06-21
PRIORITY APPLICATION NUMBER: PCT/US00/34736
PRIORITY FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 2732
TYPE: DNA
ORGANISM: Homo sapiens
US-10-168-506-2

Query Match 99.6%; Score 902.8; DB 17; Length 2732;
Best Local Similarity 99.8%; Pred. No. 4.1e-280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGGCCCATGAGATGATTTGAACCTCAAAATTTGTTACTGAGAGGTTGGTGGCTGTGCTGAA 60
538 ATGGCCCATGAGATGATTTGAACCTCAAAATTTGTTACTGAGAGGTTGGTGGCTGTGCTGAA 597
61 AGTGAACGGAAGAAAGTCTGCTAATTGATAGCCGGCCATTGTGGAATACATATCATCC 120
598 AGTGAACGGAAGAAAGTCTGCTAATTGATAGCCGGCCATTGTGGAATACATATCATCC 657
121 CACATTTTGAAGCCATTAAATATCACTGCTCCAAAGCTTTATGAGCGGAAGTTGCAACAG 180
658 CACATTTTGAAGCCATTAAATATCACTGCTCCAAAGCTTTATGAGCGGAAGTTGCAACAG 717
181 GACAAAGTGTAAATTATGAGAGCTCATCGAGATTCAGGAAACATAAGTTGACATTGAT 240
718 GACAAAGTGTAAATTATGAGAGCTCATCGAGATTCAGGAAACATAAGTTGACATTGAT 777
241 TGCACTGAGAAAGTTGATGATTAAGATCAAGCTCCCAAGATGTTGCTCTCTCTTCA 300
778 TGCACTGAGAAAGTTGATGATTAAGATCAAGCTCCCAAGATGTTGCTCTCTCTTCA 837
301 GACTGTTTCTCACTGTAATCTTGAGTAACTGGAAGAGCTTCACTTGTTCACCTG 360
838 GACTGTTTCTCACTGTAATCTTGAGTAACTGGAAGAGCTTCACTTGTTCACCTG 897
361 CTTCAGAGTGGGTTTGTGATGATCTCTGTTGTTCCCTGGCCCTGTGGAAGGAAATCC 420
898 CTTCAGAGTGGGTTTGTGATGATCTCTGTTGTTCCCTGGCCCTGTGGAAGGAAATCC 957
421 ACTCTAGTCCCTACCTGATTTCTCAGGCTTGCTTACCTGTTGCCAATTGGGCAACC 480
958 ACTCTAGTCCCTACCTGATTTCTCAGGCTTGCTTACCTGTTGCCAATTGGGCAACC 1017
481 CGAATTTCTCCCAATCTTTATCTTGAGCTGCAAGGAGATGCTTCAACAGAGCTGATA 540
1018 CGAATTTCTCCCAATCTTTATCTTGAGCTGCAAGGAGATGCTTCAACAGAGCTGATA 1077
541 CAGAGAAATGGGATTTGTTATGTTAAATGCAAGTATACCTGTCCAAAGCTTGACTT 600
1078 CAGAGAAATGGGATTTGTTATGTTAAATGCAAGTATACCTGTCCAAAGCTTGACTT 1137
601 ATCCCCGAGTCTCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
1138 ATCCCCGAGTCTCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1197
661 CCGTGTGTTGAACAATCAGTATGATTTCAATGAAAGCAAAAGCCCTCCATGATGTT 720
1198 CCGTGTGTTGAACAATCAGTATGATTTCAATGAAAGCAAAAGCCCTCCATGATGTT 1257
721 CTAATGCACTGTTTATGCTGGGATCTCCGGCTCCGCAACATGCTATGCTTACATCATG 780
1258 CTAATGCACTGTTTATGCTGGGATCTCCGGCTCCGCAACATGCTATGCTTACATCATG 1317
781 AAGAGATGACATGCTTTATGATGAGCTTACAGATTTGTGAAAGAAAGAAAGCTTACT 840

1318 AAGAGATGACATGCTTTATGATGAGCTTACAGATTTGTGAAAGAAAGAAAGCTTACT 1377
841 ATATCTCAAACTCAATTTCTGGGCGCACTCCGCACTATGAGAGAAGTTAAGAAC 900
1378 ATATCTCAAACTCAATTTCTGGGCGCACTCCGCACTATGAGAGAAGTTAAGAAC 1437
901 CAGACT 906
1438 CAGACT 1443

RESULT 6
US-10-257-026-1
Sequence 1, Application US/10257026
Publication No. US2004008659A1

GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
TITLE OF INVENTION: New dual specificity phosphatase
FILE REFERENCE: DUSP10XDS
CURRENT APPLICATION NUMBER: US/10/257,026
CURRENT FILING DATE: 2003-11-07
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 3059
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (127)..(12121)
US-10-257-026-1

Query Match 99.6%; Score 902.8; DB 17; Length 3059;
Best Local Similarity 99.8%; Pred. No. 4.3e-280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGGCCCATGAGATGATTTGAACCTCAAAATTTGTTACTGAGAGGTTGGTGGCTGTGCTGAA 60
127 ATGGCCCATGAGATGATTTGAACCTCAAAATTTGTTACTGAGAGGTTGGTGGCTGTGCTGAA 186
61 AGTGAACGGAAGAAAGTCTGCTAATTGATAGCCGGCCATTGTGGAATACATATCATCC 120
187 AGTGAACGGAAGAAAGTCTGCTAATTGATAGCCGGCCATTGTGGAATACATATCATCC 246
121 CACATTTTGAAGCCATTAAATATCACTGCTCCAAAGCTTTATGAGCGGAAGTTGCAACAG 180
247 CACATTTTGAAGCCATTAAATATCACTGCTCCAAAGCTTTATGAGCGGAAGTTGCAACAG 306
181 GACAAAGTGTAAATTATGAGAGCTCATCGAGATTCAGGAAACATAAGTTGACATTGAT 240
307 GACAAAGTGTAAATTATGAGAGCTCATCGAGATTCAGGAAACATAAGTTGACATTGAT 366
241 TGCACTGAGAAAGTTGATGATTAAGATCAAGCTCCCAAGATGTTGCTCTCTCTTCA 300
367 TGCACTGAGAAAGTTGATGATTAAGATCAAGCTCCCAAGATGTTGCTCTCTCTTCA 426
301 GACTGTTTCTCACTGTAATCTTGAGTAACTGGAAGAGCTTCACTTGTTCACCTG 360
427 GACTGTTTCTCACTGTAATCTTGAGTAACTGGAAGAGCTTCACTTGTTCACCTG 486
361 CTTCAGAGTGGGTTTGTGATGATCTCTGTTGTTCCCTGGCCCTGTGGAAGGAAATCC 420
487 CTTCAGAGTGGGTTTGTGATGATCTCTGTTGTTCCCTGGCCCTGTGGAAGGAAATCC 546
421 ACTCTAGTCCCTACCTGATTTCTCAGGCTTGCTTACCTGTTGCCAATTGGGCAACC 480
547 ACTCTAGTCCCTACCTGATTTCTCAGGCTTGCTTACCTGTTGCCAATTGGGCAACC 606
481 CGAATTTCTCCCAATCTTTATCTTGAGCTGCAAGGAGATGCTTCAACAGAGCTGATA 540
607 CGAATTTCTCCCAATCTTTATCTTGAGCTGCAAGGAGATGCTTCAACAGAGCTGATA 666

QY 541 CAGCAGAAATGGAGATGGTATGTTAAATGCGACGATATACCTGTCCAAAGCCGACTTT 600
 Db 667 CAGCAGAAATGGAGATGGTATGTTAAATGCGACGATATACCTGTCCAAAGCCGACTTT 726
 QY 601 ATCCCGAAGTCTATTTCTCGCTGCTGTGTGATGACAGCTTTTGTGAAAATTTTG 660
 Db 727 ATCCCGAAGTCTATTTCTCGCTGCTGTGTGATGACAGCTTTTGTGAAAATTTTG 786
 QY 661 CCGTGTGGACAAATCAGTAGATTTTCAATTGAGAAAGCAAAAGCTCCCAATGATGTT 720
 Db 787 CCGTGTGGACAAATCAGTAGATTTTCAATTGAGAAAGCAAAAGCTCCCAATGATGTT 846
 QY 721 CTAGTGACCTGTTTACCTGGAGATCTCCGCTCCGCAACATCCCTATCCGCTACATCAG 780
 Db 847 CTAGTGACCTGTTTACCTGGAGATCTCCGCTCCGCAACATCCGCTATCCGCTACATCAG 906
 QY 781 AAGAGATGACATGCTTATGATGAGCTTACAGATTTGTGAAAAGAAAGACTTACT 840
 Db 907 AAGAGATGACATGCTTATGATGAGCTTACAGATTTGTGAAAAGAAAGACTTACT 966
 QY 841 ATATCTCAAACTTCAATTTTCTGGGCCAACTCTGGAATGAGAAAGATTAAAGAC 900
 Db 967 ATATCTCAAACTTCAATTTTCTGGGCCAACTCTGGAATGAGAAAGATTAAAGAC 1026
 QY 901 CAGACT 906
 Db 1027 CAGACT 1032

RESULT 7

US-09-964-277-1
 ; Sequence 1, Application US/09964277
 ; Patent No. US20020137170A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Luche, Ralf M.
 ; APPLICANT: Wei, Bo
 ; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
 ; FILE REFERENCE: 200125.434
 ; CURRENT APPLICATION NUMBER: US/09/964,277
 ; CURRENT FILING DATE: 2001-09-25
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 3496
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-964-277-1

Query Match 99.6%; Score 902.8; DB 9; Length 3496;

Best Local Similarity 99.8%; Pred. No. 4,7e-280; Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCCATGAGATGATTGAACTCAATTTGTTACTGAGAGGTTGGTGGCTCTGCTGAA 60
 Db 562 ATGGCCCATGAGATGATTGAACTCAATTTGTTACTGAGAGGTTGGTGGCTCTGCTGAA 621
 QY 61 AGTGAAGGAAAAAGTCTGCTAAATGATAGCCGCCATTGTGGAATACATACATCC 120
 Db 622 AGTGAAGGAAAAAGTCTGCTAAATGATAGCCGCCATTGTGGAATACATACATCC 681
 QY 121 CACATTTTGAAGCATTAATATCAACATGCTCCAAAGCTTAAGAACCGAAGTTGCAACAG 180
 Db 682 CACATTTTGAAGCATTAATATCAACATGCTCCAAAGCTTAAGAACCGAAGTTGCAACAG 741
 QY 181 GACAAAGTGTAAATTAACAGAGCTCATCCAGATTCAGGAAACATAAGTTGATCATTTGAT 240
 Db 742 GACAAAGTGTAAATTAACAGAGCTCATCCAGATTCAGGAAACATAAGTTGATCATTTGAT 801
 QY 241 TGCAAGTGAAGGTTTGAATGATGATCAAGGCTCCCAAGATGTTGCTCTCTTCA 300
 Db 802 TGCAAGTGAAGGTTTGAATGATGATCAAGGCTCCCAAGATGTTGCTCTCTTCA 861
 QY 301 GACTGTTTTCTACTGATCTTCTGGGTAAACTGGAAGAGCTTCAACTCTGTTCACTG 360

Db 862 GACTGTTTTCTACTGATCTTCTGGGTAAACTGGAAGAGCTTCAACTCTGTTCACTG 921
 QY 361 CTGGCAGGTGGGTTTGTGAGATTCTCTGTTGTTTCCCTGGACCTGTGGAAGAAATCC 420
 Db 922 CTGGCAGGTGGGTTTGTGAGATTCTCTGTTGTTTCCCTGGACCTGTGGAAGAAATCC 981
 QY 421 ACTTAATGCTTACCTGATTTTCTCAGCTTGTCTTACTCTGTGGCAACATTTGGCCAAAC 480
 Db 982 ACTTAATGCTTACCTGATTTTCTCAGCTTGTCTTACTCTGTGGCAACATTTGGCCAAAC 1041
 QY 481 GCAATTTCTCCCAATCTTTATCTTGGCTGCGCAGGAGATGCTCCAAAGAGCTGATA 540
 Db 1042 GCAATTTCTCCCAATCTTTATCTTGGCTGCGCAGGAGATGCTCCAAAGAGCTGATA 1101
 QY 541 CAGCAGAAATGGAGATGGTATGTTAAATGCGACGATATACCTGTCCAAAGCCGACTTT 600
 Db 1102 CAGCAGAAATGGAGATGGTATGTTAAATGCGACGATATACCTGTCCAAAGCCGACTTT 1161
 QY 601 ATCCCGAAGTCTATTTCTCGCTGCTGTGTGATGACAGCTTTTGTGAAAATTTTG 660
 Db 1162 ATCCCGAAGTCTATTTCTCGCTGCTGTGTGATGACAGCTTTTGTGAAAATTTTG 1221
 QY 661 CCGTGTGGACAAATCAGTAGATTTTCAATTGAGAAAGCAAAAGCTCCCAATGATGTT 720
 Db 1222 CCGTGTGGACAAATCAGTAGATTTTCAATTGAGAAAGCAAAAGCTCCCAATGATGTT 1281
 QY 721 CTAGTGACCTGTTTACCTGGAGATCTCCGCTCCGCAACATCCCTATCCGCTACATCAG 780
 Db 1282 CTAGTGACCTGTTTACCTGGAGATCTCCGCTCCGCAACATCCCTATCCGCTACATCAG 1341
 QY 781 AAGAGATGACATGCTTATGATGAGCTTACAGATTTGTGAAAAGAAAGACTTACT 840
 Db 1342 AAGAGATGACATGCTTATGATGAGCTTACAGATTTGTGAAAAGAAAGACTTACT 1401
 QY 841 ATATCTCAAACTTCAATTTTCTGGGCCAACTCTGGAATGAGAAAGATTAAAGAC 900
 Db 1402 ATATCTCAAACTTCAATTTTCTGGGCCAACTCTGGAATGAGAAAGATTAAAGAC 1461
 QY 901 CAGACT 906
 Db 1462 CAGACT 1467

RESULT 8

US-10-370-715B-261

; Sequence 261, Application US/10370715B
 ; Publication No. US20040258678A1
 ; GENERAL INFORMATION:
 ; Patin Docket Preview
 ; APPLICANT: BODARY, SARAH C.
 ; APPLICANT: CLARK, HILARY
 ; APPLICANT: BRISBELL, HUNTE
 ; APPLICANT: JACKMAN, JANET
 ; APPLICANT: SCHOENFELD, JILL R.
 ; APPLICANT: WILLIAMS, P. MICKEY
 ; APPLICANT: WOOD, WILLIAM I.
 ; APPLICANT: WU, THOMAS D.
 ; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
 ; FILE REFERENCE: P1948R1-US
 ; CURRENT APPLICATION NUMBER: US/10/370,715B
 ; CURRENT FILING DATE: 2003-02-21
 ; NUMBER OF SEQ ID NOS: 742
 ; SEQ ID NO 261
 ; LENGTH: 3521
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-370-715B-261

Query Match 99.6%; Score 902.8; DB 18; Length 3521;
 Best Local Similarity 99.8%; Pred. No. 4,7e-280; Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCCATGAGATGATGGAATCAATTTGTAAGAGAGTTGGTGGCTCTGCTGGAA 60
DB 564 ATGGCCCATGAGATGATGGAATCAATTTGTAAGAGAGTTGGTGGCTCTGCTGGAA 623
QY 61 AGTGAACGGAAAAAGTCTGCTAATTTGATAGCCGGCCATTTTGTGAATTAACATATCC 120
DB 624 AGTGAACGGAAAAAGTCTGCTAATTTGATAGCCGGCCATTTTGTGAATTAACATATCC 683
QY 121 CACATTTTGGAAAGCATTAATTAATCACTGCTCCAAAGCTTAATGAAGCCGAAGTTTGGAAACAG 180
DB 684 CACATTTTGGAAAGCATTAATTAATCACTGCTCCAAAGCTTAATGAAGCCGAAGTTTGGAAACAG 743
QY 181 GACAAAGTTTAATTAATTAATCACTGCTCCAAAGCTTAATGAAGCCGAAGTTTGGAAACAG 240
DB 744 GACAAAGTTTAATTAATTAATCACTGCTCCAAAGCTTAATGAAGCCGAAGTTTGGAAACAG 803
QY 241 TGCAGTCAGAAAGTTGATGATTAAGATCAAAAGCTCCAAAGTTTGGCTCTCTCTTCA 300
DB 804 TGCAGTCAGAAAGTTGATGATTAAGATCAAAAGCTCCAAAGTTTGGCTCTCTCTTCA 863
QY 301 GACTGTTTCTCACTGATCTTCTGGGTAATCTGGAAGAAAGCTTCAATCTGTTCACTG 360
DB 864 GACTGTTTCTCACTGATCTTCTGGGTAATCTGGAAGAAAGCTTCAATCTGTTCACTG 923
QY 361 CTTCAGAGTGGGTTTGTGATGATCTGCTGTTTCCCTGGGCTCTGGAAGAAATCC 420
DB 924 CTTCAGAGTGGGTTTGTGATGATCTGCTGTTTCCCTGGGCTCTGGAAGAAATCC 983
QY 421 ACTCTAGTCCCTACCTGATCTTCTAGGCTTCTTACCTGTTGCAACATTTGGGCAACC 480
DB 984 ACTCTAGTCCCTACCTGATCTTCTAGGCTTCTTACCTGTTGCAACATTTGGGCAACC 1043
QY 481 CGAATTTCTTCCCAATCTTATCTTGGCTGCGCAAGAGATGCTTCAACAGAGCTGATA 540
DB 1044 CGAATTTCTTCCCAATCTTATCTTGGCTGCGCAAGAGATGCTTCAACAGAGCTGATA 1103
QY 541 CAGAGAAATGGGATTTGATGATGATTAATGCAAGCTTACCTGTCGAAGCTGACCTT 600
DB 1104 CAGAGAAATGGGATTTGATGATGATTAATGCAAGCTTACCTGTCGAAGCTGACCTT 1163
QY 601 ATCCCCGAGTCTCAATTTCTGCTGCTGCTGCTGATGATGACAGCTTTTGTGAAGAAATTTTG 660
DB 1164 ATCCCCGAGTCTCAATTTCTGCTGCTGCTGCTGATGATGACAGCTTTTGTGAAGAAATTTTG 1223
QY 661 CCGTGTGGAACAATCAATCAATGATTTCAATGAAGAAAGCAAAAGCTTCAATGATGTT 720
DB 1224 CCGTGTGGAACAATCAATCAATGATTTCAATGAAGAAAGCAAAAGCTTCAATGATGTT 1283
QY 721 CTAATGACCTGTTTATGCTGGATCTCCCGCTCCGCAACATGCTATGAGAAAGATTTAAGAC 780
DB 1284 CTAATGACCTGTTTATGCTGGATCTCCCGCTCCGCAACATGCTATGAGAAAGATTTAAGAC 1343
QY 781 AAGAGATGACATGCTTTATGATGAAGCTTACAGATTTTGAAGAAAGAAAGCTTACT 840
DB 1344 AAGAGATGACATGCTTTATGATGAAGCTTACAGATTTTGAAGAAAGAAAGCTTACT 1403
QY 841 ATATCTCCAAATCTTCAATTTTCTGGGCCAACTCTCTGACATGAGAAAGATTTAAGAC 900
DB 1404 ATATCTCCAAATCTTCAATTTTCTGGGCCAACTCTCTGACATGAGAAAGATTTAAGAC 1463
QY 901 CAGACT 906
DB 1464 CAGACT 1469

RESULT 9

US-09-816-494-1
; Sequence 1, Application US/09816494
; Patent No. US20020034807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY

; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589) ... (2583)
US-09-816-494-1

Query Match 99.8%; Score 902.8; DB 9; Length 3544;

Best Local Similarity 99.8%; Pred. No. 4.7e-280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCCATGAGATGATGGAATCAATTTGTAAGAGAGTTGGTGGCTCTGCTGGAA 60
DB 589 ATGGCCCATGAGATGATGGAATCAATTTGTAAGAGAGTTGGTGGCTCTGCTGGAA 648
QY 61 AGTGAACGGAAAAAGTCTGCTAATTTGATAGCCGGCCATTTTGTGAATTAACATATCC 120
DB 649 AGTGAACGGAAAAAGTCTGCTAATTTGATAGCCGGCCATTTTGTGAATTAACATATCC 708
QY 121 CACATTTTGGAAAGCATTAATTAATCACTGCTCCAAAGCTTAATGAAGCCGAAGTTTGGAAACAG 180
DB 709 CACATTTTGGAAAGCATTAATTAATCACTGCTCCAAAGCTTAATGAAGCCGAAGTTTGGAAACAG 768
QY 181 GACAAAGTTTAATTAATTAATCACTGCTCCAAAGCTTAATGAAGCCGAAGTTTGGAAACAG 240
DB 769 GACAAAGTTTAATTAATTAATCACTGCTCCAAAGCTTAATGAAGCCGAAGTTTGGAAACAG 828
QY 241 TGCAGTCAGAAAGTTGATGATGATTAATGCAAGCTTACCTGTCGAAGCTGACCTT 300
DB 829 TGCAGTCAGAAAGTTGATGATGATTAATGCAAGCTTACCTGTCGAAGCTGACCTT 888
QY 601 ATCCCCGAGTCTCAATTTCTGCTGCTGCTGCTGATGATGACAGCTTTTGTGAAGAAATTTTG 660
DB 889 GACTGTTTCTCACTGATCTTCTGGGTAATCTGGAAGAAAGCTTCAATCTGTTCACTG 948
QY 361 CTTCAGAGTGGGTTTGTGATGATCTGCTGTTTCCCTGGGCTCTGGAAGAAATTC 420
DB 949 CTTCAGAGTGGGTTTGTGATGATCTGCTGTTTCCCTGGGCTCTGGAAGAAATTC 1008
QY 421 ACTCTAGTCCCTACCTGATCTTCTAGGCTTCTTACCTGTTGCAACATTTGGGCAACC 480
DB 1009 ACTCTAGTCCCTACCTGATCTTCTAGGCTTCTTACCTGTTGCAACATTTGGGCAACC 1068
QY 481 CGAATTTCTTCCCAATCTTATCTTGGCTGCGCAAGAGATGCTTCAACAGAGCTGATA 540
DB 1069 CGAATTTCTTCCCAATCTTATCTTGGCTGCGCAAGAGATGCTTCAACAGAGCTGATA 1128
QY 541 CAGAGAAATGGGATTTGATGATGATTAATGCAAGCTTACCTGTCGAAGCTGACCTT 600
DB 1129 CAGAGAAATGGGATTTGATGATGATTAATGCAAGCTTACCTGTCGAAGCTGACCTT 1188
QY 601 ATCCCCGAGTCTCAATTTCTGCTGCTGCTGCTGATGATGACAGCTTTTGTGAAGAAATTTTG 660
DB 1189 ATCCCCGAGTCTCAATTTCTGCTGCTGCTGCTGATGATGACAGCTTTTGTGAAGAAATTTTG 1248
QY 661 CCGTGTGGAACAATCAATCAATGATTTCAATGAAGAAAGCAAAAGCTTCAATGATGTT 720
DB 1249 CCGTGTGGAACAATCAATCAATGATTTCAATGAAGAAAGCAAAAGCTTCAATGATGTT 1308
QY 721 CTAATGACCTGTTTATGCTGGATCTCCCGCTCCGCAACATGCTATGAGAAAGATTTAAGAC 780
DB 1309 CTAATGACCTGTTTATGCTGGATCTCCCGCTCCGCAACATGCTATGAGAAAGATTTAAGAC 1368

QY 781 AAGAGATGACATGCTTGTAGATGAAGCTTACAGATTTGTGAAGAAAAAGACCTACT 840
| | | | |
Db 1369 AAGAGATGACATGCTTGTAGATGAAGCTTACAGATTTGTGAAGAAAAAGACCTACT 1428
| | | | |
QY 841 ATATCTCCAAACTTCAATTTTCTGGCCAACTCTGAGCTATGAGAAGATTAAAGAC 900
| | | | |
Db 1429 ATATCTCCAAACTTCAATTTTCTGGCCAACTCTGAGCTATGAGAAGATTAAAGAC 1488
| | | | |
QY 901 CAGACT 906
| | | | |
Db 1489 CAGACT 1494

RESULT 10
US-10-377-072-25
; Sequence 25, Application US/10377072
; Publication No. US2004009501A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Miyoung
; APPLICANT: Teal, Fong-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; FILE REFERENCE: MPIO3-0180NMIM
; CURRENT APPLICATION NUMBER: US/10/377,072
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895,860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/843,297
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; PRIOR FILING DATE: 2001-03-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)...(2586)
US-10-377-072-25

Query Match 99.6%; Score 902.8; DB 17; Length 3544;
Best Local Similarity 99.8%; Pred. No. 4,76-280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCCATGATGATTTGAACCTCAATTTGTACTGAGAGCTTGAGCTTGTCTGGAA 60
Db 589 ATGGCCCATGATGATTTGAACCTCAATTTGTACTGAGAGCTTGAGCTTGTCTGGAA 648

QY 61 AGTGAACGGAAAAAGTGTCTGTAATTGATAGCCGGCCATTGTGGAAATCAATACATCC 120
| | | | |
Db 649 AGTGAACGGAAAAAGTGTCTGTAATTGATAGCCGGCCATTGTGGAAATCAATACATCC 708
| | | | |
QY 121 CACATTTTGAAGCCATTATATCACTGCTCCAAAGCTTATGAAAGCGAAGGTTCACAG 180
| | | | |
Db 709 CACATTTTGAAGCCATTATATCACTGCTCCAAAGCTTATGAAAGCGAAGGTTCACAG 768
| | | | |
QY 181 GACAAAGTTTAATTACAGAGCTCATCCAGCATTCAGCGAAACAAAGTTGACATTGAT 240
| | | | |
Db 769 GACAAAGTTTAATTACAGAGCTCATCCAGCATTCAGCGAAACAAAGTTGACATTGAT 828
| | | | |
QY 241 TGCAGTCAGAAAGTTTGAAGTTTAAAGATCAAGCTCCCAAGATTTGGCTCTCTCTTCA 300
| | | | |
Db 829 TGCAGTCAGAAAGTTTGAAGTTTAAAGATCAAGCTCCCAAGATTTGGCTCTCTCTTCA 888
| | | | |
QY 301 GACTGTTTCTCACTGATCTTCTGGTAAACTGAGAAAGACTTCAACTCTGTCACTG 360
| | | | |
Db 889 GACTGTTTCTCACTGATCTTCTGGTAAACTGAGAAAGACTTCAACTCTGTCACTG 948
| | | | |
QY 361 CTTCGAGTGGGTTTCTGAGTTCTCTGTTTCTCTGGCTCTGTGAAAGAAATCC 420
| | | | |
Db 949 CTTCGAGTGGGTTTCTGAGTTCTCTGTTTCTCTGGCTCTGTGAAAGAAATCC 1008
| | | | |
QY 421 ACTGTAGTCCCTACCTGATTTCTCAGCTTGTCTTACCTGTGCAATTTGGGCCAAC 480
| | | | |
Db 1009 ACTGTAGTCCCTACCTGATTTCTCAGCTTGTCTTACCTGTGCAATTTGGGCCAAC 1068
| | | | |
QY 481 CGAATTTTCCCAATCTTTAATCTTGGCTGCGAGAGATGCTTCAACAAGAGCTGATA 540
| | | | |
Db 1069 CGAATTTTCCCAATCTTTAATCTTGGCTGCGAGAGATGCTTCAACAAGAGCTGATA 1128
| | | | |
QY 541 CAGCAGATGGAGTGGTTATGTGTTAAATCCAGATATCTGTCCAAAGCTGACTTT 600
| | | | |
Db 1129 CAGCAGATGGAGTGGTTATGTGTTAAATCCAGATATCTGTCCAAAGCTGACTTT 1188
| | | | |
QY 601 ATCCCCGAGTCTCATTTCTCGCTGCTGCTGTGAATGACAGCTTTGTGGAATAATTTG 660
| | | | |
Db 1189 ATCCCCGAGTCTCATTTCTCGCTGCTGCTGTGAATGACAGCTTTGTGGAATAATTTG 1248
| | | | |
QY 661 CCGTGTGGACAATATCAGTAGATTTCAATGAGAAAGCAAAAGCTTCAATGATGTGT 720
| | | | |
Db 1249 CCGTGTGGACAATATCAGTAGATTTCAATGAGAAAGCAAAAGCTTCAATGATGTGT 1308
| | | | |
QY 721 CTAGTGAATCTTTTACTGAGATCTCCGCTCGCCACATGCTATGCCCTTACATCAG 780
| | | | |
Db 1309 CTAGTGAATCTTTTACTGAGATCTCCGCTCGCCACATGCTATGCCCTTACATCAG 1368
| | | | |
QY 781 AAGAGATGACATGCTTGTAGATGAAGCTTACAGATTTGTGAAGAAAAAGACCTACT 840
| | | | |
Db 1369 AAGAGATGACATGCTTGTAGATGAAGCTTACAGATTTGTGAAGAAAAAGACCTACT 1428
| | | | |
QY 841 ATATCTCCAAACTTCAATTTTCTGGCCAACTCTGAGCTATGAGAAGATTAAAGAC 900
| | | | |
Db 1429 ATATCTCCAAACTTCAATTTTCTGGCCAACTCTGAGCTATGAGAAGATTAAAGAC 1488
| | | | |
QY 901 CAGACT 906
| | | | |
Db 1489 CAGACT 1494

RESULT 11
US-10-377-072-25
; Sequence 25, Application US/10377072
; Publication No. US20040157221A9
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.

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APPLICANT: Chun, Myoung
APPLICANT: Tsai, Fong-Ying
TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: MP103-0180MIM
CURRENT APPLICATION NUMBER: US/10/377,072
PRIOR FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US 09/895,860
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,370
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/723,806
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/187,455
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/843,297
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199,801
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: US 09/861,801
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205,508
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/816,494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/815,419
PRIOR FILING DATE: 2001-03-22
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 3544
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (589)...(2586)
US-10-377-072-25

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Query Match 99.6%; Score 902.8; DB 18; Length 3544;
Best Local Similarity 99.8%; Pred. No. 4.7e-280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCCATGAGATGATGGAATCAATTTGTAAGAGAGTGGTCTGTGTGAA 60
DB 589 ATGGCCCATGAGATGATGGAATCAATTTGTAAGAGAGTGGTCTGTGTGAA 648
QY 61 AGTGAACGAAAAAGTCTGTAATGATAGCGGCATTTGTGGAATACATCATCC 120
DB 649 AGTGAACGAAAAAGTCTGTAATGATAGCGGCATTTGTGGAATACATCATCC 708
QY 121 CACATTTGGAAGCCATTATATCAACTGCTCAAGCTTATGAGCGAAGTTGCAACG 180
DB 709 CACATTTGGAAGCCATTATATCAACTGCTCAAGCTTATGAGCGAAGTTGCAACG 768
QY 181 GACAAAGTTTATTAACAGACTCATCCAGCATTTAGGAAACATTAAGTGAATGAT 240
DB 769 GACAAAGTTTATTAACAGACTCATCCAGCATTTAGGAAACATTAAGTGAATGAT 828
QY 241 TGCAGTCGAGAGTTGTGATTAAGATCAAGCTCCCAAGATGTTGCTCTCTCTCA 300
DB 829 TGCAGTCGAGAGTTGTGATTAAGATCAAGCTCCCAAGATGTTGCTCTCTCTCA 888
QY 301 GACTGTTTCTCACTGATCTTCTGGGTAACGTGAGAAAGCTTCAACTCTGTTCACTG 360
DB 889 GACTGTTTCTCACTGATCTTCTGGGTAACGTGAGAAAGCTTCAACTCTGTTCACTG 948
QY 361 CTTCGAGGTGGTGTGCTGAGATCTCTGTTGTTCCCTGCGCTCTGGAAGAAATCC 420
DB 949 CTTCGAGGTGGTGTGCTGAGATCTCTGTTGTTCCCTGCGCTCTGGAAGAAATCC 1008
QY 421 ACTCTAGTCCTACCTGATTTCTAGCTTGTCTTACTGTTGCCAATTTGGGCAATCC 480

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DB 1009 ACTCTAGTCCTACCTGATTTCTAGCTTGTCTTACTGTTGCCAATTTGGGCAATCC 1068
QY 481 GGAATTTCTCCCAATCTTATCTTGCGGCGCAAGAGATGTCCTCAAGAGGCTGATA 540
DB 1069 GGAATTTCTCCCAATCTTATCTTGCGGCGCAAGAGATGTCCTCAAGAGGCTGATA 1128
QY 541 CAGCAGAAATGGATGTTATGATGTTAATGCAAGCTATACCTGTCCAAAGCTGACTTT 600
DB 1129 CAGCAGAAATGGATGTTATGATGTTAATGCAAGCTATACCTGTCCAAAGCTGACTTT 1188
QY 601 ATCCCGAGTCTCATTTCTGCGTGTGCTGTAATGACAGCTTTGTGAGAAATTTTG 660
DB 1189 ATCCCGAGTCTCATTTCTGCGTGTGCTGTAATGACAGCTTTGTGAGAAATTTTG 1248
QY 661 CCGTGTGGAACAATGATGATTTCAATTGAGAAAGAAAGCCTCCAAATGAGATGTT 720
DB 1249 CCGTGTGGAACAATGATGATTTCAATTGAGAAAGAAAGCCTCCAAATGAGATGTT 1308
QY 721 CTAGTCAGCTGTTTATGCTGGATCTCCGCTCCGCAACATGCTATGCTCATCATG 780
DB 1309 CTAGTCAGCTGTTTATGCTGGATCTCCGCTCCGCAACATGCTATGCTCATCATG 1368
QY 781 AAGAGATGACATGCTTTAGATGAGACTTACAGATTTGTGAAAGAAAGAAAGCTTACT 840
DB 1369 AAGAGATGACATGCTTTAGATGAGACTTACAGATTTGTGAAAGAAAGAAAGCTTACT 1428
QY 841 ATATCTCCAACTTCAATTTTCTGGGCGCACTCTCGAGCTATGAGAAAGATTAAGAC 900
DB 1429 ATATCTCCAACTTCAATTTTCTGGGCGCACTCTCGAGCTATGAGAAAGATTAAGAC 1488
QY 901 CAGACT 906
DB 1489 CAGACT 1494

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RESULT 12
US-10-425-114-26234
; Sequence 26234, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26234
; LENGTH: 3625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4119-028-H6_FLI
US-10-425-114-26234

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Query Match 99.6%; Score 902.8; DB 17; Length 3625;
Best Local Similarity 99.8%; Pred. No. 4.8e-280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCCCATGAGATGATGGAATCAATTTGTAAGAGAGTGGTCTGTGTGAA 60
DB 692 ATGGCCCATGAGATGATGGAATCAATTTGTAAGAGAGTGGTCTGTGTGAA 751
QY 61 AGTGAACGAAAAAGTCTGTAATGATAGCGGCATTTGTGGAATACATCATCC 120
DB 752 AGTGAACGAAAAAGTCTGTAATGATAGCGGCATTTGTGGAATACATCATCC 811

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QY 121 CACATTTTGAAGCCATTAATATCACTGCTCCAGCTTATGAAGCGAAGTTGCAACG 180
Db 812 CACATTTTGAAGCCATTAATATCACTGCTCCAGCTTATGAAGCGAAGTTGCAACG 871
QY 181 GACAAATGTTAATTAAGAGCTCATCAGACATTCAGCGAACAATAAGTTGACATTGAT 240
Db 872 GACAAATGTTAATTAAGAGCTCATCAGACATTCAGCGAACAATAAGTTGACATTGAT 931
QY 241 TGCAGTCAGAGGTTGATGTTTACGATCAAGCTCCCAAGATGTTGCTCTCTCTCA 300
Db 932 TGCAGTCAGAGGTTGATGTTTACGATCAAGCTCCCAAGATGTTGCTCTCTCTCA 991
QY 301 GACTGTTTCTCACTGTAATCTTCTGGGTAACCTGAGAAAGCTTCAACTCTGTTCACTG 360
Db 992 GACTGTTTCTCACTGTAATCTTCTGGGTAACCTGAGAAAGCTTCAACTCTGTTCACTG 1051
QY 361 CTTCGAGTGAGGTTTGTGAGTCTCTCGTGTGTTTCCCTGGCTCTGTGAAGAAATCC 420
Db 1052 CTTCGAGTGAGGTTTGTGAGTCTCTCGTGTGTTTCCCTGGCTCTGTGAAGAAATCC 1111
QY 421 ACTTAGTCCCTTACCTGCAATTTCTCAGCCTTGCTTACCTGTTGCCAATGGGCCAAC 480
Db 1112 ACTTAGTCCCTTACCTGCAATTTCTCAGCCTTGCTTACCTGTTGCCAATGGGCCAAC 1171
QY 481 CGAATTTCTCCCAATCTTTATCTTGCTGCTGCAGCGAGATGCTCTCAACAGAGCTGATA 540
Db 1172 CGAATTTCTCCCAATCTTTATCTTGCTGCTGCAGCGAGATGCTCTCAACAGAGCTGATA 1231
QY 541 CAGCAGAAATGGGATGTTATGTTAATGCAAGCTATACCTGTCCAAAGCTCACTT 600
Db 1232 CAGCAGAAATGGGATGTTATGTTAATGCAAGCTATACCTGTCCAAAGCTCACTT 1291
QY 601 ATCCCGAGTCTCATTTCTCGCTGCTGCTGTAATGACAGCTTTTGTGAGAAATTTTG 660
Db 1292 ATCCCGAGTCTCATTTCTCGCTGCTGCTGTAATGACAGCTTTTGTGAGAAATTTTG 1351
QY 661 CGGTGTTGGAACAATCACTATGATTCATTGAGAAAGCAAAAGCTCCCAATGATGTT 720
Db 1352 CGGTGTTGGAACAATCACTATGATTCATTGAGAAAGCAAAAGCTCCCAATGATGTT 1411
QY 721 CTAGTGCACTGTTTATGCTGGGATCTCCGCTCCGCAACATGCTATGCGCTACATCATG 780
Db 1412 CTAGTGCACTGTTTATGCTGGGATCTCCGCTCCGCAACATGCTATGCGCTACATCATG 1471
QY 781 AAGAGATGACATGCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAGAAAGCTTACT 840
Db 1472 AAGAGATGACATGCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAGAAAGCTTACT 1531
QY 841 ATATCTCCAAATCTCAATTTCTGGGCAACTCCGCACTATGAGAAAGATTTAAGAC 900
Db 1532 ATATCTCCAAATCTCAATTTCTGGGCAACTCCGCACTATGAGAAAGATTTAAGAC 951
QY 901 CAGACT 906
Db 1592 CAGACT 1597

RESULT 13
US-10-343-357-17
; Sequence 17, Application US/10343357
; Publication No. US20040058341A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. TOM
; APPLICANT: ELLIOTT, Vicki S.; RAMKUMAR, Jayalaxmi
; APPLICANT: YAO, Monique G.; BUREFORD, Neil
; APPLICANT: WANG, Yumei B.; STEWART, Elizabeth A.
; APPLICANT: GANDHI, Ameena R.; ARVIZU, Chandra S.
; APPLICANT: LEE, Ernestine A.; HAPALIA, April J.A.
; APPLICANT: LU, Dying Aina M.; TRIBOULEY, Catherine M.
; APPLICANT: GRIFPIN, Jennifer A.; BAUGHN, Mariah R.
; APPLICANT: YUE, Henry; WARREN, Bridget A.
; APPLICANT: NGUYEN, Daniel B.; CHAWLA, Nalinder K.
; APPLICANT: KEARNEY, Liam
```

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; TITLE OF INVENTION: PROTEIN PHOSPHATASES
; FILE REFERENCE: PI-0173 PCT
; CURRENT APPLICATION NUMBER: US/10/343,357
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: PCT/US01/23716
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 60/221,679
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/223,272
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/224,309
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 60/226,728
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/229,254
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: US 60/231,366
; PRIOR FILING DATE: 2000-09-08
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 3766
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040058341A1 7480570CB1
US-10-343-357-17

Query Match 99.6%; Score 902.8; DB 17; Length 3766;
Best Local Similarity 99.8%; Pred. No. 4,9e-280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGCCCATGAGATGATGGAAGTCAATTTGTTACTGAGAGTTGGTCTGCTGGAA 60
Db 538 ATGCCCATGAGATGATGGAAGTCAATTTGTTACTGAGAGTTGGTCTGCTGGAA 597
QY 61 AGTGAACGAAAAAGTGTCTAATTTGATAGCCGGCATTTGTGAAATCAATACATCC 120
Db 598 AGTGAACGAAAAAGTGTCTAATTTGATAGCCGGCATTTGTGAAATCAATACATCC 657
QY 121 CACATTTTGAAGCCATTAATATCACTGCTCCAGCTTATGAAGCGAAGTTGCAACG 180
Db 658 CACATTTTGAAGCCATTAATATCACTGCTCCAGCTTATGAAGCGAAGTTGCAACG 717
QY 181 GACAAATGTTAATTAAGAGCTCATCAGACATTCAGCGAACAATAAGTTGACATTGAT 240
Db 718 GACAAATGTTAATTAAGAGCTCATCAGACATTCAGCGAACAATAAGTTGACATTGAT 777
QY 241 TGCAGTCAGAGGTTGATGTTTACGATCAAGCTCCCAAGATGTTGCTCTCTCTCA 300
Db 778 TGCAGTCAGAGGTTGATGTTTACGATCAAGCTCCCAAGATGTTGCTCTCTCTCA 837
QY 301 GACTGTTTCTCACTGTAATCTTCTGGGTAACCTGAGAAAGCTTCAACTCTGTTCACTG 360
Db 838 GACTGTTTCTCACTGTAATCTTCTGGGTAACCTGAGAAAGCTTCAACTCTGTTCACTG 897
QY 361 CTTCGAGTGAGGTTTGTGAGTCTCTCGTGTGTTTCCCTGGCTCTGTGAAGAAATCC 420
Db 898 CTTCGAGTGAGGTTTGTGAGTCTCTCGTGTGTTTCCCTGGCTCTGTGAAGAAATCC 957
QY 421 ACTTAGTCCCTTACCTGCAATTTCTCAGCCTTGCTTACCTGTTGCCAATGGGCCAAC 480
Db 958 ACTTAGTCCCTTACCTGCAATTTCTCAGCCTTGCTTACCTGTTGCCAATGGGCCAAC 1017
QY 481 CGAATTTCTCCCAATCTTTATCTTGCTGCTGCAGCGAGATGCTCTCAACAGAGCTGATA 540
Db 1018 CGAATTTCTCCCAATCTTTATCTTGCTGCTGCAGCGAGATGCTCTCAACAGAGCTGATA 1077
QY 541 CAGCAGAAATGGGATGTTATGTTAATGCAAGCTATACCTGTCCAAAGCTCACTT 600
Db 1078 CAGCAGAAATGGGATGTTATGTTAATGCAAGCTATACCTGTCCAAAGCTCACTT 1137
```


Qy 601 ATCCCCGAGTCTCATTTCTGCGTGTGCTGTAATGACAGCTTTTGTGAGAAAATTTTG 660
Db 1138 ATCCCCGAGTCTCATTTCTGCGTGTGCTGTAATGACAGCTTTTGTGAGAAAATTTTG 1197
Qy 661 CCGTGGTGGACAAATCAGTAGATTTTCATTTGAGAAAGCAAAAGCTTCCAAATGAGATGTT 720
Db 1198 CCGTGGTGGACAAATCAGTAGATTTTCATTTGAGAAAGCAAAAGCTTCCAAATGAGATGTT 1257
Qy 721 CTAGTGCATGTTTGTAGTGGATCTCCGCTCCGACACATGCTATGCGCTACATCATG 780
Db 1258 CTAGTGCATGTTTGTAGTGGATCTCCGCTCCGACACATGCTATGCGCTACATCATG 1317
Qy 781 AAGAGATGACATGCTTTTGTAGTGAAGCTTACAGATTTGTGAGAAAAGAAAGCTTACT 840
Db 1318 AAGAGATGACATGCTTTTGTAGTGAAGCTTACAGATTTGTGAGAAAAGAAAGCTTACT 1377
Qy 841 ATATCTCCAAATCTTAATTTTCTGGGCCAATCTCTGGAATGAGAGAAAGATTAAAGAC 900
Db 1378 ATATCTCCAAATCTTAATTTTCTGGGCCAATCTCTGGAATGAGAGAAAGATTAAAGAC 1437
Qy 901 CAGACT 906
Db 1438 CAGACT 1443

RESULT 14

US-10-648-593-115
; Sequence 115, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 115
; LENGTH: 4790
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-648-593-115

Query Match 99.6%; Score 902.8; DB 18; Length 4790;
Best Local Similarity 99.8%; Pred. No. 5,6e-280;
Matches 904; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGCCCCATGAGATGATGGAATCAAAATGTTACTGAGAGGTTGGTGGCTCTGCTGAA 60
Db 184 ATGCCCCATGAGATGATGGAATCAAAATGTTACTGAGAGGTTGGTGGCTCTGCTGAA 243
Qy 61 AGTGAAGGAAAAGTCTGTATTTATGAGCGGCAATTTGGGAATTAACATCATCC 120
Db 244 AGTGAAGGAAAAGTCTGTATTTATGAGCGGCAATTTGGGAATTAACATCATCC 303
Qy 121 CACATTTTGAAGCATTAATATCAACTGCTCCAAAGTTTGAAGCGAAGTTGCAAG 180
Db 304 CACATTTTGAAGCATTAATATCAACTGCTCCAAAGTTTGAAGCGAAGTTGCAAG 363
Qy 181 GACAAAGTGTATTAATACAGAGCTCATCCAGCATTCAGCGAAACATTAAGTTGACATTGAT 240
Db 364 GACAAAGTGTATTAATACAGAGCTCATCCAGCATTCAGCGAAACATTAAGTTGACATTGAT 423
Qy 241 TGCAGTCAAGAGTGTAGTTAGATCAAGAGTCCCAAGAGTTGCTCTCTCTCA 300
Db 424 TGCAGTCAAGAGTGTAGTTAGATCAAGAGTCCCAAGAGTTGCTCTCTCTCA 483
Qy 301 GACTGTTTCTCACTGTAATCTTCTGGTAAACTGAGAGAGCTTCAACTCTTTCACTG 360
Db 483 GACTGTTTCTCACTGTAATCTTCTGGTAAACTGAGAGAGCTTCAACTCTTTCACTG 543

Db 484 GACTGTTTCTCACTGTAATCTTCTGGTAAACTGAGAGAGCTTCAACTCTTTCACTG 543
Qy 361 CTGCAAGGTGGATTTGCTGAGATCTCTGTTGTTTCCCTGGGCTCTGTAAGAAATCC 420
Db 544 CTGCAAGGTGGATTTGCTGAGATCTCTGTTGTTTCCCTGGGCTCTGTAAGAAATCC 603
Qy 421 ACTTAGTCCCTACCTGATTTCTCAGCTTGTCTTACCTGTTGGCCAAATGGGCAAC 480
Db 604 ACTTAGTCCCTACCTGATTTCTCAGCTTGTCTTACCTGTTGGCCAAATGGGCAAC 663
Qy 481 CGAATCTTCCCAATCTTATCTTGTGCTGCCAGAGATGCTCTTAACAGAGAGCTGATA 540
Db 664 CGAATCTTCCCAATCTTATCTTGTGCTGCCAGAGATGCTCTTAACAGAGAGCTGATA 723
Qy 541 CAGCAAGTGGATTTGTTAGTGTAAATGCAAGCTTATCTGTCGCAAGCTGACTT 600
Db 724 CAGCAAGTGGATTTGTTAGTGTAAATGCAAGCTTATCTGTCGCAAGCTGACTT 783
Qy 601 ATCCCCGAGTCTCATTTCTGCGTGTGCTGTAATGACAGCTTTTGTGAGAAAATTTTG 660
Db 784 ATCCCCGAGTCTCATTTCTGCGTGTGCTGTAATGACAGCTTTTGTGAGAAAATTTTG 843
Qy 661 CCGTGGTGGACAAATCAGTAGATTTTCATTTGAGAAAGCAAAAGCTTCCAAATGAGATGTT 720
Db 844 CCGTGGTGGACAAATCAGTAGATTTTCATTTGAGAAAGCAAAAGCTTCCAAATGAGATGTT 903
Qy 721 CTAGTGCATGTTTGTAGTGGATCTCCGCTCCGACACATGCTATGCGCTACATCATG 780
Db 904 CTAGTGCATGTTTGTAGTGGATCTCCGCTCCGACACATGCTATGCGCTACATCATG 963
Qy 904 CAGACT 906
Db 1084 CAGACT 1089

RESULT 15

US-10-357-930-20824
; Sequence 20824, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 6232
; SOFTWARE: FastSeq for Windows Version 4.0

QY	173	GCCTTCAGTCAGAGTAAAGCTGTGTGGAGCCCGGAGCAAAAGTAAAGATATATTAATG	232
Db	224	GCTTTCAGTCCAGTGTAAAGCTGTGTGAGCCCGGAGCAAAAGTAAAGATATTAATG	283
QY	233	CGCTGGCTGCTCCAAAGCATCTTTTGTGTGGAAATGTATTCAGTCATCTCTTTATGA	292
Db	284	CGCTGGCTGCTCCAAAGCATCTTTTGTGTGGAAATGTATTCAGTCATCTCTTTATGA	343
QY	293	ATCAAAATGTAGGGGGCTGTGTGTGTGGAGAGAGTCTTTGGCAAGACATCAACGGGAA	352
Db	344	ATCAAAATGTAGGGGGCTGTGTGTGTGGAGAGAGTCTTTGGCAAGACATCAACGGGAA	403
QY	353	GAGAAAGAGACATTCATTTGGAGGGGCTCTTGCTGTAATAATGGGTTTAACTCTCTTTGAC	412
Db	404	GAGAAAGAGACATTCATTTGGAGGGGCTCTTGCTGTAATAATGGGTTTAACTCTCTTTGAC	463
QY	413	AGTCACCAACCAAGCTGACCTGCATACACTTTTATGATCAATGAGATGGCTTGAGCTTGAAC	472
Db	464	AGTCACCAACCAAGCTGACCTGCATACACTTTTATGATCAATGAGATGGCTTGAGCTTGAAC	523
QY	473	ACACCAACCATTAATCATCTGTGGCAATTTAAAGAAAGAGTGGGAAAAGAGACTTATTG	532
Db	524	ACACCAACCATTAATCATCTGTGGCAATTTAAAGAAAGAGTGGGAAAAGAGACTTATTG	583
QY	533	TTGTCAATGGCCCATGAGATGATGTGAAACTCAAAATTTGTAAGTGAAGGTGGTGGCTGAC	592
Db	584	TTGTCAATGGCCCATGAGATGATGTGAAACTCAAAATTTGTAAGTGAAGGTGGTGGCTGAC	643
QY	593	TGGAAGGTGAAACGGAAAAAGTGTGCTGAATTTGATAGCCGGCCATTTGTGAAATCAATA	652
Db	644	TGGAAGGTGAAACGGAAAAAGTGTGCTGAATTTGATAGCCGGCCATTTGTGAAATCAATA	703
QY	653	CATCCCACTTTTGGAAAGCCATTAAATCAACTGTCTCCAAGCTTATGAAAGCAAGTTGC	712
Db	704	CATCCCACTTTTGGAAAGCCATTAAATCAACTGTCTCCAAGCTTATGAAAGCAAGTTGC	763
QY	713	AAACGAGCAAAAGTGTAAATTCACAGCTGCATCCAGCACTTCAGCGGAAACATAAAGTTGACA	772
Db	764	AAACGAGCAAAAGTGTAAATTCACAGCTGCATCCAGCACTTCAGCGGAAACATAAAGTTGACA	823
QY	773	TTGATTTGAGTCAGAAAGGTTGTAGTTTATGCATCAAAAGCTCCCAAGATGTGGCTCTCTCT	832
Db	824	TTGATTTGAGTCAGAAAGGTTGTAGTTTATGCATCAAAAGCTCCCAAGATGTGGCTCTCTCT	883
QY	833	CTTCAGACTGTCTTCTCACTGTACTCTTGCGTAAACGTGAGAAAGACTTCAACTGTGTTT	892
Db	884	CTTCAGACTGTCTTCTCACTGTACTCTTGCGTAAACGTGAGAAAGACTTCAACTGTGTTT	943
QY	893	ACCTGCTTTCAGAGTGGGTTTGTCTGAGTCTCTCGTTGTTTCCCTGAGCTCTGTGAAGAA	952
Db	944	ACCTGCTTTCAGAGTGGGTTTGTCTGAGTCTCTCGTTGTTTCCCTGAGCTCTGTGAAGAA	1003
QY	953	AATCCACTGTATGCCCATCTGACGCAATTTCTGAGCCCTGTCTACCTGTTCGCAACATTTGGAC	1012
Db	1004	AATCCACTGTATGCCCATCTGACGCAATTTCTGAGCCCTGTCTACCTGTTCGCAACATTTGGAC	1063
QY	1013	CAACCCGAAATTCCTCCCAATCTTTATCTTTGCTGCCAGCGAGATGTCTCTCAACAAGAGAC	1072
Db	1064	CAACCCGAAATTCCTCCCAATCTTTATCTTTGCTGCCAGCGAGATGTCTCTCTCAACAAGAGAC	1122
QY	1073	TGATACAGACGAATGGGATTTGTATGTCTTAAATGCCAGCTATACCTGTCCAAAGCTGC	1133

Db 1124 TGATGAGAGAAATGGAGTGGTTATATGATTAATAATGCGAAGCAATACCTGTCGAAAGCCG 1183
QY 1133 ACTTTATCCCGAGTCTCAATTTCTGCGTGTGCTGTGAATGACAGCTTTTGTGAGAAAA 1192
Db 1184 ACTTTATCCCGAGTCTCAATTTCTGCGTGTGCTGTGAATGACAGCTTTTGTGAGAAAA 1243
QY 1193 TTTTGCCTGTGTGAGCAAAATCAGTAGATTTCAATTTGAGAAAGCAAAAGCTCCATATGAT 1252
Db 1244 TTTTGCCTGTGTGAGCAAAATCAGTAGATTTCAATTTGAGAAAGCAAAAGCTCCATATGAT 1303
QY 1253 GGTGTTCTAGTGCATCTTTTACGTGGATCTCCGCTCCGCAACATCGCTATCGCTCA 1312
Db 1304 GTGTTCTAGTGCATCTTTTACGTGGATCTCCGCTCCGCAACATCGCTATCGCTCA 1363
QY 1313 TCATGAAAGAGATGACATGCTTTTATGATGAAGCTTACAGATTTGTGAAAGAAAAAGAC 1372
Db 1364 TCATGAAAGAGATGACATGCTTTTATGATGAAGCTTACAGATTTGTGAAAGAAAAAGAC 1423
QY 1373 CTACTATATCTCCAAACTTCAATTTTCTGAGCCAACTCCTGAGCTATAGAGAAAGATTA 1432
Db 1424 CTACTATATCTCCAAACTTCAATTTTCTGAGCCAACTCCTGAGCTATAGAGAAAGATTA 1483
QY 1433 AGAACAAGACTGAGAGATCAGAGCCAAAGAGCAAACTCAAGCTGTGCACTGTGAGAGC 1492
Db 1484 AGAACAAGACTGAGAGATCAGAGCCAAAGAGCAAACTCAAGCTGTGCACTGTGAGAGC 1543
QY 1493 CAAATGAACTGTGCTGCTGTCTGTCAAGAGGTGAGCAAGAAAGAGAGAGCCCTCAAGTC 1552
Db 1544 CAAATGAACTGTGCTGCTGTCTGTCAAGAGGTGAGCAAGAAAGAGAGAGCCCTCAAGTC 1603
QY 1553 CACCTGTGCGCACTGTCTACTCTCAAGAGGAGAGAGCAAAAGCCCTGTGATCCGCCA 1612
Db 1604 CACCTGTGCGCACTGTCTACTCTCAAGAGGAGAGAGCAAAAGCCCTGTGATCCGCCA 1663
QY 1613 GCGTGCCCGAGGTGCCAGAGGTGAGAGCCGTCTGTGAGAGCAAGCCCGCTGTGATCCGCCA 1672
Db 1664 GCGTGCCCGAGGTGCCAGAGGTGAGAGCCGTCTGTGAGAGCAAGCCCGCTGTGATCCGCCA 1723
QY 1673 GCGTCAGTGGCTGCACTGTCTGCGAGAGAGGTGAGAGCAAGCTTAAGCTCAAGCGTT 1732
Db 1724 GCGTCAGTGGCTGCACTGTCTGCGAGAGAGGTGAGAGCAAGCTTAAGCTCAAGCGTT 1783
QY 1733 CCTTCTCTGAGATCAATCAATGCTTCAATTTCAAGCCAGATGAGCACTCTTAAATG 1792
Db 1784 CCTTCTCTGAGATCAATCAATGCTTCAATTTCAAGCCAGATGAGCACTCTTAAATG 1843
QY 1793 GCTTCTCTCATCAAGAGATGCTTTGAGAACTTCAAAACCTTCACTACTTGTGATGGA 1852
Db 1844 GCTTCTCTCATCAAGAGATGCTTTGAGAACTTCAAAACCTTCACTACTTGTGATGGA 1903
QY 1853 CCAACAAGCTATGCGAGTTCTCCCTGTTCAGAACTATCGAGACAGACTCCGAAACCA 1912
Db 1904 CCAACAAGCTATGCGAGTTCTCCCTGTTCAGAACTATCGAGACAGACTCCGAAACCA 1963
QY 1913 GTTCTGATTAAGAGAGAGCAATCCCAAGAGCTGAGAGCCGCGAGGCTTTCAGACA 1972
Db 1964 GTTCTGATTAAGAGAGAGCAATCCCAAGAGCTGAGAGCCGCGAGGCTTTCAGACA 2023
QY 1973 GCCAAGAGAGAGATTTGATTCGCTCAAGAACCAAGCAAGTGTGCAACCGGCGAGAGGTGCC 2032
Db 2024 GCCAAGAGAGAGATTTGATTCGCTCAAGAACCAAGCAAGTGTGCAACCGGCGAGAGGTGCC 2083
QY 2033 TTTTATCTCCATGATCAAGAGAGAGCACTCAAGAGTGTGCTGTGAGGCTTTAAGGCT 2092
Db 2084 TTTTATCTCCATGATCAAGAGAGAGCACTCAAGAGTGTGCTGTGAGGCTTTAAGGCT 2143
QY 2093 TCGGCTTTTCAACAGAGCAAGCACTCAAGAGTGTGCTGTGAGGCTTTAAGGCT 2152
Db 2144 TCGGCTTTTCAACAGAGCAAGCACTCAAGAGTGTGCTGTGAGGCTTTAAGGCT 2203
QY 2153 GCGACTGGAATCTTTGGCCCGCCAGACCTTCAACCCCTTCCCTGACAGGCTGCTGTATTT 2212
Db 2212 GCGACTGGAATCTTTGGCCCGCCAGACCTTCAACCCCTTCCCTGACAGGCTGCTGTATTT 2263
QY 2213 TTGCGCAGAGGTCTCAACTTTCTACTGCTGCTGCAAGCATCTACGAGAGCTGTATTT 2272
Db 2264 TTGCGCAGAGGTCTCAACTTTCTACTGCTGCTGCAAGCATCTACGAGAGCTGTATTT 2323
QY 2273 ACTCTGCTTACAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCT 2332
Db 2324 ACTCTGCTTACAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCT 2383
QY 2333 GCGCGAGAGGCAAGTGAAGAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCT 2392
Db 2384 GCGCGAGAGGCAAGTGAAGAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCT 2443
QY 2393 TTGAAAGAGCTTTTAAAGCAGAGAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCT 2452
Db 2444 TTGAAAGAGCTTTTAAAGCAGAGAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCT 2503
QY 2453 AGAACAAGTCAAGGAGAGCTGCGGAGAGAGTGGAGAGTCAAGTCACTTTTGGGAGCA 2512
Db 2504 AGAACAAGTCAAGGAGAGCTGCGGAGAGAGTGGAGAGTCAAGTCACTTTTGGGAGCA 2563
QY 2513 TGAATATCATTTAGAGTCTCTGAGAGAGAGCACTGTGACTTTCTATAGACATTTT 2572
Db 2564 TGAATATCATTTAGAGTCTCTGAGAGAGAGCACTGTGACTTTCTATAGACATTTT 2622
QY 2573 TTTTCTGTTCACAAAAAATTTCCCTGTATATCTGAAATATATATATATATATATAT 2632
Db 2623 TTTTCTGTTCACAAAAAATTTCCCTGTATATCTGAAATATATATATATATATATATAT 2682
QY 2633 TATTTTGGAAAAATGAGCTATGATGTAATAAGCAACAGGTGATCAACCCAGTTGTA 2692
Db 2683 TATTTTGGAAAAATGAGCTATGATGTAATAAGCAACAGGTGATCAACCCAGTTGTA 2742
QY 2693 CTCTTAACATCTGCACTTTGAGAGATCACTTAATCTTCTGTCAACAAAAATGAGAGGCA 2752
Db 2743 CTCTTAACATCTGCACTTTGAGAGATCACTTAATCTTCTGTCAACAAAAATGAGAGGCA 2802
QY 2753 GATGCTAAGATCCCTCTGAGACGAGAGAAACATTTTATTCAGTAAATTCACATCC 2812
Db 2803 GATGCTAAGATCCCTCTGAGACGAGAGAAACATTTTATTCAGTAAATTCACATCC 2862
QY 2813 TTGTTCTTAAAAAAGCAAGGTCTTTGTTGTGAGAGCAAAATCCCTACATTTTCA 2872
Db 2863 TTGTTCTTAAAAAAGCAAGGTCTTTGTTGTGAGAGCAAAATCCCTACATTTTCA 2922
QY 2873 GTTGTGCTATAGAGATCTCAATATATAGTCTTGTCCGAGCCCTTCATATGTAACCT 2932
Db 2923 GTTGTGCTATAGAGATCTCAATATATAGTCTTGTCCGAGCCCTTCATATGTAACCT 2982
QY 2933 TAGCGTGAAGCTGAGCAAGCTTTGGGGGTCAAGTATGACCTGTTAAGGAGACAGGCC 2992
Db 2983 TAGCGTGAAGCTGAGCAAGCTTTGGGGGTCAAGTATGACCTGTTAAGGAGACAGGCC 3042
QY 2993 TAGTGTAAATCCAGAGAAATGATCTTCAAAAGCTGATTCACAAACCCAGCTCA 3052
Db 3043 TAGTGTAAATCCAGAGAAATGATCTTCAAAAGCTGATTCACAAACCCAGCTCA 3102
QY 3053 TGAACGCCAGGAGACAGAGCACTCACTGCTGAGAGCACTTATAGGAGGCTTGGCAAG 3112
Db 3103 TGAACGCCAGGAGACAGAGCACTCACTGCTGAGAGCACTTATAGGAGGCTTGGCAAG 3162
QY 3113 TCTACTTTAGAGCAAACTCAAGTACTGAGACAGAGAAAGTGGGGCTTTGACATACAT 3172
Db 3163 TCTACTTTAGAGCAAACTCAAGTACTGAGACAGAGAAAGTGGGGCTTTGACATACAT 3222
QY 3173 ATCTGTAGCCCATTTTCTAGAGATTTGAGATTTAGTATAGTATGACATTTTCA 3232
Db 3223 ATCTGTAGCCCATTTTCTAGAGATTTGAGATTTAGTATAGTATGACATTTTCA 3282
QY 3233 CCAATTTCAATTTGTCATAGCAAAATTTCCGAGGCTTATAGAGATTAATTTT 3292
Db 3283 CCAATTTCAATTTGTCATAGCAAAATTTCCGAGGCTTATAGAGATTAATTTT 3342

QY 3293 CTTCTACCTTTATGAGAGAGAGAACTGTCTAGATTGAGTCAAGTCAACACAGAAAC 3352
DB 3343 CTTCTACCTTTATGAGAGAGAGAGAACTGTCTAGATTGAGTCAACACAGAAAC 3402
QY 3353 TGGCAACATCAAGATTTAAGCTTAAGCTTGGAGGCTAAAGAGTCTACCTCTCTTTGTA 3412
DB 3403 TGGCAACATCAAGATTTAAGCTTGGAGGCTAAAGAGTCTACCTCTCTTTGTA 3462
QY 3413 AATCAAGAAATTTGTTAAATGGAGTGTCAATCCTTTAAATTAAGATGAATGGTTTC 3472
DB 3463 AATCAAGAAATTTGTTAAATGGAGTGTCAATCCTTTAAATTAAGATGAATGGTTTC 3522
QY 3473 AA 3474
DB 3523 AA 3524

RESULT 2
US-09-816-494-3
; Sequence 3, Application US/09816494
; Patent No. 6664089
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-816-494-3

Query Match 34.8%; Score 1896; DB 4; Length 1998;
Bee Local Similarity 99.9%; Pred. No. 0;
Matches 1996; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 538 ATGGCCCATGAGATGATGAACTCAATTTGTTACTGAGAGTGGTGGCTCTGCTGGA 597
DB 1 ATGGCCCATGAGATGATGAACTCAATTTGTTACTGAGAGTGGTGGCTCTGCTGGA 60
QY 598 AGTGAACGAGAAAGTCTCTAATTGATAGCCGGCCATTTGTGAAATACATATCATCC 657
DB 61 AGTGAACGAGAAAGTCTCTAATTGATAGCCGGCCATTTGTGAAATACATATCATCC 120
QY 658 CACATTTTGAAGCATTAATATCAAGCTCTCAAGCTTTAAGAACCGAAAGTTGCAAG 717
DB 121 CACATTTTGAAGCATTAATATCAAGCTCTCAAGCTTTAAGAACCGAAAGTTGCAAG 180
QY 718 GACAAAGTGAATTAATACAGAGTCAATCAGAGTTCAGGAAACATTAAGTTGACATTGAT 777
DB 181 GACAAAGTGAATTAATACAGAGTCAATCAGAGTTCAGGAAACATTAAGTTGACATTGAT 240
QY 778 TGCAAGTGAAGAGTTGATGATTAAGATCAAGAGTCTCCAAAGATTTGCTCTCTTCA 837
DB 241 TGCAAGTGAAGAGTTGATGATTAAGATCAAGAGTCTCCAAAGATTTGCTCTCTTCA 300
QY 838 GACGTGTTTCTCACTGTAATCTTGGGTAACTGAGAAAGAGCTTCAATCTGTTCACTG 897
DB 301 GACGTGTTTCTCACTGTAATCTTGGGTAACTGAGAAAGAGCTTCAATCTGTTCACTG 360
QY 898 CTTGCAAGTGGGTTTGTGAGTCTCTGTTGTTTCCCTGGCTCTGAGAAAGAAATCC 957
DB 361 CTTGCAAGTGGGTTTGTGAGTCTCTGTTGTTTCCCTGGCTCTGAGAAAGAAATCC 420
QY 958 ACTGTAGTCCCTACCTGCAATTTCTAGGCTTACTGTTGCCAATTTGGGCAAC 1017

DB 421 ACTGTAGTCCCTACCTGCAATTTCTAGGCTTGTACTGTTGCCAATTTGGGCAAC 480
QY 1018 CGAATTTCTCCCAATCTTTATCTTGGCTGAGGAGATGCTCAACAGAGAGCTGATA 1077
DB 481 CGAATTTCTCCCAATCTTTATCTTGGCTGAGGAGATGCTCAACAGAGAGCTGATA 540
QY 1078 CAGCAAGATGGAGTTGTTATGTTAAATCCAGATTAATCTGTCCAAAGCTGACTTT 1137
DB 541 CAGCAAGATGGAGTTGTTATGTTAAATCCAGATTAATCTGTCCAAAGCTGACTTT 600
QY 1138 ATCCCCGAGTCTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1197
DB 601 ATCCCCGAGTCTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 1198 CCGTGTGTTGACCAATCAGTATGATTTCTTGAAGAAAGCAAGCTCCATGATGATG 1257
DB 661 CCGTGTGTTGACCAATCAGTATGATTTCTTGAAGAAAGCAAGCTCCATGATGATG 720
QY 1258 CTAGTGCACTGTTAGCTGGAGTCTCCGCTCCGCAACATCGCTATCGCTACATCAG 1317
DB 721 CTAGTGCACTGTTAGCTGGAGTCTCCGCTCCGCAACATCGCTATCGCTACATCAG 780
QY 1318 AAGAGATGACATGCTTTTATGATGAAGCTTACAGATTTGTGAAGAAAAAGACTTCT 1377
DB 781 AAGAGATGACATGCTTTTATGATGAAGCTTACAGATTTGTGAAGAAAAAGACTTCT 840
QY 1378 ATATCTCCAACTCAATTTCTGAGGCACTCCGCTGATGATGAAGATTAAGAAC 1437
DB 841 ATATCTCCAACTCAATTTCTGAGGCACTCCGCTGATGATGAAGATTAAGAAC 900
QY 1438 CAGACTGAGAGTCAAGGCGCAAGAGCAATCAAGCTGTGCACTGAGAGAGCAAT 1497
DB 901 CAGACTGAGAGTCAAGGCGCAAGAGCAATCAAGCTGTGCACTGAGAGAGCAAT 960
QY 1498 GAACCTGTCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1557
DB 961 GAACCTGTCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1558 TGTGCGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1617
DB 1021 TGTGCGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1618 CCCAGCGTCCAGAGCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1677
DB 1081 CCCAGCGTCCAGAGCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1678 AGTGGGCTGACCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1737
DB 1141 AGTGGGCTGACCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 1738 TCTCTGATATCAATGATGATTTCAATTCAGCCAGCATGAGAGATCCTTACATGCTTC 1797
DB 1201 TCTCTGATATCAATGATGATTTCAATTCAGCCAGCATGAGAGATCCTTACATGCTTC 1260
QY 1798 TCTCTCATGAAAGATGCTTTGGAATTAATCAAACTTCACTGATGAGAGCAAC 1857
DB 1261 TCTCTCATGAAAGATGCTTTGGAATTAATCAAACTTCACTGATGAGAGCAAC 1320
QY 1858 AAGCTATGCAAGTCTCCCTGTTCAAGAACTATCGAGAGACTCCGAAACAGATCT 1917
DB 1321 AAGCTATGCAAGTCTCCCTGTTCAAGAACTATCGAGAGACTCCGAAACAGATCT 1380
QY 1918 GATTAAGAGAGAGAGCAATCCCAAGAGTGAAGCCGCAAGCTTGAAGAGCAG 1977
DB 1381 GATTAAGAGAGAGAGCAATCCCAAGAGTGAAGCCGCAAGCTTGAAGAGCAG 1440
QY 1978 AGCAAGGATTTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2037
DB 1441 AGCAAGGATTTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 2038 TCTCACTGATCGAAGTGGAGGCTGAGAGCAATTAACACACAGCTTCTTTTGGC 2097
DB 1501 TCTCACTGATCGAAGTGGAGGCTGAGAGCAATTAACACACAGCTTCTTTTGGC 1560

QY	2098	CTTTCCACGAGCAGACAGACCTCCAGAAAGTCTGTGGCTTGGGCTTAAAGGCTGGAC	2157
Db	1561	CTTTCCACGAGCAGACAGACCTCCAGAAAGTCTGTGGCTTGGGCTTAAAGGCTGGAC	1620
QY	2158	TCGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACCAGCAGCTGGTATTTTGGC	2217
Db	1621	TCGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACCAGCAGCTGGTATTTTGGC	1680
QY	2218	ACAGAGTCTCTACACTTTCTACTCTGACCTCAGCACTTACCGAGGCAATGTCCTTACTCT	2277
Db	1681	ACAGAGTCTCTACACTTTCTACTCTGACCTCAGCACTTACCGAGGCAATGTCCTTACTCT	1740
QY	2278	GCTTACAGCTGACGACGACTGCCCCACTTGGGAGACCAAGTCTTATCTGTGCGAGGCGG	2337
Db	1741	GCTTACAGCTGACGACGACTGCCCCACTTGGGAGACCAAGTCTTATCTGTGCGAGGCGG	1800
QY	2338	CAGAAAGCCAAATGACAGAGCTGACTCTGGCGGCGAGCTGGCAATGAAAGAGAGCCCTTTGAA	2397
Db	1801	CAGAAAGCCAAATGACAGAGCTGACTCTGGCGGCGAGCTGGCAATGAAAGAGAGCCCTTTGAA	1860
QY	2398	AAGCAGTTTAAACGCAGAGCTGCCAAATTGGAAATTGGAGAGACATCATGTCCAGAAAC	2457
Db	1861	AAGCAGTTTAAACGCAGAGCTGCCAAATTGGAAATTGGAGAGACATCATGTCCAGAAAC	1920
QY	2458	AGGTCAACGGGAAGAGCTGGGGAAGATGGGCAATGAGTCTAGCTTTTGGGCGAGCATGAA	2517
Db	1921	AGGTCAACGGGAAGAGCTGGGGAAGATGGGCAATGAGTCTAGCTTTTGGGCGAGCATGAA	1980
QY	2518	ATCATTTAGAGTCTCTCTGA	2535
Db	1981	ATCATTTAGAGTCTCTCTGA	1998

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1      RESULT 3
2      US-09-016-434-91
3      ; Sequence 91, Application US/09016434
4      Patent No. 6500938
5      ; GENERAL INFORMATION:
6      APPLICANT: Janice Au-Young
7      APPLICANT: Jeffrey J. Seilheimer
8      TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
9      TITLE OF INVENTION: PATHWAY GENE EXPRESSION
10     NUMBER OF SEQUENCES: 1490
11     ; CORRESPONDENCE ADDRESS:
12     ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
13     STREET: 3174 PORTER DRIVE
14     CITY: PALO ALTO
15     STATE: CALIFORNIA
16     COUNTRY: USA
17     ZIP: 94304
18     ; COMPUTER READABLE FORM:
19     MEDIUM TYPE: Floppy disk
20     COMPUTER: IBM PC compatible
21     OPERATING SYSTEM: PC-DOS/MS-DOS
22     SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
23     CURRENT APPLICATION DATA:
24     APPLICATION NUMBER: US/09/016,434
25     FILING DATE: HERewith
26     CLASSIFICATION:
27     PRIOR APPLICATION DATA:
28     APPLICATION NUMBER:
29     FILING DATE:
30     CLASSIFICATION:
31     ATTORNEY/AGENT INFORMATION:
32     NAME: Zeller, Karen J.
33     REGISTRATION NUMBER: 37,071
34     REFERENCE/DOCKET NUMBER: PA-0002 US
35     TELECOMMUNICATION INFORMATION:
36     TELEPHONE: (650) 855-0555
37     TELEFAX: (650) 845-4166
38     INFORMATION FOR SEQ. ID NO: 91:
39     SEQUENCE CHARACTERISTICS:

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; LENGTH: 279 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGEF03
; CLONE: 1234795
US-09-016-434-91

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Query Match	4.5%;	Score 247;	DB 4;	Length 279;
Best Local Similarity	100.0%;	Pred. No. 7.2e-113;		
Matches 247;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	GGGAAAAGAGCACTTATGTGTGCATGGCCCATGAGATGATTGGAACTCAATTTACT	573
Db	1 GGGAAAAGAGCACTTATGTGTGCATGGCCCATGAGATGATTGGAACTCAATTTACT	60
QY	GAGAGGTTTGCGCTTCGCTGGAAAAGTGGAACGAAAAAGTGCCTAATTGATGCCGG	633
Db	61 GAGAGGTTTGCGCTTCGCTGGAAAAGTGGAACGAAAAAGTGCCTAATTGATGCCGG	120
QY	CCATTGTGGAATAACAATACATCCCACATTTGGAGCATTATATCAATGCMCCAG	693
Db	121 CCATTGTGGAATAACAATACATCCCACATTTGGAGCATTATATCAATGCTCCAAG	180
QY	CTTATGAAGCGAAGGTTCACACGACCAAAGTGTTAATTACAGAGCTCATCCACATTCA	753
Db	181 CTTATGAAGCGAAGGTTCACACGACCAAAGTGTTAATTACAGAGCTCATCCACATTCA	240
QY	GCGAAAC 760	
Db	241 GCGAAAC 247	

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RESULT 4
US-09-513-999C-2877
Sequence 2877, Application US/0951399C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 2877
LENGTH: 333
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 127..333
FEATURE:
NAME/KEY: misc_feature
LOCATION: 17
OTHER INFORMATION: h=a or c or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18
OTHER INFORMATION: y=c or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 19
OTHER INFORMATION: k=g or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 36

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OTHER INFORMATION: n=a, g, c or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 58
OTHER INFORMATION: r=a or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: 237
OTHER INFORMATION: w=a or t
FEATURE:
NAME/KEY: UNSURE
LOCATION: 37
OTHER INFORMATION: xaa=His or Gln
US-09-513-999C-2877

Query Match 3.8%; Score 205; DB 4; Length 333;
Best Local Similarity 99.6%; Pred. No. 8e-92;
Matches 255; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 648 CAATACATCCCATTTTGAAGCATTATATATCAAGCTCCAGCTTATGAAGCGAAG 707
DB 78 CAATACATCCCATTTTGAAGCATTATATATCAAGCTCCAGCTTATGAAGCGAAG 137
QY 708 GTTGCAACAGACAAAGTTTATATACAGAGCTCATCCAGCATTCAGGAAAATTAAGT 767
DB 138 GTTGCAACAGACAAAGTTTATATACAGAGCTCATCCAGCATTCAGGAAAATTAAGT 197
QY 768 TGACATTATATGCAATGCAAGAGTTGATTACATCAAGCTCCCAAGATGTTGCTC 827
DB 198 TGACATTATATGCAATGCAAGAGTTGATTACATCAAGCTCCCAAGATGTTGCTC 257
QY 828 TCTCTCTCAGAGCTTTTCTGCTGTAAGCTTGAAGAGAGCTTCAAGCTC 887
DB 258 TCTCTCTCAGAGCTTTTCTGCTGTAAGCTTGAAGAGAGCTTCAAGCTC 317
QY 888 TGTTCACCTGCTTGCA 903
DB 318 TGTTCACCTGCTTGCA 333

RESULT 5
US-09-513-999C-3684/C
Sequence 3684, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Ducleit, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513, 999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 3684
LENGTH: 378
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 216..377
FEATURE:
NAME/KEY: misc_feature
LOCATION: 164
OTHER INFORMATION: k=g or t
US-09-513-999C-3684

Query Match 3.4%; Score 187; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 8.3e-83;
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 581 TGTGCTCTGCTGGAAGTGAACGGAAGAGTCTGTAATGATAGCCGCCATTG 640
DB 378 TGTGCTCTGCTGGAAGTGAACGGAAGAGTCTGTAATGATAGCCGCCATTG 319
QY 641 TGAATACATATATATCCCAATTTTGAAGCATTATATATCAAGCTCCCAAGTTATGA 700
DB 318 TGAATACATATATATCCCAATTTTGAAGCATTATATATCAAGCTCCCAAGTTATGA 259
QY 701 AGCGAAGTTGCAACAGACAAAGTTTATATACAGAGCTCATCCAGATTCAGGAAAC 760
DB 258 AGCGAAGTTGCAACAGACAAAGTTTATATACAGAGCTCATCCAGATTCAGGAAAC 199
QY 761 ATTAAGT 767
DB 198 ATTAAGT 192

RESULT 6
US-09-513-999C-24342
Sequence 24342, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Ducleit, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513, 999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 24342
LENGTH: 259
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 230
OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-24342

Query Match 2.3%; Score 128; DB 4; Length 259;
Best Local Similarity 100.0%; Pred. No. 2.9e-53;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 102 GTGTAAGTTGATGGAAGAGCTGTAATGTTAATATGATATATGTTGTTGAAGT 161
QY 5038 AAGCCAGCTGTTGAACGTTAACTGTGATTTCTCATTTTGAAGTGTATGTTA 5097
DB 162 AAGCCAGCTGTTGAACGTTAACTGTGATTTCTCATTTTGAAGTGTATGTTA 221
QY 5098 ATGTATGA 5105
DB 222 ATGTATGA 229

Search completed: February 15, 2005, 21:20:50
Job time : 824 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: February 15, 2005, 15:22:58 ; Search time 2769 Seconds
(without alignments)
11613.401 Million cell updates/sec

Title: US-10-029-345a-108
Perfect score: 5450
Sequence: 1 gaaagaagacgagagagag.....ctgattccagacacacaaag 5450

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 5378673 seqs, 2950229984 residues

Word size : 100

Total number of hits satisfying chosen parameters: 84

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

Published Applications_MA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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- 19: /cgn2_6/ptodata/1/pubpna/US10F_NEW_PUB.seq:*
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- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	4413	81.0	5145	18	US-10-357-930-20824
2	4413	81.0	5145	18	US-10-357-930-20969
3	4413	81.0	5145	18	US-10-357-930-21071
4	4413	81.0	5145	18	US-10-357-930-21083
5	4413	81.0	5145	18	US-10-357-930-21103
6	4413	81.0	5145	18	US-10-357-930-21130
7	4413	81.0	5145	18	US-10-357-930-21307
8	4413	81.0	5145	18	US-10-357-930-22820
9	4413	81.0	5145	18	US-10-357-930-26659
10	4413	81.0	5145	18	US-10-357-930-26815
11	4413	81.0	5145	18	US-10-357-930-26912
					Sequence 26923, A

12	4413	81.0	5145	18	US-10-357-930-27145	Sequence 27145, A
13	4413	81.0	5145	18	US-10-357-930-27149	Sequence 27149, A
14	4413	81.0	5145	18	US-10-357-930-28675	Sequence 28675, A
15	4262	78.2	4790	18	US-10-648-593-115	Sequence 115, App
16	3482	63.9	3766	17	US-10-343-357-17	Sequence 17, Appl
17	3238	59.4	3625	17	US-10-425-114-26234	Sequence 26234, A
18	3118	57.2	3496	9	US-09-964-277-1	Sequence 1, Appl1
19	3079	56.5	3544	9	US-09-816-494-1	Sequence 1, Appl1
20	3079	56.5	3544	17	US-10-377-072-25	Sequence 25, Appl
21	3079	56.5	3544	18	US-10-377-072-25	Sequence 25, Appl
22	3069	56.3	3521	18	US-10-370-715B-261	Sequence 261, App
23	2837	52.1	3059	17	US-10-257-026-1	Sequence 1, Appl1
24	2624	48.1	2966	17	US-10-296-115-520	Sequence 520, App
25	2459	45.1	2732	9	US-10-168-506-2	Sequence 2, Appl1
26	2117	38.8	2332	17	US-09-964-277-20	Sequence 20, Appl
27	2098	38.5	2558	17	US-10-104-047-1750	Sequence 1750, App
28	1896	34.8	1998	9	US-09-816-494-3	Sequence 3, Appl1
29	1896	34.8	1998	17	US-10-377-072-27	Sequence 27, Appl
30	1896	34.8	1998	18	US-10-377-072-27	Sequence 27, Appl
31	1889	34.7	2102	17	US-10-094-749-673	Sequence 673, App
32	1889	27.3	1916	17	US-10-108-260A-2429	Sequence 2429, App
33	1318	24.2	2071	17	US-10-072-012-257	Sequence 257, App
34	1225	22.5	2200	17	US-10-072-012-255	Sequence 255, App
35	940	17.2	940	17	US-10-172-118-2599	Sequence 2599, App
36	940	17.2	940	17	US-10-342-887-2599	Sequence 2599, App
37	631	11.6	860	13	US-10-027-632-144266	Sequence 144266, Sequence 144266, Sequence 147620, Sequence 147620, A
38	631	11.6	860	17	US-10-027-632-144266	Sequence 24920, A
39	600	11.0	841	13	US-10-027-632-147620	Sequence 24920, A
40	600	11.0	841	17	US-10-027-632-147620	Sequence 24920, A
41	541	9.9	803	13	US-10-027-632-24930	Sequence 24930, A
42	541	9.9	803	17	US-10-027-632-24930	Sequence 24930, A
43	541	9.9	803	17	US-10-027-632-24930	Sequence 24930, A
44	541	9.9	803	17	US-10-027-632-24930	Sequence 24930, A
45	431	7.9	518	18	US-10-357-930-43560	Sequence 43560, A
46	431	7.6	425	18	US-10-357-930-10717	Sequence 10717, A
47	414	7.6	467	18	US-10-357-930-11909	Sequence 31909, A
48	414	7.6	467	18	US-10-357-930-10868	Sequence 40868, A
49	414	7.6	467	17	US-10-357-930-11017	Sequence 41017, A
50	403	7.4	789	17	US-10-220-891-86	Sequence 86, Appl
51	400	7.3	408	18	US-10-357-930-10898	Sequence 10898, A
52	398	7.3	438	18	US-10-357-930-12077	Sequence 32077, A
53	391	7.2	399	18	US-10-357-930-13561	Sequence 13561, A
54	391	7.2	442	18	US-10-357-930-14703	Sequence 34703, A
55	381	7.0	877	9	US-09-764-853-158	Sequence 158, App
56	343	6.3	390	9	US-09-880-107-177	Sequence 177, App
57	335	5.1	456	18	US-10-357-930-13392	Sequence 43392, App
58	321	5.9	489	18	US-10-357-930-1296	Sequence 1296, App
59	316	5.7	787	17	US-10-220-891-85	Sequence 85, Appl
60	309	5.7	309	10	US-09-960-706-887	Sequence 887, App
61	309	5.7	309	10	US-09-873-119-580	Sequence 580, App
62	296	5.4	355	18	US-10-357-930-1729	Sequence 1729, App
63	291	5.3	478	10	US-09-918-995-25801	Sequence 25801, A
64	283	5.2	383	18	US-09-803-719-1233	Sequence 1233, App
65	263	4.8	418	18	US-10-357-930-11243	Sequence 11243, App
66	262	4.8	461	18	US-10-357-930-32416	Sequence 32416, A
67	262	4.8	461	18	US-10-357-930-41000	Sequence 41000, A
68	262	4.8	461	18	US-10-357-930-41346	Sequence 41346, A
69	253	4.6	411	18	US-10-357-930-1548	Sequence 1548, App
70	249	4.6	452	9	US-09-880-107-1941	Sequence 1941, App
71	247	4.5	277	18	US-10-637-855-29	Sequence 29, Appl
72	247	4.5	279	17	US-10-305-720-91	Sequence 91, Appl
73	242	4.4	345	18	US-10-357-930-11236	Sequence 11236, A
74	241	4.4	345	18	US-10-357-930-2067	Sequence 2067, App
75	240	4.4	377	18	US-10-357-930-32409	Sequence 32409, A
76	240	4.4	377	18	US-10-357-930-41339	Sequence 41339, A
77	224	4.1	419	18	US-10-357-930-32060	Sequence 32060, A
78	224	4.1	422	18	US-10-357-930-2074	Sequence 2074, App
79	224	4.1	427	18	US-10-357-930-10878	Sequence 10878, App
80	217	4.0	246	17	US-10-257-026-3	Sequence 3, Appl1
81	217	4.0	823	18	US-10-357-930-10465	Sequence 10465, A
82	189	3.5	823	18	US-10-357-930-31662	Sequence 31662, A
83	165	3.0	483	18	US-10-357-930-40631	Sequence 40631, A
84	123	2.3	326	18	US-10-357-930-1709	Sequence 1709, App

ALIGNMENTS

RESULT 1

US-10-357-930-20824
Sequence 20824, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Morahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357, 930
PRIOR APPLICATION NUMBER: 2003-02-04
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20824
LENGTH: 5145
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1, 5144, 5145
OTHER INFORMATION: n = A,T,C or G
US-10-357-930-20824

Query Match 81.0%; Score 4413; DB 18; Length 5145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4683; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Db 2144 TCGGCGTTTTCACACGAGCAGGAGACCTCAGAAAGTCTGGGCTGGGCTTTAAGGCT 2203
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Db 4903 TGGCTGG 4909
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RESULT 2
US-10-357-930-20969
; Sequence 20969, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John
; APPLICANT: Nedeege, Wilson
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BON
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/189,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20969
; LENGTH: 5145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 5144, 5145
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-20969

Query Match 81.0%; Score 4413; DB 18; Length 5145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4683; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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RESULT 3
US-10-357-930-21071
; Sequence 21071, Application US/10357930


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1  PublicationNo. US20040259086A1
2  GENERAL INFORMATION:
3  APPLICANT: Schlegel, Robert
4  APPLICANT: Endege, Wilson
5  APPLICANT: Monahan, John
6  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
7  TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
8  TITLE OF INVENTION: HUMAN PROSTATE CANCER
9  FILE REFERENCE: MRI-0078CN
10 CURRENT FILING DATE: US/10/357,930
11 CURRENT FILING DATE: 2003-02-04
12 PRIOR APPLICATION NUMBER: 09/785,276
13 PRIOR FILING DATE: 2003-02-16
14 PRIOR APPLICATION NUMBER: 60/183,319
15 PRIOR FILING DATE: 2000-02-17
16 PRIOR APPLICATION NUMBER: 60/189,862
17 PRIOR FILING DATE: 2000-03-16
18 PRIOR APPLICATION NUMBER: 60/207,454
19 PRIOR FILING DATE: 2000-05-25
20 PRIOR APPLICATION NUMBER: 60/211,314
21 PRIOR FILING DATE: 2000-06-09
22 PRIOR APPLICATION NUMBER: 60/219,007
23 PRIOR FILING DATE: 2000-07-18
24 PRIOR APPLICATION NUMBER: 60/255,281
25 PRIOR FILING DATE: 2000-12-13
26 NUMBER OF SEQ ID NOS: 62232
27 SOFTWARE: FastSeq for Windows Version 4.0
28 SEQ ID NO 21071
29 LENGTH: 5145
30 TYPE: DNA
31 ORGANISM: Homo sapiens
32 FEATURE:
33 NAME/KEY: misc_feature
34 LOCATION: 1, 5144, 5145
35 OTHER INFORMATION: n = A,T,C or G
36 US-10-357-930-21071

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Db 4903 TGGCTGG 4909

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RESULT 4
US-10-357-930-21083
; Sequence 21083, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson

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; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21083
; LENGTH: 5145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 5144, 5145
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-21083

Query Match 81.0%; Score 4413; DB 18; Length 5145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4683; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Qy 3833 CCATTTAGTTTGTATCAATTTGAAATAGAGTCAAGCAATGAGCCAACTGTTTGGAA 3892
Db 3883 CCATTTAGTTTGTATCAATTTGAAATAGAGTCAAGCAATGAGCCAACTGTTTGGAA 3942
Qy 3893 ACGCTGCGGCGGTCTTCTAGTGGAGAAAGCAATCAAAATGAGCAGAGCAAGAGGG 3952
Db 3943 ACGCTGCGGCGGTCTTCTAGTGGAGAAAGCAATCAAAATGAGCAGAGCAAGAGGG 4002
Qy 3953 GGTCTCTAGTCTTCAACCTCAATCATCTGTATGAAATCGTCTTGGCAGCTGAACATAG 4012
Db 4003 GGTCTCTAGTCTTCAACCTCAATCATCTGTATGAAATCGTCTTGGCAGCTGAACATAG 4062

Qy 4013 AGGTCACTGGAACAAGTAGTAGTAGATTTGGCTTCAAAACATCTCTGCTGAGTT 4072
Db 4063 AGGTCACTGGAACAAGTAGTAGTAGATTTGGCTTCAAAACATCTCTGCTGAGTT 4122
Qy 4073 TATCAGCTCAATGTGGCTCTCTTTGAAGCTTAAATTCACACAGACGCTTTTGGG 4132
Db 4123 TATCAGCTCAATGTGGCTCTCTTTGAAGCTTAAATTCACACAGACGCTTTTGGG 4182
Qy 4133 GTGGGCTGGGCGGTGTGATGATGTTTCTTCCCTCTGTAAGTGTGCTAGTTGCTG 4192
Db 4183 GTGGGCTGGGCGGTGTGATGATGTTTCTTCCCTCTGTAAGTGTGCTAGTTGCTG 4242
Qy 4193 CCTGTATCTCAGGTTTCTCTGTTTGAAGAAATGACAGTTTGTGACAGATG 4252
Db 4243 CCTGTATCTCAGGTTTCTCTGTTTGAAGAAATGACAGTTTGTGACAGATG 4302
Qy 4253 ACTTATGTTTCTATGAGTACTTAAACAGACAGAAATGATATGCTCAACAGAG 4312
Db 4303 ACTTATGTTTCTATGAGTACTTAAACAGACAGAAATGATATGCTCAACAGAG 4362
Qy 4313 CCGACTTGTATGAGGATGATGAGCCGACAGACTTCACTAGTTGTGACAAATATGT 4372
Db 4363 CCGACTTGTATGAGGATGATGAGCCGACAGACTTCACTAGTTGTGACAAATATGT 4422
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Db 4423 GCTATGATGGGCTTAAAGTGAAGCAGAGAGGCTCAGCCGATTTGATATGATCTGG 4482
Qy 4433 AAGGTCTGTCAACGATTTGATGATTTTGAATATATATGAAATCTTAAATCAGAC 4492
Db 4483 AAGGTCTGTCAACGATTTGATGATTTTGAATATATATGAAATCTTAAATCAGAC 4542
Qy 4493 ATTCTCAAGTTTCAACAGTATTTTGAATATATATGATATATATGATATATGAT 4552
Db 4543 ATTCTCAAGTTTCAACAGTATTTTGAATATATATGATATATATGATATATGAT 4602
Qy 4553 GTTCAACATCTCAGAGTGTGTCAATGCCCAAAACATGTTTAAAGAAAGAGAGTAC 4612
Db 4603 GTTCAACATCTCAGAGTGTGTCAATGCCCAAAACATGTTTAAAGAAAGAGAGTAC 4662
Qy 4613 TCTTTGCTAACGATTTTCAAGAGGTTTGGGCACTTGTATTAATGAGCTTCTGAT 4672
Db 4663 TCTTTGCTAACGATTTTCAAGAGGTTTGGGCACTTGTATTAATGAGCTTCTGAT 4722
Qy 4673 TAGGCTTCTTGGCCATGTCCTCTTCTTGAACCTGTGATGATGATCATCTAC 4732
Db 4723 TAGGCTTCTTGGCCATGTCCTCTTCTTGAACCTGTGATGATGATCATCTAC 4782
Qy 4733 AGCTTTAGTGTGTTTCAATGATGCTCAATTAATCAATTTGAAATGAGCTGCGGTG 4792
Db 4783 AGCTTTAGTGTGTTTCAATGATGCTCAATTAATCAATTTGAAATGAGCTGCGGTG 4842
Qy 4793 GCGAAGGAGGCTCGAGAGCAGGCTGTGAGCTGTTGATGTTTGAAGTGGGCTG 4852
Db 4843 GCGAAGGAGGCTCGAGAGCAGGCTGTGAGCTGTTGATGTTTGAAGTGGGCTG 4902
Qy 4853 TGGCTGG 4859
Db 4903 TGGCTGG 4909

RESULT 5
US-10-357-930-21303
; Sequence 21303, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilbert
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER

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/ FILE REFERENCE: MRI-007BCN
/ CURRENT APPLICATION NUMBER: US/10/357,930
/ CURRENT FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: 09/785,276
/ PRIOR FILING DATE: 2003-02-16
/ PRIOR APPLICATION NUMBER: 60/183,319
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: 60/189,862
/ PRIOR FILING DATE: 2000-03-16
/ PRIOR APPLICATION NUMBER: 60/207,454
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: 60/211,314
/ PRIOR FILING DATE: 2000-06-09
/ PRIOR APPLICATION NUMBER: 60/219,007
/ PRIOR FILING DATE: 2000-07-18
/ PRIOR APPLICATION NUMBER: 60/255,281
/ PRIOR FILING DATE: 2000-12-13
/ NUMBER OF SEQ ID NOS: 62232
/ SOFTWARE: PASCSeq for Windows Version 4.0
/ SEQ ID NO 21303
/ LENGTH: 5145
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1, 5144, 5145
/ OTHER INFORMATION: n = A,T,C or G
US-10-357-930-21303
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Query Match      81.0%; Score 4413; DB 18; Length 5145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4693; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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DB      224 GCTTTCAGTCCAGTGTAAAGCTGTTGAGAGCGGAGCAAGGTAAAGATGATGATG 283
QY      233 CGCTGGCTCTCCAAAGCATCTTTTGTGTGAATGTTTATTCAGTCATCTTTTATGA 292
DB      284 CGCTGGCTCTCCAAAGCATCTTTTGTGTGAATGTTTATTCAGTCATCTTTTATGA 343
QY      293 ATCAATGTGAGGGGCTGTTGTGAGAGGAGTCCCTTTCAGAGACATCAACGGGAAA 352
DB      344 ATCAATGTGAGGGGCTGTTGTGAGAGGAGTCCCTTTCAGAGACATCAACGGGAAA 403
QY      353 GAGAAAGAGACATTCATTGAGAGGCTCTTGCTGAAAAATGGTTTAACTCTCTTTTGGC 412
DB      404 GAGAAAGAGACATTCATTGAGAGGCTCTTGCTGAAAAATGGTTTAACTCTCTTTTGGC 463
QY      413 AGTCACCAAGCCCTGAGCTCATATACCTTTTATGTAATGAGATGAGCTGAGCTTTTGAAC 472
DB      464 AGTCACCAAGCCCTGAGCTCATATACCTTTTATGTAATGAGATGAGCTGAGCTTTTGAAC 523
QY      473 ACACCACCATTAATCATCTGCTGCAAAATTAAGAGAGGAGGAAAAAGAGACTTAATG 532
DB      524 ACACCACCATTAATCATCTGCTGCAAAATTAAGAGAGGAGGAAAAAGAGACTTAATG 583
QY      533 TTGTATATGGCCCATGAGATGATGTAATGAACTCAAAATTTTACTGAGAGGTTGGTGGCTGCG 592
DB      584 TTGTATATGGCCCATGAGATGATGTAATGAACTCAAAATTTTACTGAGAGGTTGGTGGCTGCG 643
QY      593 TGGAAAGTGGAAAGGAAAAAGTGTGCTAAATTTGATTAACCCGGCCCTTTGTGGAATACATA 652
DB      644 TGGAAAGTGGAAAGGAAAAAGTGTGCTAAATTTGATTAACCCGGCCCTTTGTGGAATACATA 703
QY      653 CATCCACATTTTGGAAAGCATTAATATCAATGCTCAAGCTTAATGAGAGGATGCG 712
DB      704 CATCCACATTTTGGAAAGCATTAATATCAATGCTCAAGCTTAATGAGAGGATGCG 763
QY      713 AACGAGCAAAAGCTTAATTAACAGAGCTCATCCAGCATTAAGCGAAACATTAAGGTTGACA 772
DB      764 AACGAGCAAAAGCTTAATTAACAGAGCTCATCCAGCATTAAGCGAAACATTAAGGTTGACA 823
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QY      773 TTGATTCAGTCAGAGGTTGTAGTTTACGATCAAAAGCTCCCAAGATGTGCTCTCT 832
DB      824 TTGATTCAGTCAGAGGTTGTAGTTTACGATCAAAAGCTCCCAAGATGTGCTCTCTCT 883
QY      833 CTTCAAGCTGTTTCTCACTGACTGACTTCTGGGTTAACTGAGAAAGACTTCACTGTTC 892
DB      884 CTTCAAGCTGTTTCTCACTGACTGACTTCTGGGTTAACTGAGAAAGACTTCACTGTTC 943
QY      893 ACCCTGTCAGAGTGGGTTTCTGAGTCTCTGCTGTTTCCCTGGCCCTGTGAGAGAA 952
DB      944 ACCCTGTCAGAGTGGGTTTCTGAGTCTCTGCTGTTTCCCTGGCCCTGTGAGAGAA 1003
QY      953 AATCCACTTATGCTCCTTACCTGCAATTTTCAAGCTTGTCTTACCTGTTGCCAATTTGGGC 1012
DB      1004 AATCCACTTATGCTCCTTACCTGCAATTTTCAAGCTTGTCTTACCTGTTGCCAATTTGGGC 1063
QY      1013 CAACCCGAATCTTCCCAATCTTTATCTGTGGCTGCGAGGAGATGCTCAACAGAGAGC 1072
DB      1064 CAACCCGAATCTTCCCAATCTTTATCTGTGGCTGCGAGGAGATGCTCAACAGAGAGC 1123
QY      1073 TGAATACAGCAAGATGGGATGGTTATGTGTAAATGCAAGCTATACCTGTCCAAAGCCTG 1132
DB      1124 TGAATACAGCAAGATGGGATGGTTATGTGTAAATGCAAGCTATACCTGTCCAAAGCCTG 1183
QY      1133 ACTTATATCCCGAGCTCATTTTCTGCGTGTGCTGTGAATGACAGCTTTGTGAGAAA 1192
DB      1184 ACTTATATCCCGAGCTCATTTTCTGCGTGTGCTGTGAATGACAGCTTTGTGAGAAA 1243
QY      1193 TTTTGGCGTGGTTGAGCAAAATCAGTAGATTTCAATTTGAGAAAGCAAAAGCTCCAAATGAG 1252
DB      1244 TTTTGGCGTGGTTGAGCAAAATCAGTAGATTTCAATTTGAGAAAGCAAAAGCTCCAAATGAG 1303
QY      1253 GTGTTCTAGTGCACTGTTTGTGCTGGATCTCCGCTCCGCAATCATGCTATGCGCTACA 1312
DB      1304 GTGTTCTAGTGCACTGTTTGTGCTGGATCTCCGCTCCGCAATCATGCTATGCGCTACA 1363
QY      1313 TCATGAAGAGATGAGCAATGCTTTTATGATGAACCTTACGATTTGTGAAAGAAAAGAGC 1372
DB      1364 TCATGAAGAGATGAGCAATGCTTTTATGATGAACCTTACGATTTGTGAAAGAAAAGAGC 1423
QY      1373 CTACTATATCTCCAAACTTCAATTTTCTGGGCAATCTCTGCACTATGAGAAAGATTA 1432
DB      1424 CTACTATATCTCCAAACTTCAATTTTCTGGGCAATCTCTGCACTATGAGAAAGATTA 1483
QY      1433 AGAACCAAGCTGAGAGATCAGAGGCCCAAGAGCAAACTCAAGCTGTGCACTGAGAGAGC 1492
DB      1484 AGAACCAAGCTGAGAGATCAGAGGCCCAAGAGCAAACTCAAGCTGTGCACTGAGAGAGC 1543
QY      1493 CAATGAACCTGTCCCTGCTGTCTCAGAGGGTGAACAGAAAGCGAGCCCTCAAGTC 1552
DB      1544 CAATGAACCTGTCCCTGCTGTCTCAGAGGGTGAACAGAAAGCGAGCCCTCAAGTC 1603
QY      1553 CACCTGTGCGCACTGTGCTACCTCAGAGGCAAGGCAAAAGGCCGTGCAATCCGCA 1612
DB      1604 CACCTGTGCGCACTGTGCTACCTCAGAGGCAAGGCAAAAGGCCGTGCAATCCGCA 1663
QY      1613 GCGTGGCCAGCGGCGCAGGCGTGAAGCGCTGCTTTGAGAGCAAGCCCGCTGTGATGAG 1672
DB      1664 GCGTGGCCAGCGGCGCAGGCGTGAAGCGCTGCTTTGAGAGCAAGCCCGCTGTGATGAG 1723
QY      1673 CGCTCAGTGGGCTGCACTGTGCGCAGACAGGCTGGAAGACAGCAATTAAGCTCAAGCCTT 1732
DB      1724 CGCTCAGTGGGCTGCACTGTGCGCAGACAGGCTGGAAGACAGCAATTAAGCTCAAGCCTT 1783
QY      1733 CTTTCTCTCTGATATCAAAATCAATGTTTATATTCAGCCAGATGAGCAATCCATTAATG 1792
DB      1784 CTTTCTCTCTGATATCAAAATCAATGTTTATATTCAGCCAGATGAGCAATCCATTAATG 1843
QY      1793 GCTTCTCTCATCAGAAAGCTTTTGAATCTCAAACTTTCACATCTGTGATGGGA 1852
DB      1844 GCTTCTCTCATCAGAAAGCTTTTGAATCTCAAACTTTCACATCTGTGATGGGA 1903
QY      1853 CCAACAGACTATGCCAGTTTCTCCCTGTTCAGAACTATGCGAGCAGACTCCCGAAACA 1912
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Dp	1904	CCAAACAGCTATGCCAGTTCTCCCTGTCAGAAACTATCGAGAGACTCCGAAACCA	1963
Qy	1913	GTCTCGATTAAGGAGGAGCCAGCATCCCCAAGAACTCGACAGCCGACGGCTTCAGACA	1972
Dp	1964	GTCTCGATTAAGGAGGAGGAGCAGCATCCCAAGAACTCGACAGCCGACGGCTTCAGACA	2022
Qy	1973	GCCAGAGCAAGCGATTGCATTCGGTCAGAACGAGCAGCAGTGCGACCGGCCAGAGTCCC	2033
Dp	2024	GCCAGAGCAAGCGATTGCATTCGGTCAGAACGAGCAGCAGTGCGACCGGCCAGAGTCCC	2083
Qy	2033	TTTTTATCTCCACTGCATGGAATGTGGGAGCGTGGAGAGCAATTACACACAGCTTCCTT	2092
Dp	2084	TTTTTATCTCCACTGCATGGAATGTGGGAGCGTGGAGAGCAATTACACACAGCTTCCTT	2143
Qy	2093	TCGGGCTTTCACACAGCAGCAGCACTCAACGAGTCTGTGGCTGGGGCTTTAAGGGCT	2155
Dp	2144	TCGGGCTTTCACACAGCAGCAGCACTCAACGAGTCTGTGGCTGGGGCTTTAAGGGCT	2202
Qy	2153	GGCACCTGGGATATCTTGGGCCCCCAGACCTCTACCCCTTCCCTGACAGCAGCTGGTAT	2212
Dp	2204	GGCACCTGGGATATCTTGGGCCCCCAGACCTCTACCCCTTCCCTGACAGCAGCTGGTAT	2262
Qy	2213	TTGGCACAAGAGTCTTCACACTTCTATCTGTGCTCAGCCATCTACGGAGGCAATGCCAGT	2272
Dp	2264	TTGGCACAAGAGTCTTCACACTTCTATCTGTGCTCAGCCATCTACGGAGGCAATGCCAGT	2322
Qy	2273	ACTGTGCTTACAGCTGCAGCCAGCTGCCCATTTGGGAGAACCAAGTCTATTCTGTGGCCA	2333
Dp	2324	ACTGTGCTTACAGCTGCAGCCAGCTGCCCATTTGGGAGAACCAAGTCTATTCTGTGGCCA	2383
Qy	2333	GGCGGCAGAGCCAGATGACAGAGCTGACTGGCGCGAGCTGGCATGAGAGAGCCCT	2392
Dp	2384	GGCGGCAGAGCCAGATGACAGAGCTGACTGGCGCGAGCTGGCATGAGAGAGCCCT	2443
Qy	2393	TTGAAAACAGATTTTAAAGCGCAGAGCTGCCAAATGGAAATTTGGAGAGAGCATATGTGAG	2455
Dp	2444	TTGAAAACAGATTTTAAAGCGCAGAGCTGCCAAATGGAAATTTGGAGAGAGCATATGTGAG	2503
Qy	2453	AGAACAGGTCAACGGGAGAGGCTGGGGAAAGTGGGGAGTCAAGCTGATCTTTTCGGGCAGCA	2512
Dp	2504	AGAACAGGTCAACGGGAGAGGCTGGGGAAAGTGGGGAGTCAAGCTGATCTTTTCGGGCAGCA	2562
Qy	2513	TGGAATCATTTGAGGCTCTCTGAGAGAGAAAGACACTTGTGACTTCTATAGACAAATTTTT	2572
Dp	2564	TGGAATCATTTGAGGCTCTCTGAGAGAGAAAGACACTTGTGACTTCTATAGACAAATTTTT	2622
Qy	2573	TTTTTCTTGTCACAAAAAAATTCCTGTGAATCTGAATATATATATGTACATACATATA	2633
Dp	2623	TTTTTCTTGTCACAAAAAAATTCCTGTGAATCTGAATATATATATGTACATACATATA	2682
Qy	2633	TATTTTGGAAAAATGAGCTATGCTGTAAAGCAACAGTGGATCAACCCAGTTGTATCT	2692
Dp	2683	TATTTTGGAAAAATGAGCTATGCTGTAAAGCAACAGTGGATCAACCCAGTTGTATCT	2743
Qy	2693	CTCTTAAACATCTGCATTTTGAGAGATCAGCTATATCTTCTCTCAACAAAAATGGAAGGCA	2752
Dp	2743	CTCTTAAACATCTGCATTTTGAGAGATCAGCTATATCTTCTCTCAACAAAAATGGAAGGCA	2802
Qy	2753	GATGCTAAGATCCCCCTTGAACGAGAGGAAAAACATTTTATTCAGGAAATTCACATCTCTC	2812
Dp	2803	GATGCTAAGATCCCCCTTGAACGAGAGGAAAAACATTTTATTCAGGAAATTCACATCTCTC	2862
Qy	2813	TTGTCTTAAAAAAAGCAAGTGTCTTGGGTGGGAGCAAAATCCCTCAACATTTTAC	2872
Dp	2863	TTGTCTTAAAAAAAGCAAGTGTCTTGGGTGGGAGCAAAATCCCTCAACATTTTAC	2922
Qy	2873	GTGTGTACTAAGAGATCTCAAAATATTAGTCTTGTCCGAGCCCTTCATATGTAACCT	2933
Dp	2923	GTGTGTACTAAGAGATCTCAAAATATTAGTCTTGTCCGAGCCCTTCATATGTAACCT	2982
Qy	2933	TAGCGCTAGACTGAGCCAGCTTGGGGGTCAAGTATGATAGACCTGTTTAGGAGCAGAGCC	2992

Db	2993	TAGGCGTGAACCTGAGCCAGCTTGGGGGTGAGTAAAGTAAAGCTCTGTTAAGGACAGAGCC	3042
Qy	2993	TAGTGTAAATCCAAAGAAATGATCTCTATCCAAAGCTGATTCAAAACCCACGCTCAC	3052
Db	3043	TAGTGTAAATCCAAAGAAATGATCTCTATCCAAAGCTGATTCAAAACCCACGCTCAC	3102
Qy	3053	TGACAGCCGAGGGACAGAGCATCACTCTGTGGAAGGACCATTTAGGGGCTTGGCAAG	3112
Db	3103	TGACAGCCGAGGGACAGAGCATCACTCTGTGGAAGGACCATTTAGGGGCTTGGCAAG	3162
Qy	3113	TCCTACCTTAGAGCAAAACCCAGTACTCAGACAGAAAGTCGGGGCTTTGACCACTACAT	3172
Db	3163	TCCTACCTTAGAGCAAAACCCAGTACTCAGACAGAAAGTCGGGGCTTTGACCACTACAT	3222
Qy	3173	ATCTGTAGCCCATTTTCTAGGCAATGTGAAATAGTAGTAGTCACTTTTCAGA	3232
Db	3223	ATCTGTAGCCCATTTTCTAGGCAATGTGAAATAGTAGTAGTCACTTTTCAGA	3282
Qy	3233	COAATTCAACTGTCTATGCAAAAATTTCCCGTGGCCCTAGATGGAGATATTTTTTTTT	3292
Db	3283	COAATTCAACTGTCTATGCAAAAATTTCCCGTGGCCCTAGATGGAGATATTTTTTTTT	3342
Qy	3293	CTTCTACGCTTTAAGAAAGAAAGGAAACGTCTAGAAATTCAGCTGAACCAACGAGAAC	3352
Db	3343	CTTCTACGCTTTAAGAAAGAAAGGAAACGTCTAGAAATTCAGCTGAACCAACGAGAAC	3402
Qy	3353	TGGCAACATCAGATTTAAGCTAAAGTGGAGGCTAACAGTCACTCCCTCTTTGTA	3412
Db	3403	TGGCAACATCAGATTTAAGCTAAAGTGGAGGCTAACAGTCACTCCCTCTTTGTA	3462
Qy	3413	AATCAAGAATGTTTAAATGGGATTGTCAATCTTTAAATAAAGTGAACCTTGGTTTC	3472
Db	3463	AATCAAGAATGTTTAAATGGGATTGTCAATCTTTAAATAAAGTGAACCTTGGTTTC	3522
Qy	3473	AAGCCAAATGGAATTTATTTGGGTGGTGGAGAGAGAGAGAGACCTTCAAAATTCAGC	3532
Db	3523	AAGCCAAATGGAATTTATTTGGGTGGTGGAGAGAGAGAGAGACCTTCAAAATTCAGC	3582
Qy	3533	CAAAAGCAGATTTTTCCTTCCTTCTGCTTCATCTGATGATACAGTTGTTAAATGTAAAT	3592
Db	3583	CAAAAGCAGATTTTTCCTTCCTTCTGCTTCATCTGATGATACAGTTGTTAAATGTAAAT	3642
Qy	3593	AAATAAGCAGATTTTATAGGAAACCTTCTAGGAGGTAAATTATGCGAAAGATTAGAAA	3652
Db	3643	AAATAAGCAGATTTTATAGGAAACCTTCTAGGAGGTAAATTATGCGAAAGATTAGAAA	3702
Qy	3653	GGTACAAATTCCTAGAGAGAAAGCAAGAAACCTGTTTCTTAATGAGGCTTTATCCCTCGG	3712
Db	3703	GGTACAAATTCCTAGAGAGAAAGCAAGAAACCTGTTTCTTAATGAGGCTTTATCCCTCGG	3762
Qy	3713	CATCGATAGGGGCTGATGTTTCTATGATGCTCAGACTTTCACATTTACTAGTAGGGCT	3772
Db	3763	CATCGATAGGGGCTGATGTTTCTATGATGCTCAGACTTTCACATTTACTAGTAGGGCT	3822
Qy	3773	GAGAGAGCTTTAGTGAAGAAAGAAATATTCAGATTAATAACCGTTGAGAAAGCTGAGAA	3832
Db	3823	GAGAGAGCTTTAGTGAAGAAAGAAATATTCAGATTAATAACCGTTGAGAAAGCTGAGAA	3882
Qy	3833	CCATTGATTTTGAATCAGTTGTGAATAGAGTGCAAACCCATGGCCAGCTGTTTTTGAA	3892
Db	3883	CCATTGATTTTGAATCAGTTGTGAATAGAGTGCAAACCCATGGCCAGCTGTTTTTGAA	3942
Qy	3893	ACGCTGAGCCGCGTGTCTTCAGTGGAAAAAGCAAAATCAAAATGGAGCGAGACAAAGGGG	3952
Db	3943	ACGCTGAGCCGCGTGTCTTCAGTGGAAAAAGCAAAATCAAAATGGAGCGAGACAAAGGGG	4002
Qy	3953	CGTCCCTAGTCTTCAACCTACATCACTGATGGAATCGGTCTGAGCTGAACATAGG	4012
Db	4003	CGTCCCTAGTCTTCAACCTACATCACTGATGGAATCGGTCTGAGCTGAACATAGG	4062
Qy	4013	AGGTCACTGGAACAAGTATAGTGCAGATTTGGCTTTCAACATCTCTCTGGCTTGAATTT	4072
Db	4063	AGGTCACTGGAACAAGTATAGTGCAGATTTGGCTTTCAACATCTCTCTGGCTTGAATTT	4122

QY 4073 TATACGTACATGATGGGCTCTTTTGAAGCCTTATTCACAACAGAGCTTTTGGGG 4132
DB 4123 TATCAGCTACAGTGGGCTCTTTTGAAGCCTTATTCACAACAGAGCTTTTGGGG 4182
QY 4133 GTGGGGCTGGGCGGGGTGTGTCAATGTTCTTCTCTGTAAAGTGTGGTCTG 4192
DB 4183 GTGGGGCTGGGCGGGGTGTGTCAATGTTCTTCTCTGTAAAGTGTGGTCTG 4242
QY 4193 CCTGATCTCAGGTTTTCTCGTTTTGAGAAATGACAGTTTTTTGACCGAGATGG 4252
DB 4243 CCTGATCTCAGGTTTTCTCGTTTTGAGAAATGACAGTTTTTTGACCGAGATGG 4302
QY 4253 ACTTCATGTTTCTTATGTGACTTCTTAAACACGACAGATGATGACTCAACAGA 4312
DB 4303 ACTTCATGTTTCTTATGTGACTTCTTAAACACGACAGATGATGACTCAACAGA 4362
QY 4313 CCGACTTGTATGAGGATGATGACCGGACAGCTCACTAGTTGTGCACAATATGT 4372
DB 4363 CCGACTTGTATGAGGATGATGACCGGACAGCTCACTAGTTGTGCACAATATGT 4422
QY 4373 GCTATGATGGGCTGTAAGTGAAGGACAGAAAGGGTCAAGCCGATTTGATGATCTGG 4432
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QY 4433 AAAAGTCTGTCAACGATTTGAGTTAGTTTATATATATATATATATATATATATAT 4492
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QY 4673 TAGGCTTCTCTGGGCAATGTCCTCTCTGGAATCTGATGATGATGATGATGATG 4732
DB 4723 TAGGCTTCTCTGGGCAATGTCCTCTCTGGAATCTGATGATGATGATGATGATG 4782
QY 4733 AGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4792
DB 4783 AGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4842
QY 4793 GCGAAGGGGTGCGCTCGGAGGAGGCTTGGAGCTGCTGATGATGATGATGATGATG 4852
DB 4843 GCGAAGGGGTGCGCTCGGAGGAGGCTTGGAGCTGCTGATGATGATGATGATGATG 4902
QY 4853 TGGCTGG 4859
DB 4903 TGGCTGG 4909

RESULT 6
US-10-357-930-21307
Sequence 21307, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276

PRIOR FILING DATE: 2003-02-15
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21307
LENGTH: 5145
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 1, 514, 5145
OTHER INFORMATION: n = A,T,C or G
US-10-357-930-21307
Query Match 81.0%; Score 4413; DB 18; Length 5145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4683; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 173 GCTTTCAGTCCAGTGAAGCTGTGAGCGCGGAGCAAGGTAAAGATGATGATG 232
DB 224 GCTTTCAGTCCAGTGAAGCTGTGAGCGCGGAGCAAGGTAAAGATGATGATG 283
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DB 284 CGCTGGCTGCTCCAAAGCATCTTTGTTGTGTAATGTTATTCAGTCACTCTTTATGA 343
QY 293 ATCAATGATGAGGGGCTGTTGTGACGAGGCTTTGCAAGAGCAATCAACGGGAAA 352
DB 344 ATCAATGATGAGGGGCTGTTGTGACGAGGCTTTGCAAGAGCAATCAACGGGAAA 403
QY 353 GAGAAAGACATTCATCTTGAGAGGCTCTTGCTGAATAATGAGTTAACTCTCTTTTGGC 412
DB 404 GAGAAAGACATTCATCTTGAGAGGCTCTTGCTGAATAATGAGTTAACTCTCTTTTGGC 463
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; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/207,454
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/211,314
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: 60/219,007
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: 60/255,281
 ; PRIOR FILING DATE: 2000-12-13
 ; NUMBER OF SEQ ID NOS: 62232
 ; SOFTWARE: ParseSeq for Windows Version 4.0
 ; SEQ ID NO: 22820
 ; LENGTH: 5145
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 1, 5144, 5145
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-357-930-22820

Query Match 81.0%; Score 4413; DB 18; Length 5145;

Beet Local Similarity 99.9%; Pred. No. 0;

Matches 4683; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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 QY 293 ATCAATGTGAGGGCTGCTTGTGTGGAGCGAGTCTTTGGCAAGACATCAAGCGGAAA 352
 DB 344 ATCAATGTGAGGGCTGCTTGTGTGGAGCGAGTCTTTGGCAAGACATCAAGCGGAAA 403
 QY 353 GAGAAAGACATTCATCTGGAGGGCTGTGGTGAATGGTTTAACTCTCTTTGCC 412
 DB 404 GAGAAAGACATTCATCTGGAGGGCTGTGGTGAATGGTTTAACTCTCTTTGCC 463
 QY 413 AGTCACCAAGCCTGACCTCATACCTTTTATGATCAATGAGTGGCTGAGCCTTTGAGC 472
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RESULT 9
 US-10-357-930-26815
 ; Sequence 26815, Application US/10357930
 ; Publication No. US20040259086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Endege, Wilson
 ; APPLICANT: Monahan, John
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 ; TITLE OF INVENTION: HUMAN PROSTATE CANCER
 ; FILE REFERENCE: MRI-007BCN
 ; CURRENT APPLICATION NUMBER: US/10/357,930
 ; CURRENT FILING DATE: 2003-02-04
 ; PRIOR APPLICATION NUMBER: 09/785,276
 ; PRIOR FILING DATE: 2003-02-16
 ; PRIOR APPLICATION NUMBER: 60/183,319
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: 60/189,862
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/207,454
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/211,314
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: 60/219,007
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: 60/255,281

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: PRIOR FILING DATE: 2000-11-13
: NUMBER OF SEQ ID NOS: 62232
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: SEQ ID NO: 26815
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: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1, 5144, 5145
: OTHER INFORMATION: n = A,T,C or G
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Query Match	81.0%	Score 4413;	DB 18;	Length 5145;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 4683; Conservative	0;	Mismatches 3;	Indels 1;	Gaps 1;

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Db 2863 TTGTTCTTAAAAAGCAAGTGTCTTGGTGTGAGACAAAAATCCCTACCATTTTAC 2922
Qy 2873 GTTGTCTACTAAGAGATCTCAAAATATTAGTCTTTGTCCGAGCCCTTCATATGACCT 2932
Db 2923 GTTGTCTACTAAGAGATCTCAAAATATTAGTCTTTGTCCGAGCCCTTCATATGACCT 2982
Qy 2933 TAGGGCTGAGACTGAGCCAGCTTGGGGGTGAGATAGTAAACCTGTGTAAGGACAGAGC 2992
Db 2983 TAGGGCTGAGACTGAGCCAGCTTGGGGGTGAGATAGTAAACCTGTGTAAGGACAGAGC 3042
Qy 2993 TAGTGTAAATTCAGAGAAATGATCTATCCAAAGTGTATTCACAAACCCACGCTGAC 3052
Db 3043 TAGTGTAAATTCAGAGAAATGATCTATCCAAAGTGTATTCACAAACCCACGCTGAC 3102
Qy 3053 TGAAGCCGAGAGGACAGAGATCTCTGTCTGAGACGAGCATTTAGGGGCTTTCAGAG 3112
Db 3103 TGAAGCCGAGAGGACAGAGATCTCTGTCTGAGACGAGCATTTAGGGGCTTTCAGAG 3162
Qy 3113 TCTACCTTAAGCAAAACCAATGACTGAGACAGAAAGTGGGGCTTGAACATATACAT 3172
Db 3163 TCTACCTTAAGCAAAACCAATGACTGAGACAGAAAGTGGGGCTTGAACATATACAT 3222
Qy 3173 ATTCGTAGCCCATTTTGAAGCATTTGGAATAGGTAGGTAGTCACTTTTCAGA 3232

Db 3223 ATTCGTAGCCCATTTTGAAGCATTTGGAATAGGTAGGTAGTCACTTTTCAGA 3282
Qy 3233 CCATTTCAACTGTCTATGACAAAAATCCCGTGGGCTTGAATGAGATTAATTTTTTT 3292
Db 3283 CCATTTCAACTGTCTATGACAAAAATCCCGTGGGCTTGAATGAGATTAATTTTTTT 3342
Qy 3293 CTTCAGCTTTATGAGAGAGAGGAACTGTCTAGATTGAGTCAACACAGAAACC 3352
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Qy 3353 TGGCAACATCAAGATTAAAGTTAGGTTGGAGGCTAACAGAGTCACTCCCTTTGTA 3412
Db 3403 TGGCAACATCAAGATTAAAGTTAGGTTGGAGGCTAACAGAGTCACTCCCTTTGTA 3462
Qy 3413 AATCAAAATTTGTTTAAATGGAATTTGGAATTTGGAATTTGGAATTTGGAATTTG 3472
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Db 3523 AAGCCAAATTTGGAATTTTATTTGGTTGTTAGACAGACAGACCTTCAAAATCTCAGC 3582
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Db 3583 CAAGCAGATGTTTTCCTTTCCTTTCCTTCACTGATGATTAACATTTGTAAT 3642
Qy 3593 AATATGAGAAATTTTATAGAAACTTCTAGGAGTAAATTTATGGAATTAAGAA 3652
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Qy 3653 GGTAAATTTGCTGAGAGAGAGCAAGAAACCTGTTTCTTATGAGCTTTTATCCCTGAG 3712
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Qy 3713 CATGAGATGGGCTGATGTTTCTATGATTTGCTCAGATTTTCACTTATAGAGGCT 3772
Db 3763 CATGAGATGGGCTGATGTTTCTATGATTTGCTCAGATTTTCACTTATAGAGGCT 3822
Qy 3773 GAGAGAGCTTTATGAGAGAGAAATTTCAAGATTAACGTTGAGAAAGCTGAGAA 3832
Db 3823 GAGAGAGCTTTATGAGAGAGAAATTTCAAGATTAACGTTGAGAAAGCTGAGAA 3882
Qy 3833 CCATTTAGTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3892
Db 3883 CCATTTAGTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3942
Qy 3893 ACGCTGCGCGCGTGTCTTCACTGAGAAAGCAAAATGAGAGCAGAGCAAAAGGG 3952
Db 3943 ACGCTGCGCGCGTGTCTTCACTGAGAAAGCAAAATGAGAGCAGAGCAAAAGGG 4002
Qy 3953 GGTCTCAGTCTCAACCTCAATCACTGATGATGATGATGATGATGATGATGATG 4012
Db 4003 GGTCTCAGTCTCAACCTCAATCACTGATGATGATGATGATGATGATGATGATG 4062
Qy 4013 AGGTCACTGAAACAAGTATGATGATGATGATGATGATGATGATGATGATGATG 4072
Db 4063 AGGTCACTGAAACAAGTATGATGATGATGATGATGATGATGATGATGATGATG 4122
Qy 4073 TATCAGCTCAATGAGTGTCTCTTTTGAAGCTTAAATTCACAAAGAGCTTTTGGGG 4132
Db 4123 TATCAGCTCAATGAGTGTCTCTTTTGAAGCTTAAATTCACAAAGAGCTTTTGGGG 4182
Qy 4133 GTGGGGCTGGGGGTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 4192
Db 4183 GTGGGGCTGGGGGTGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 4242
Qy 4193 CTTGTATCTCAGATTTTCTCTGTTTGTGGAATGAGACGTTTGTGACAGAGATG 4252
Db 4243 CTTGTATCTCAGATTTTCTCTGTTTGTGGAATGAGACGTTTGTGACAGAGATG 4302
Qy 4253 ACTTCATGTTTCTATGATGATCTTAAACACAGACAGATGATGATGATGATGATG 4312
Db 4303 ACTTCATGTTTCTATGATGATCTTAAACACAGACAGATGATGATGATGATGATG 4362

QY	4313	CCGACTTGGTTAATGGGGAGATGAGCCGCCACAGACCTCACTAGTTGTGACAAATAATGT	43172
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QY	4373	GCTATGATGGGGTGTAAATGAAAGCAGAAAGAGGGTCAAGCCGATGTTATGATATCTGGG	44322
Db	4423	GCTATGATGGGGTGTAAATGAAAGCAGAAAGAGGGTCAAGCCGATGTTATGATATCTGGG	44822
QY	4433	AAAGTCTGTGTCAAGATTTGAATTTAGATTTAATATATCAATTTGAAATCTTTAATCAAGC	44922
Db	4483	AAAGTCTGTGTCAAGATTTGAATTTAGATTTAATATATCAATTTGAAATCTTTAATCAAGC	45422
QY	4493	AATTCAGAGTTTCAACAGTAGTATTTTATGATATGTAACAACAACCAATATGTGTACA	45522
Db	4543	AATTCAGAGTTTCAACAGTAGTATTTTATGATATGTAACAACAACCAATATGTGTACA	46022
QY	4553	GTTTCAACACTTCCAGAGTGTGTCAATGCCAAAACATGTTTAAAGAAAGAAAGAGTAGC	46122
Db	4603	GTTTCAACACTTCCAGAGTGTGTCAATGCCAAAACATGTTTAAAGAAAGAAAGAGTAGC	46622
QY	4613	TCTTTGCTTAACGATGTTTCAAGAGGTTTGGGGCACTTGTTTAAATGAGCTTGTCAAT	46722
Db	4663	TCTTTGCTTAACGATGTTTCAAGAGGTTTGGGGCACTTGTTTAAATGAGCTTGTCAAT	47222
QY	4673	TAGGGCTTCTCTGGGCCAATGGTCCCTCTCTTGGAACATGTGATATGATACATCTTAC	47322
Db	4723	TAGGGCTTCTCTGGGCCAATGGTCCCTCTCTTGGAACATGTGATATGATACATCTTAC	47822
QY	4733	AGCCTTATGATCTGTGTTCACTAGTGTCAATGATCAATCAATCTTGGAATCGAGACTGCCGTG	47922
Db	4783	AGCCTTATGATCTGTGTTCACTAGTGTCAATGATCAATCAATCTTGGAATCGAGACTGCCGTG	48422
QY	4793	GCGAAGGGGTGGCTTCGGAGGCAAGCTCTGAGCTGCTTGATGTCTTTAGTGGGGGTGG	48522
Db	4843	GCGAAGGGGTGGCTTCGGAGGCAAGCTCTGAGCTGCTTGATGTCTTTAGTGGGGGTGG	49022
QY	4853	TGGCTGG 4859	
Db	4903	TGGCTGG 4909	
RESULT 10			
US-10-357-930-26912			
Sequence 26912, Application US/10357930			
Publication No. US20040259086A1			
GENERAL INFORMATION:			
APPLICANT: Schlegel, Robert			
APPLICANT: Endege, Wilson			
APPLICANT: Monahan, John			
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR			
IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF			
TITLE OF INVENTION: HUMAN PROSTATE CANCER			
FILE REFERENCE: MRI-007BCN			
CURRENT APPLICATION NUMBER: US/10/357,930			
CURRENT FILING DATE: 2003-02-04			
PRIOR APPLICATION NUMBER: 09/785,276			
PRIOR FILING DATE: 2003-02-16			
PRIOR APPLICATION NUMBER: 60/183,319			
PRIOR FILING DATE: 2000-02-17			
PRIOR APPLICATION NUMBER: 60/189,862			
PRIOR FILING DATE: 2000-03-16			
PRIOR APPLICATION NUMBER: 60/207,454			
PRIOR FILING DATE: 2000-05-25			
PRIOR APPLICATION NUMBER: 60/211,314			
PRIOR FILING DATE: 2000-06-09			
PRIOR APPLICATION NUMBER: 60/219,007			
PRIOR FILING DATE: 2000-07-18			
PRIOR APPLICATION NUMBER: 60/255,281			
PRIOR FILING DATE: 2000-12-13			
NUMBER OF SEQ ID NOS: 62232			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 26912			

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; LENGTH: 5145
; TYPE: DNA
; ORGANISM: Homo sapiens
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 5144, 5145
;
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-26912

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Query Match	81.0%;	Score 4413;	DB 18;	Length 5145;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 4683;	Conservative	0;	Mismatches 3;	Indels 1; Gaps 1

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QY	223	CGCTGGCTCTCCAAAGACCTTTTGTGTGTGAAATGGTAAATTCAGTCATCTCTTTATGA	292
Db	284	CGCTGGCTCTCCAAAGACCTTTTGTGTGTGAAATGGTAAATTCAGTCATCTCTTTATGA	343
QY	229	ATCCAAATGTGAGGGGGGTCTTTGTGTGACGGAATCCTTTTCCAAAGACATCAACGGGAAA	352
Db	344	ATCCAAATGTGAGGGGGGTCTTTGTGTGACGGAATCCTTTTCCAAAGACATCAACGGGAAA	403
QY	353	GAGAAAGAGACATTCATCTGAGGGGCTCTTGTGTGAAATAGGGTTTAACTCTCTTTGGC	412
Db	404	GAGAAAGAGACATTCATCTGAGGGGCTCTTGTGTGAAATAGGGTTTAACTCTCTTTGGC	463
QY	413	AGTCACCAACGACGCTGACCTCTATACTTTTATGTAACAATGAGTGGCTGAGCTTTGAGC	472
Db	464	AGTCACCAACGACGCTGACCTCTATACTTTTATGTAACAATGAGTGGCTGAGCTTTGAGC	523
QY	473	ACACCACCATTAATCATCATCTGTGTGGCAAAATTAAAGAGAGGTGGGAAAAGAGACCTTATG	532
Db	524	ACACCACCATTAATCATCATCTGTGTGGCAAAATTAAAGAGAGGTGGGAAAAGAGACCTTATG	583
QY	533	TTGTATGTGCCCATGATGATGATTGGAATCTCAATTTGTATCTGAGAGTTGTGTGGCTTGC	592
Db	584	TTGTATGTGCCCATGATGATGATTGGAATCTCAATTTGTATCTGAGAGTTGTGTGGCTTGC	643
QY	593	TGGAAAGTGGAAACGGAAAAGTGCCTGTAATTGATAGCGGCACTTTGTGGAATTAACATA	652
Db	644	TGGAAAGTGGAAACGGAAAAGTGCCTGTAATTGATAGCGGCACTTTGTGGAATTAACATA	703
QY	653	CATCCACATTTTGGAGCCATTAATATCAATGCTGCCAAGCTTTATGAAAGCGAAGTTGC	712
Db	704	CATCCACATTTTGGAGCCATTAATATCAATGCTGCCAAGCTTTATGAAAGCGAAGTTGC	763
QY	713	AACAGGACAAATGTGTAATTACAGAGCTCATCCAGCATTTACGCCAAACATAAGTTTGACA	772
Db	764	AACAGGACAAATGTGTAATTACAGAGCTCATCCAGCATTTACGCCAAACATAAGTTTGACA	823
QY	773	TTGATTGACATCAGAAAGGTTGTAGTTTACATCAAAAGCTCCCAAGATGTTGGCTCTCT	832
Db	824	TTGATTGACATCAGAAAGGTTGTAGTTTACATCAAAAGCTCCCAAGATGTTGGCTCTCT	883
QY	833	CTTCAAGACTGTTTCTCACTGTACTTCTGGGTTAACTGAGAAAGCTTCAACTCTGTTC	892
Db	884	CTTCAAGACTGTTTCTCACTGTACTTCTGGGTTAACTGAGAAAGCTTCAACTCTGTTC	943
QY	893	ACCTGCTTGCAGGTGGGGTTGTGTAGTTCTCTGTTGTTCCCTGGGCTCTGTGAAGGAA	952
Db	944	ACCTGCTTGCAGGTGGGGTTGTGTAGTTCTCTGTTGTTCCCTGGGCTCTGTGAAGGAA	1003
QY	953	AATCACTTAAGTCCCTACCTGCAATTTCTAGCCTTGTTACCTGTGTGCCCAATTTGGC	1012
Db	1004	AATCACTTAAGTCCCTACCTGCAATTTCTAGCCTTGTTACCTGTGTGCCCAATTTGGC	1063
QY	1013	CAACCCGAATTTCTCCAAATCTTTATCTGTGGTCCACGCGAATGTCTCTCAACAAGAGC	1072
Db	1064	CAACCCGAATTTCTCCAAATCTTTATCTGTGGTCCACGCGAATGTCTCTCAACAAGAGC	1123

Qy 1073 TGATACAGCAGAAATGGATGGTTATGTGTAAATGCGACGTATACCTGTCCAAAGCTG 1132
Db 1124 TGATGACAGCAAAATGGATGGTTATGTGTAAATGCGACAAATACCTGTCCAAAGCTG 1183
Qy 1133 ACTTATATCCCGAGCTCATTTTCCCTGCGTGGCCCTGTAAATGACAGCTTTTGTGAGAAA 1192
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Qy 1253 GTGTTCTAGTCACTGTTTAACTGGAGATCTCCCGCTCCGCAACAATCGCTATCGCTTCA 1312
Db 1304 GTGTTCTAGTCACTGTTTAACTGGAGATCTCCCGCTCCGCAACAATCGCTATCGCTTCA 1363
Qy 1313 TCATGAAAGAGATGGAATGTCTTTAATGAAGCTTACAGATTTGTGAAAGAAAAGAC 1372
Db 1364 TCATGAAAGAGATGGAATGTCTTTAATGAAGCTTACAGATTTGTGAAAGAAAAGAC 1423
Qy 1373 CTACATATCTCCAACTTCAATTTTCTGGGCAACCTCTGGACATATGAGAAAGATTA 1432
Db 1424 CTACATATCTCCAACTTCAATTTTCTGGGCAACCTCTGGACATATGAGAAAGATTA 1483
Qy 1433 AGAACAGACTGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGTGACCTGAGAAAGC 1492
Db 1484 AGAACAGACTGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGTGACCTGAGAAAGC 1543
Qy 1493 CAATGAACTGTCTGTCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCTCAATC 1552
Db 1544 CAATGAACTGTCTGTCTGTCTCAGAGGGTGGACAGAAAAGCGAGACGCCCTCAATC 1603
Qy 1553 CACCTGTGCGGACCTGTCTACCTCAGAGGAGAGCAAAAGCCCGTGAATCCCGCA 1612
Db 1604 CACCTGTGCGGACCTGTCTACCTCAGAGGAGAGCAAAAGCCCGTGAATCCCGCA 1663
Qy 1613 GCGTGCACAGCGTGCACAGCGTGCAGCCGTGTGTAGAGAACAGCCCGTGTATCAGG 1672
Db 1664 GCGTGCACAGCGTGCACAGCGTGCAGCCGTGTGTAGAGAACAGCCCGTGTATCAGG 1723
Qy 1673 CGCTCAGTGGGCTGACCTGTCTCCGAGACAGGCTGGAAGACAGCAATTAAGCTCAAGC 1732
Db 1724 CGCTCAGTGGGCTGACCTGTCTCCGAGACAGGCTGGAAGACAGCAATTAAGCTCAAGC 1783
Qy 1733 CCTTCTCTCTGGAATATCAATCAAGTTTCAATTAATTCAGACAGATGGACACATCTTAAC 1792
Db 1784 CCTTCTCTCTGGAATATCAATCAAGTTTCAATTAATTCAGACAGATGGACACATCTTAAC 1843
Qy 1793 GCTTCTCTCTCAGAAAGATCTTGGAAATCTAACAACTTCCACTCTCTGATGGGA 1852
Db 1844 GCTTCTCTCTCAGAAAGATCTTGGAAATCTAACAACTTCCACTCTCTGATGGGA 1903
Qy 1853 CCAACAAAGCTATGCGAGTTCTCCCTGTTCAGGAATATCGAAGAGACCTCCGAAACCA 1912
Db 1904 CCAACAAAGCTATGCGAGTTCTCCCTGTTCAGGAATATCGAAGAGACCTCCGAAACCA 1963
Qy 1913 GTCTGATTAAGAGAGAACCCAGCATCCCAAGAAAGCTCAGACCGGAGCTTCAAGCA 1972
Db 1964 GTCTGATTAAGAGAGAACCCAGCATCCCAAGAAAGCTCAGACCGGAGCTTCAAGCA 2033
Qy 1973 GCGAGAGCAGATGATTCGATTCGATTCAGAACAGAGAGATGGACCGCCAGAGATCC 2032
Db 2024 GCGAGAGCAGATGATTCGATTCGATTCAGAACAGAGATGGACCGCCAGAGATCC 2083
Qy 2033 TTTTATCTCACTGATGAAAGTGGAGCGTGGAGAACAAATTAACAACAAGCTTCTTT 2092
Db 2084 TTTTATCTCACTGATGAAAGTGGAGCGTGGAGAACAAATTAACAACAAGCTTCTTT 2143
Qy 2093 TCGGCTTTTCAACGAGCAGACCTCAGGAATGTCTGTGGCTTGGGCTTTAAGGCT 2152
Db 2144 TCGGCTTTTCAACGAGCAGACCTCAGGAATGTCTGTGGCTTGGGCTTTAAGGCT 2203
Qy 2153 GGCACCTGGATATCTTGGCCCCCGAGACCTTACCCCTTCCCTGAACAGAGCTGTAT 2212

Db 2204 GGCACCTGGATATCTTGGCCCCCGAGACCTTACCCCTTCCCTGAACAGAGCTGTAT 2263
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Db 2264 TTGCAACAGATCTCCACATTTACTGTGCTAGACCATCTAGAGAGAGTGCAGCT 2323
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Db 2564 TGAATATCATTTAGCTCTCTGAGAGAAAGACATTTGTGACCTTATAGACAA-TTTT 2622
Qy 2573 TTTTCTGTTCACAAAAATTTCCCTGTAAATCTGAAATATATATATATATATATAT 2632
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Qy 2693 CTCTTAACATCTGATTTGAGAGATCAGCTAATATCTTCTCAACAAAAATGAAAGGCA 2752
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Qy 2753 GATGCTAAGATCCCCCTTACGAGAGAGAAACATTTTATCAATGAAATTAACATCTC 2812
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Db 2923 GTTGTGCTACTAAGAGATCTCAAAATATTAATCTTGTCCGAGCCCTTCAATGACACT 2982
Qy 2933 TAGCGCTGAGACTGAGCCAGCTTGGGGTCAAGTATGATGACCCCTGTTAAGGAGACAG 2992
Db 2983 TAGCGCTGAGACTGAGCCAGCTTGGGGTCAAGTATGATGACCCCTGTTAAGGAGACAG 3042
Qy 2993 TAGTGTAAATCCAAAGAAATGATCTATCCAAAGCTGATTCAAACCAAGCTCAC 3052
Db 3043 TAGTGTAAATCCAAAGAAATGATCTATCCAAAGCTGATTCAAACCAAGCTCAC 3102
Qy 3053 TGAAGCGAGAGGACAGAGCATCTCTGTGACGAGCACTTAAGGGCTTTCAGAG 3112
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Qy 3113 TCTACCTTAAGCAAAACCCAGTACTCAGACAGAAAGTGGGCTTTCAGCACTACAT 3172
Db 3163 TCTACCTTAAGCAAAACCCAGTACTCAGACAGAAAGTGGGCTTTCAGCACTACAT 3222
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Db 3223 ATCTGTAGCCCATTTTCTAGGCAATGTGAATAGTATGATGATGATGATGATGATGAT 3282
Qy 3233 CCAATTCAACTGTCTATGACAAAAATTCCTGGGCTAGATGAGATTAATTTTTTTT 3292

Db	3283	CCAAATTCAAACCTGCTATGCAAAAATTTCCCGTGGCCATGATGAGATAAATTTTTTTTT	3342
Qy	3293	CTTCTGAGCTTTTAGAAGAGAGGAAACTGCTCTAGATTCAGCTGAACACACAGAAAC	3352
Db	3343	CTTCTCAGCTTTATGAAGAGAGGAAAAGTGTCTAGATTCTGAGCTGAACACAGAAAC	3402
Qy	3353	TGGCAACATACGATTTTAAAGCTAAAGTTGGAGAGCTAACAGATCTAAGCTCTTTGTA	3412
Db	3403	TGGCAACATACGATTTTAAAGCTAAAGTTGGAGAGCTAACAGATCTAAGCTCTTTGTA	3462
Qy	3413	AATCAAGAAATGTTTAAATGGAGATTGTCATTCCTTTAAATAAGATGAAGCTGGTTC	3472
Db	3463	AATCAAGAAATGTTTAAATGGAGATTGTCATTCCTTTAAATAAGATGAAGCTGGTTC	3522
Qy	3473	AAGCCAAATGTAATTTATTTGGGTGGTAGACAGACGACGACCTTCAAAATTCAGC	3532
Db	3523	AAGCCAAATGTAATTTATTTGGGTGGTAGACAGACGACGACCTTCAAAATTCAGC	3582
Qy	3533	CAAAAGAGATGTTTTTGCCCTTCTGCTTCACTGATGATACAGTTGGTAAATGAT	3592
Db	3583	CAAAAGAGATGTTTTTGCCCTTCTGCTTCACTGATGATACAGTTGGTAAATGAT	3642
Qy	3593	AATATGGCAGATTTTATATAGAAAAGCTCTAGAGAGTAAATTAATGGAGATTAAGAAA	3652
Db	3643	AATATGGCAGATTTTATATAGAAAAGCTCTAGAGAGTAAATTAATGGAGATTAAGAAA	3702
Qy	3653	GGTACAAATTGCTAGAGAGAACACAGAAAACGTTTCCTTAGGCTTTATCCCTCGG	3712
Db	3703	GGTACAAATTGCTAGAGAGAACACAGAAAACGTTTCCTTAGGCTTTATCCCTCGG	3762
Qy	3713	CATGCGATGGGCGTGAATGTTCTATGATGCTCAGACTTTCACATTTACTAGTAGGCT	3772
Db	3763	CATGCGATGGGCGTGAATGTTCTATGATGCTCAGACTTTCACATTTACTAGTAGGCT	3822
Qy	3773	GAGAGAGCTTTATAGTAGAGAGGAATATTCAGATTAATAACGTTGAGAAAAGCTGAGAA	3832
Db	3823	GAGAGAGCTTTATAGTAGAGAGGAATATTCAGATTAATAACGTTGAGAAAAGCTGAGAA	3882
Qy	3833	CCATTAAGTTTGAATCAAGTTGGAATAGTAGCAAAAGCCATGAGCTGTTTGGAA	3892
Db	3883	CCATTAAGTTTGAATCAAGTTGGAATAGTAGCAAAAGCCATGAGCTGTTTGGAA	3942
Qy	3893	ACGCTGGCCGGCGGTCTTCACTAGTGGAAAAGCAAAATCAAAATGAGCGAGAGCAAAAGGG	3952
Db	3943	ACGCTGGCCGGCGGTCTTCACTAGTGGAAAAGCAAAATCAAAATGAGCGAGAGCAAAAGGG	4002
Qy	3953	CGTCTCAGTCTCAACCTACATCACTGTATGGAATCGGTCTGCGACGTGAACAATAG	4012
Db	4003	CGTCTCAGTCTCAACCTACATCACTGTATGGAATCGGTCTGCGACGTGAACAATAG	4062
Qy	4013	AGGTACATGGAACAAGATATGTGCAAGATTTGGCTTTCAAAACATCTCTCGGCTTGATTT	4072
Db	4063	AGGTACATGGAACAAGATATGTGCAAGATTTGGCTTTCAAAACATCTCTCGGCTTGATTT	4122
Qy	4073	TATACGCTACATGTGGGTCTCTTTTGAAGCCTTAATTCAACAAGAGCTTTTGGGG	4132
Db	4123	TATACGCTACATGTGGGTCTCTTTTGAAGCCTTAATTCAACAAGAGCTTTTGGGG	4182
Qy	4133	GTGGGCGCTGGCGGGGTGTGTCAATGTTCTTTCCCTTCTGTAAGTGTGCTAGTTGGCTG	4192
Db	4183	GTGGGCGCTGGCGGGGTGTGTCAATGTTCTTTCCCTTCTGTAAGTGTGCTAGTTGGCTG	4242
Qy	4193	CCTGTATCTCAGGTTTTCTCGTTTTTGAAGAAATGGAACAGTTTTTTTGAACAGAGATGTG	4252
Db	4243	CCTGTATCTCAGGTTTTCTCGTTTTTGAAGAAATGGAACAGTTTTTTTGAACAGAGATGTG	4302
Qy	4253	ACTTCATGTTTTCTATGTGACTTTAAACACAGACAGATGATGATGCTCAACACGA	4312
Db	4303	ACTTCATGTTTTCTATGTGACTTTAAACACAGACAGATGATGATGCTCAACACGA	4362
Qy	4313	CCGACTGTTTTAATGGGAGATAGAGCGGACAGACCTCACTATGTTGTGCAAAATATGT	4372
Db	4363	CCGACTGTTTTAATGGGAGATAGAGCGGACAGACCTCACTATGTTGTGCAAAATATGT	4422

QY	4373	GCTATGATGGCGGTGTAAGTGAAGCCAGAAAGAGGTCAAGCCGACATGTTATGATCTGGG	4432
Db	4423	GCTATGAATGGGATGTAAAGTAAAGCCAGAAAGAGGTCAAGCCGACATGTTATGATCTGGG	4482
QY	4433	AAAGTCTGTGTCACAGATTTGAGTTAGTTTATGATATATACATTGAATCTTTATCGAC	4492
Db	4483	AAAGTCTGTGTCACAGATTTGAGTTAGTTTATGATATATACATTGAATCTTTATCGAC	4542
QY	4493	ATTCGAGTTTCACACAGTAGTTTGTGATGTATATGACACACACCAATGTGTACA	4552
Db	4543	ATTCGAGTTTCACACAGTAGTTTGTGATGTATATGACACACACCAATGTGTACA	4602
QY	4553	GTTTCACCACTTCAGAGTGTGTATGCCCAAAACATGTTTAAAGAAAGAAACAGTAGC	4612
Db	4603	GTTTCACCACTTCAGAGTGTGTATGCCCAAAACATGTTTAAAGAAAGAAACAGTAGC	4662
QY	4613	TCCTTGCTTAACGANTTTACAGAGGTTTGAGGACATTGTTTTAATGAGCTTGTCAAT	4672
Db	4663	TCCTTGCTTAACGANTTTACAGAGGTTTGAGGACATTGTTTTAATGAGCTTGTCAAT	4722
QY	4673	TAGGAGCTTCTCTTGAGGCATGATGCCCTTCCCTTGCGAAACGTGATATGATCAATCTAC	4732
Db	4723	TAGGAGCTTCTCTTGAGGCATGATGCCCTTCCCTTGCGAAACGTGATATGATCAATCTAC	4782
QY	4733	AGCCTTAGTGTCTGTTCACTAGTGTCAATTAATCAATTCAGATTCAGACTGCCGTG	4792
Db	4783	AGCCTTAGTGTCTGTTCACTAGTGTCAATTAATCAATTCAGATTCAGACTGCCGTG	4842
QY	4793	GCGAAGAGGATGGCCTCGGAGAGCAGGCGCTCGAGACTCTGGAGTCTTTAGTGGGATGG	4852
Db	4843	GCGAAGAGGATGGCCTCGGAGAGCAGGCGCTCGAGACTCTGGAGTCTTTAGTGGGATGG	4902
QY	4853	TGCGCTGG 4859	
Db	4903	TGCGCTGG 4909	
RESULT 11			
US-10-357-930-26923			
/ Sequence 26923, Application US/10357930			
/ Publication No. US20040259086A1			
/ GENERAL INFORMATION:			
/ APPLICANT: Schlegel, Robert			
/ APPLICANT: Endege, Wilson			
/ APPLICANT: Monahan, John			
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR			
/ TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF			
/ FILE REFERENCE: MRI -007BCN			
/ CURRENT APPLICATION NUMBER: US/10/357, 930			
/ PRIOR FILING DATE: 2003-02-04			
/ PRIOR APPLICATION NUMBER: 09/785, 276			
/ PRIOR FILING DATE: 2003-02-16			
/ PRIOR APPLICATION NUMBER: 60/183, 319			
/ PRIOR FILING DATE: 2000-02-17			
/ PRIOR APPLICATION NUMBER: 60/189, 862			
/ PRIOR FILING DATE: 2000-03-16			
/ PRIOR APPLICATION NUMBER: 60/207, 454			
/ PRIOR FILING DATE: 2000-05-25			
/ PRIOR APPLICATION NUMBER: 60/211, 314			
/ PRIOR FILING DATE: 2000-06-09			
/ PRIOR APPLICATION NUMBER: 60/219, 007			
/ PRIOR FILING DATE: 2000-07-18			
/ PRIOR APPLICATION NUMBER: 60/255, 281			
/ PRIOR FILING DATE: 2000-12-13			
/ NUMBER OF SEQ ID NOS: 62232			
/ SOFTWARE: FastSeq for Windows Version 4.0			
/ SEQ ID NO 26923			
/ LENGTH: 5145			
/ TYPE: DNA			
/ ORGANISM: Homo sapiens			
FEATURE:			

NAME/KEY: misc_feature
LOCATION: 1, 5144, 5145
OTHER INFORMATION: n = A,T,C or G
US-10-357-930-26923

Query Match 81.0%; Score 4413; DB 18; Length 5145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4683; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 173 GCTTCACATCCAGTGTAAAGCTGTGGAGCCCGGAGAGAAAGTAAAGATGCTATG 232
DB 224 GCTTCACATCCAGTGTAAAGCTGTGGAGCCCGGAGAGAAAGTAAAGATGCTATG 283
QY 223 CGCTGGCTGCTCAAGCATCTTTGTGTGAATGTTATTCAGATCTCTTATGA 292
DB 284 CGCTGGCTGCTCAAGCATCTTTGTGTGAATGTTATTCAGATCTCTTATGA 343
QY 293 ATCAATGTGAGGGCTCTTTGTGAGCGAGTCTTTGCAAGACACATCAACGGGAAA 352
DB 344 ATCAATGTGAGGGCTCTTTGTGAGCGAGTCTTTGCAAGACACATCAACGGGAAA 403
QY 353 GAGAAAGACATTCATTTGAGGGCTCTTGTGAAAATGGTTAACTCTCTTTGCC 412
DB 404 GAGAAAGACATTCATTTGAGGGCTCTTGTGAAAATGGTTAACTCTCTTTGCC 463
QY 413 AGTCAACCAAGCTGACCTCATATACCTTTAGTACATGAGTGGCTGAGCTTTGAGC 472
DB 464 AGTCAACCAAGCTGACCTCATATACCTTTAGTACATGAGTGGCTGAGCTTTGAGC 523
QY 473 ACACCAACCATTAATCATCTGTGGCAATTAAGAAAGGTGGAAAAGAGACTTATG 532
DB 524 ACACCAACCATTAATCATCTGTGGCAATTAAGAAAGGTGGAAAAGAGACTTATG 583
QY 533 TTGTCAATGGCCCATGAGATGATTTGAACTCAATTTGTACTGAGAGTTGGTCTGCG 592
DB 584 TTGTCAATGGCCCATGAGATGATTTGAACTCAATTTGTACTGAGAGTTGGTCTGCG 643
QY 593 TGGAAAGTGAACGGAAAAGTGTCTAATTTGATGAGCGGCAATTTGTGAAATCAATA 652
DB 644 TGGAAAGTGAACGGAAAAGTGTGTCTAATTTGATGAGCGGCAATTTGTGAAATCAATA 703
QY 653 CATCCACATTTTGGAGCCATTAATATCAATGCTCCAGCTTAATGAGGAAAGTTC 712
DB 704 CATCCACATTTTGGAGCCATTAATATCAATGCTCCAGCTTAATGAGGAAAGTTC 763
QY 713 AACGAGAAAGTGTAAATTAACAGCTCATCCAGCATTCAGCGAAACATAAGTTGACA 772
DB 764 AACGAGAAAGTGTAAATTAACAGCTCATCCAGCATTCAGCGAAACATAAGTTGACA 823
QY 773 TTGATTTGAGTCAGAAAGTGTGATTTAGATCAAGCTCCCAAGATGTTGCTCTCT 832
DB 824 TTGATTTGAGTCAGAAAGTGTGATTTAGATCAAGCTCCCAAGATGTTGCTCTCT 883
QY 833 CTTCAGACTGTTTTCTCACTGATCTTCTGGGTAAACTGAGAAAGCTTCACTCTGTC 892
DB 884 CTTCAGACTGTTTTCTCACTGATCTTCTGGGTAAACTGAGAAAGCTTCACTCTGTC 943
QY 893 ACCTGCTTGACAGTGGGTTTGTGCTGAGTCTCTGTTGTTCCCTGGCTCTGTGAAGAA 952
DB 944 ACCTGCTTGACAGTGGGTTTGTGCTGAGTCTCTGTTGTTCCCTGGCTCTGTGAAGAA 1003
QY 953 AATCACTCTAGTCCCTACCTGACATTTCTCAGCCCTGTTTACCTGTTGCCAAACATTGGGC 1012
DB 1004 AATCACTCTAGTCCCTACCTGACATTTCTCAGCCCTGTTTACCTGTTGCCAAACATTGGGC 1063
QY 1013 CAACCCGAATCTTCCCAATCTTTATCTTGCTGCGCAGAGAGATGCTCTCAACAGAGGC 1072
DB 1064 CAACCCGAATCTTCCCAATCTTTATCTTGCTGCGCAGAGAGATGCTCTCAACAGAGGC 1123
QY 1073 TGAATACAGAGAAATGGATGTTGTTATGTTAAATGCAAGCTATACCTGTCAAAGCTG 1132
DB 1124 TGAATACAGAGAAATGGATGTTGTTATGTTAAATGCAAGCTATACCTGTCAAAGCTG 1183

QY 1133 ACTTATCCCGAGTCTCATTTCTGCTGTGCTGTGATGACAGCTTTTGTGAGAAA 1192
DB 1184 ACTTATCCCGAGTCTCATTTCTGCTGTGCTGTGATGACAGCTTTTGTGAGAAA 1243
QY 1193 TTTTGGCGGTGTGGACAAATCAGTAAATTTTCAATTTGAGAAAAGCAAAAGCTTCAATGAT 1252
DB 1244 TTTTGGCGGTGTGGACAAATCAGTAAATTTTCAATTTGAGAAAAGCAAAAGCTTCAATGAT 1303
QY 1253 GTGTTCTAGTGCACGTGTTTACCTGGGATCTCCGCTCCGACCAATGCTATGCTTCA 1312
DB 1304 GTGTTCTAGTGCACGTGTTTACCTGGGATCTCCGCTCCGACCAATGCTATGCTTCA 1363
QY 1313 TCATGAAGAGATGACATGCTTTAGTGAAGCTTACATGTTGTGAAAAGAAAAGAC 1372
DB 1364 TCATGAAGAGATGACATGCTTTAGTGAAGCTTACATGTTGTGAAAAGAAAAGAC 1423
QY 1424 CTACTATATCTCCAAACTTCAATTTTGTGGCCCAACTCTGACTATGAGAAAGATTA 1483
DB 1433 AGAACCAAGCTGAGCATCAAGGCGCAAGAGCAAACTCAAGCTCTGACCTGAGAGAGC 1492
QY 1484 AGAACCAAGCTGAGCATCAAGGCGCAAGAGCAAACTCAAGCTCTGACCTGAGAGAGC 1543
QY 1493 CAATGAACCTGTCCCTGCTGTCTCAGAGGTTGACAGAAAAGCGAGAGAGCCCTCAGTC 1552
DB 1544 CAATGAACCTGTCCCTGCTGTCTCAGAGGTTGACAGAAAAGCGAGAGAGCCCTCAGTC 1603
QY 1553 CACCTGTGCGGACTCTGTCTAATCTTCAAGAGGACAGACAAAGGCCGTGATCCGCCA 1612
DB 1604 CACCTGTGCGGACTCTGTCTAATCTTCAAGAGGACAGACAAAGGCCGTGATCCGCCA 1663
QY 1613 GCGTCCCAAGGTCGCCAGCGGTGACAGCCGTGCTGTTAAGAGACAGCCCGTGTGACAGG 1672
DB 1664 GCGTCCCAAGGTCGCCAGCGGTGACAGCCGTGCTGTTAAGAGACAGCCCGTGTGACAGG 1723
QY 1673 CGCTCAGTGGGCTCAGCTGTCCGACAGCAGGCTGSAAGACAGCAATAGCTCAAGCGTT 1732
DB 1724 CGCTCAGTGGGCTCAGCTGTCCGACAGCAGGCTGSAAGACAGCAATAGCTCAAGCGTT 1783
QY 1733 CTTTCTCTGTGATATCAATCAATTCATATTTAGCCAGCAGATGAGCATCTTACATG 1792
DB 1784 CTTTCTCTGTGATATCAATCAATTCATATTTAGCCAGCAGATGAGCATCTTACATG 1843
QY 1793 GCTTCTCTCATCAGAAATGCTTTGAAATCTACAACTTCCATCTCTGTGATGGA 1852
DB 1844 GCTTCTCTCATCAGAAATGCTTTGAAATCTACAACTTCCATCTCTGTGATGGA 1903
QY 1853 CCAACAGCTATGCAAGTCTCCCTGTTCAGAACTATGAGAGACATCCCGAAACCA 1912
DB 1904 CCAACAGCTATGCAAGTCTCCCTGTTCAGAACTATGAGAGACATCCCGAAACCA 1963
QY 1913 GTCTGTAAAGAGAAAGCCAGATCCCAAGAAAGCTGACAGCCGACGCTTACAGCA 1972
DB 1964 GTCTGTAAAGAGAAAGCCAGATCCCAAGAAAGCTGACAGCCGACGCTTACAGCA 2023
QY 1973 GCGAGAGCAAGCATTTGATTCGTTCAAGAACACAGCAGTGGCAACGCGCCAGAGGTTCC 2032
DB 2024 GCGAGAGCAAGCATTTGATTCGTTCAAGAACACAGCAGTGGCAACGCGCCAGAGGTTCC 2083
QY 2033 TTTTATCTCCATCTGACATGAAAGTGGAGCGTGGAGGACAAATTAACACACAGCTTCTT 2092
DB 2084 TTTTATCTCCATCTGACATGAAAGTGGAGCGTGGAGGACAAATTAACACACAGCTTCTT 2143
QY 2093 TCGGCTTTTCCACAGCAGCAGACCTCAAGAGTCTGTGCGCTGAGCTTAAAGGCT 2152
DB 2144 TCGGCTTTTCCACAGCAGCAGACCTCAAGAGTCTGTGCGCTGAGCTTAAAGGCT 2203
QY 2153 GGCACCTGGATATTTTGGCCCGCCAGAACCTTACCTCTCTTCAACAGCAGCTGTATTT 2212
DB 2204 GGCACCTGGATATTTTGGCCCGCCAGAACCTTACCTCTCTTCAACAGCAGCTGTATTT 2263
QY 2213 TTGCAACAGAGTCTTCACTTCTGCTCAGGCATCTACGAGGAGGAGTGCAGTT 2272

Db	2264	TTGGCAGAGTCTCTCACTTTACTCTGCTCAAGCCATTCACGAGGCACTGTCCAACTT	2233
Qy	2273	ACTTGTGCTTACAGCTGTGAGCCAGACTGCCCCACTTGTGCGAGAACCAAGTCAATTTGTGCGCA	2232
Db	2324	ACTGTGCTTACAGCTGTGAGCCAGACTGCCCCACTTGTGCGAGAACCAAGTCAATTTGTGCGCA	2383
Qy	2333	GGGGCGAAGCCCACTGACACAGCTGACTCCGGCGGAGCTGTGCATGAAGAGCCCTT	2392
Db	2384	GGGGCGAAGCCCAAGTGAACAGCTGACTCCGGCGGAGCTGTGCATGAAGAGCCCTT	2443
Qy	2393	TTGAAAAGCAGTTTAAACCGACAGAGTGTCCAAATGGAATTTTGAAGAGCAATGTCAG	2452
Db	2444	TTGAAAAGCAGTTTAAACCGACAGAGTGTCCAAATGGAATTTTGAAGAGCAATGTCAG	2503
Qy	2453	AGAAACGTCACGGGAAGAGCTGTGGGAAAAGTGCGAGTCACTAGCTTTTTCGGGACAGA	2512
Db	2504	AGAAACGTCACGGGAAGAGCTGTGGGAAAAGTGCGAGTCACTAGCTTTTTCGGGACAGA	2563
Qy	2513	TGGAATTCATYAGAGTCTCCTGAGAAAGAACATCTGACCTTCATATAGCAATTTTTT	2572
Db	2564	TGGAATTCATYAGAGTCTCCTGAGAAAGAACATCTGACCTTCATATAGCAAA-TTTTT	2622
Qy	2573	TTTTCTTGTTCACAAAAAATTCCTGTAAATCTGAAAATATATATATATGATCATATATA	2632
Db	2623	TTTTCTTGTTCACAAAAAATTCCTGTAAATCTGAAAATATATATATATGATCATATATA	2682
Qy	2633	TATTTTGGAAAAATGAGCTATGTGTATAAAGCAACAGTGTGATCAACCAAGTTGTACT	2692
Db	2683	TATTTTGGAAAAATGAGCTATGTGTATAAAGCAACAGTGTGATCAACCAAGTTGTACT	2742
Qy	2693	CTCTTAACATCTGCATTTTGAGAGATCAGCTAATCTTCTCAACAAAAATGGAAGGCA	2752
Db	2743	CTCTTAACATCTGCATTTTGAGAGATCAGCTAATCTTCTCAACAAAAATGGAAGGCA	2802
Qy	2753	GATGCTAAGATATCCCCCTTGAACGAGAGAAAAACATTTTATTCAGTGAATTAACATCTTC	2812
Db	2803	GATGCTAAGATATCCCCCTTGAACGAGAGAAAAACATTTTATTCAGTGAATTAACATCTTC	2862
Qy	2813	TTGTTCTTAAAAAAGCAAGTCTTTTGGTGTGTGAGAGCAAAAATCCCCCTCAATTTTCAC	2872
Db	2863	TTGTTCTTAAAAAAGCAAGTCTTTTGGTGTGTGAGAGCAAAAATCCCCCTCAATTTTCAC	2922
Qy	2873	GTGTGTCTATCAAGAGATCTCAATATTTAGTCTTTTGTCCGAGCCCTTCAATAGTACACT	2932
Db	2923	GTGTGTCTATCAAGAGATCTCAATATTTAGTCTTTTGTCCGAGCCCTTCAATAGTACACT	2982
Qy	2933	TAGCGCTGAGCTGAGCAGCTTGAGGGGTCAAGTAGTAAACCTGTATTGGGACACAGGC	2992
Db	2983	TAGCGCTGAGCTGAGCAGCTTGAGGGGTCAAGTAGTAAACCTGTATTGGGACACAGGC	3042
Qy	2993	TAGTGTAAATCCCAAGAGAAATGATCTTATTCAAAGCTGATTCACAAACCCAGCGTCAAC	3052
Db	3043	TAGTGTAAATCCCAAGAGAAATGATCTTATTCAAAGCTGATTCACAAACCCAGCGTCAAC	3102
Qy	3053	TGACAGCCGAGAGACACAGAGTCACTCTGTGGAAGAGCAATTAGAGGCGCTTGGCAAG	3112
Db	3103	TGACAGCCGAGAGACACAGAGTCACTCTGTGGAAGAGCAATTAGAGGCGCTTGGCAAG	3162
Qy	3113	TCATACCTTAGAGCAAAACCCAGTACCTTCAGACAGAAAAGTCCGAGCTTTGACCACTACAT	3172
Db	3163	TCATACCTTAGAGCAAAACCCAGTACCTTCAGACAGAAAAGTCCGAGCTTTGACCACTACAT	3222
Qy	3173	ATCAGGTAGCCCAATTTCTTAGGCAATGTGTAAATAGTAGTAGTCACTTTTTCAGA	3232
Db	3223	ATCAGGTAGCCCAATTTCTTAGGCAATGTGTAAATAGTAGTAGTCACTTTTTCAGA	3282
Qy	3233	CCAAATTCAAACTGTCTATGACACAAAATCCCGTGGGCTAGATGTGAGAGATTAATTTTTTT	3292
Db	3283	CCAAATTCAAACTGTCTATGACACAAAATCCCGTGGGCTAGATGTGAGAGATTAATTTTTTT	3342
Qy	3293	CTTCTAGCTTTATGAAAGAGAGAAATCTGTAGAGTTCACTGAAACCAAGAAACC	3352

Db	3434	CTTCTCAGCTTTATGAAAGAAAGGAAACTGTCTAGATTAAGCTGAACCAACAGAAC	3402
Qy	3353	TGGCAACATCAGCATTTTAAGTAAAGTTGGAGGCTAAACGAATCACTCCCTCTTTGTA	3412
Db	3403	TGGCAACATCAGCATTTTAAGTAAAGTTGGAGGCTAAACGAATCACTCCCTCTTTGTA	3462
Qy	3413	AATCAAGAAATTGTTAAATGGGAAATGTCATCTCTTAAATAAAGATGAACCTTGGTTTC	3472
Db	3463	AATCAAGAAATTGTTAAATGGGAAATGTCATCTCTTAAATAAAGATGAACCTTGGTTTC	3522
Qy	3473	AAGCCAAAGTAAATTTATTTGGTTGGAGCAGCAGCAGCACTTCAAAATCTCAGC	3532
Db	3523	AAGCCAAAGTAAATTTATTTGGTTGGAGCAGCAGCAGCACTTCAAAATCTCAGC	3582
Qy	3533	CAAGCAGATGTTTTTGGCCTTTCTGCTCACTGCATGATACAGTTGGTAAATGTAT	3592
Db	3583	CAAGCAGATGTTTTTGGCCTTTCTGCTCACTGCATGATACAGTTGGTAAATGTAT	3642
Qy	3593	AATATGGCAGATTTTATATAGGAACTTCCTAGGAGAGTAAATTAATGGAAATTAAGAA	3652
Db	3643	AATATGGCAGATTTTATATAGGAACTTCCTAGGAGAGTAAATTAATGGAAATTAAGAA	3702
Qy	3653	GGTACAAATTGCTGAGAGAAAGCAGAAACCTGTTCTTATGAGGCTTTATCCCTCG	3712
Db	3703	GGTACAAATTGCTGAGAGAAAGCAGAAACCTGTTCTTATGAGGCTTTATCCCTCG	3762
Qy	3713	CATGGAGTGGGGCTGATGCTTTCTATAGATGCTCAGACTTTCACATTTACTATAGGCT	3772
Db	3763	CATGGAGTGGGGCTGATGCTTTCTATAGATGCTCAGACTTTCACATTTACTATAGGCT	3822
Qy	3773	GAGAGAGCTTTAGTAGAGAAAGAAATATCAGATATAACCGTTGAGAAAGCTGAGAGA	3832
Db	3823	GAGAGAGCTTTAGTAGAGAAAGAAATATCAGATATAACCGTTGAGAAAGCTGAGAGA	3882
Qy	3833	CCATTGAATTTTGAATCAGTTGTGAATAGATGCAAAGCCATGSCCAAGCTGTTTGGAA	3892
Db	3883	CCATTGAATTTTGAATCAGTTGTGAATAGATGCAAAGCCATGSCCAAGCTGTTTGGAA	3942
Qy	3893	ACGCTGCGCGGCGTGTCTTCAGTGTGAAAAAGCAAAATCAAAAATGGACGAGCAAAAGGG	3952
Db	3943	ACGCTGCGCGGCGTGTCTTCAGTGTGAAAAAGCAAAATCAAAAATGGACGAGCAAAAGGG	4002
Qy	3953	CGTCTCAGTCTCTAACCTTACATCACTGTATGAAATCGGCTCTGGCAGCTGAACATAG	4012
Db	4003	CGTCTCAGTCTCTAACCTTACATCACTGTATGAAATCGGCTCTGGCAGCTGAACATAG	4062
Qy	4013	AGGTCACTGGAAACAAGATAGAGAGATGGCTTCAAAACATCCCTCGGCTTGATTT	4072
Db	4063	AGGTCACTGGAAACAAGATAGAGAGATGGCTTCAAAACATCCCTCGGCTTGATTT	4122
Qy	4073	TATCAGCTCAATGTGGGTCCTCTTTGAAAGCCTTAATCAACAACAGCAGCTTTTGGGG	4132
Db	4123	TATCAGCTCAATGTGGGTCCTCTTTGAAAGCCTTAATCAACAACAGCAGCTTTTGGGG	4182
Qy	4133	GTGGGGCTGGGCGGGGTGTGATATGTTTCTTCCCTCTGTAAATGTGTGCAATTTGCTG	4192
Db	4183	GTGGGGCTGGGCGGGGTGTGATATGTTTCTTCCCTCTGTAAATGTGTGCAATTTGCTG	4242
Qy	4193	CTTGATATCAGATTTTCTCGTTTGTGAAAAATGACATTTTGTGACAGGATG	4252
Db	4243	CTTGATATCAGATTTTCTCGTTTGTGAAAAATGACATTTTGTGACAGGATG	4302
Qy	4253	ACTTCATGTTTCTTATGTGATCTTTCTTAAACCAAGCAACGAATGATATGATCTCAACAGA	4312
Db	4303	ACTTCATGTTTCTTATGTGATCTTTCTTAAACCAAGCAACGAATGATATGATCTCAACAGA	4362
Qy	4313	CCGACTTGGTTATGGGAGTATGAGCGGACAGACTCACTAGTTGTGACAAATTAATGT	4372
Db	4363	CCGACTTGGTTATGGGAGTATGAGCGGACAGACTCACTAGTTGTGACAAATTAATGT	4422
Qy	4373	GCTATGATGGGTTGTAAGTGAAGCAAGAGGTCAGCCGACATTTGTTATGATATCGG	4432
Db	4423	GCTATGATGGGTTGTAAGTGAAGCAAGAGGTCAGCCGACATTTGTTATGATATCGG	4482

QY	4433	AAAGGCTGGGCAACGA	TTTGAGTTAGTTT	TAGTATACAT	GTGAAATCTT	TATACGAC	44932
Db	4443	AAAGGCTGGGCAACGA	TTTGAGTTAGTTT	TAGTATACAT	GTGAAATCTT	TATACGAC	45424
QY	4493	ATTCTCAAGTTTCACAC	AGTAGTATTTT	GATGTATAT	GACACACACCA	CCAAATGTGTAA	CA
Db	4543	ATTCTCAAGTTTCACAC	AGTAGTATTTT	GATGTATAT	GACACACCA	CCAAATGTGTAA	CA
QY	4553	GTTACCACTTCCAGAGT	GTGTCA	TGCCAAACAT	TTGTTAAGAAAG	GAAGCATGAC	46122
Db	4603	GTTACCACTTCCAGAGT	GTGTCA	TGCCAAACAT	TTTAAAGAAAG	GAAGCATGAC	46622
QY	4613	TCCTTGTCTAACGAT	GTTCAGAGGTTT	GGGGCACTT	GTGTTTATGAT	GACTTCTGTCA	TT
Db	4663	TCCTTGTCTAACGAT	GTTCAGAGGTTT	GGGGCACTT	GTGTTTATGAT	GACTTCTGTCA	TT
QY	4673	TAGGGCTTCTCTTGCC	CAATGTCCTT	TCCTTCTGGA	ACCTGATGAT	CAATCCTTAC	47322
Db	4723	TAGGGCTTCTCTTGCC	CAATGTCCTT	TCCTTCTGGA	ACCTGATGAT	CAATCCTTAC	47822
QY	4733	AGCCTTAGTCTGGT	GTCTACTAGTAT	GCAGATAT	CAGTTCTT	TGGAATGGA	ACGCGGTG
Db	4783	AGCCTTAGTCTGGT	GTCTACTAGTAT	GCAGATAT	CAGTTCTT	TGGAATGGA	ACGCGGTG
QY	4793	GCGAAGGGGTGACCT	CGAGGCAAGGCT	CTGAGCTGCTT	GTGATGTCTT	TAGTGGGGGTG	48522
Db	4843	GCGAAGGGGTGACCT	CGAGGCAAGGCT	CTGAGCTGCTT	GTGATGTCTT	TAGTGGGGGTG	49022
QY	4853	TGGCTGG	4859				
Db	4903	TGGCTGG	4909				

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RESULT 12
US-10-357-930-27145
: Publication 27145, Application US/10357930
: GENERAL INFORMATION:
: APPLICANT: Schlegel, Robert
: APPLICANT: Endege, Wilson
: APPLICANT: Monahan, John
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
: TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
: FILE REFERENCE: MRI-007BCN
: CURRENT APPLICATION NUMBER: US/10/357,930
: CURRENT FILING DATE: 2003-02-04
: PRIOR APPLICATION NUMBER: 09/785,276
: PRIOR FILING DATE: 2003-02-16
: PRIOR APPLICATION NUMBER: 60/183,319
: PRIOR FILING DATE: 2000-02-17
: PRIOR APPLICATION NUMBER: 60/189,862
: PRIOR FILING DATE: 2000-03-16
: PRIOR APPLICATION NUMBER: 60/207,454
: PRIOR FILING DATE: 2000-05-25
: PRIOR APPLICATION NUMBER: 60/211,314
: PRIOR FILING DATE: 2000-06-09
: PRIOR APPLICATION NUMBER: 60/219,007
: PRIOR FILING DATE: 2000-07-18
: PRIOR APPLICATION NUMBER: 60/255,281
: PRIOR FILING DATE: 2000-12-13
: NUMBER OF SEQ ID NOS: 62232
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 27145
: LENGTH: 5145
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: 1, 5144, 5145
: OTHER INFORMATION: n = A,T,C or G
US-10-357-930-27145

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Query Match	81.0%;	Score 4413;	DB 18;	Length 5145;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 4683;	Conservative	0;	Mismatches 3;	Indels 1;
			Gaps	1.

QY	173	GCTTCACTCCAGGTAAAGCTGTTGGAGCCGCGGAGCAAAAGGTAAAGATGAATGAATG	232
Db	224	GCTTCACTCCAGGTAAAGCTGTTGGAGCCGCGGAGCAAAAGGTAAAGATGAATGAATG	283
QY	233	CGTGGCTGCTCCAAAGCATCTTTTGTGTGGAAATGTTATTTCCAGTCATCTCTTATGA	292
Db	284	CGTGGCTGCTCCAAAGCATCTTTTGTGTGGAAATGTTATTTCCAGTCATCTCTTATGA	343
QY	293	ATCAAAATGTAGGGGCTGCTTTGTGGAGGAGTCTTTGGCAAGGACATCAACGGGAAA	352
Db	344	ATCAAAATGTAGGGGCTGCTTTGTGGAGGAGTCTTTGGCAAGGACATCAACGGGAAA	403
QY	353	GAGAAAGAGACATTCATCTTGGAGGGGCTCTTGCTGTAATAATGGGTTTAACTCTCTTTGGC	412
Db	404	GAGAAAGAGACATTCATCTTGGAGGGGCTCTTGCTGTAATAATGGGTTTAACTCTCTTTGGC	463
QY	413	AGTCAACACAGCCTGACCTTATACACTTTTATAGTCAATGTAGTGGCTTGAAGC	472
Db	464	AGTCAACACAGCCTGACCTTATACACTTTTATAGTCAATGTAGTGGCTTGAAGC	523
QY	473	ACACCAACATTACATCATCTGTGGCAAAATTAAGAAGAGGTGGGAAAAGAGACATTATG	532
Db	524	ACACCAACATTACATCATCTGTGGCAAAATTAAGAAGAGGTGGGAAAAGAGACATTATG	583
QY	533	TTGTTCATGGCCCATGAGATGATTTGGAACTCAAAATTTGTACTGAGAGTGTGGCTGTGC	592
Db	584	TTGTTCATGGCCCATGAGATGATTTGGAACTCAAAATTTGTACTGAGAGTGTGGCTGTGC	643
QY	593	TGAAAGGTGAAACGGAAAAAGTGTCTTAATTGATAGCCGCGCATTTGTGAAATCAATA	652
Db	644	TGAAAGGTGAAACGGAAAAAGTGTCTTAATTGATAGCCGCGCATTTGTGAAATCAATA	703
QY	653	CATCCCACTTTTGGAGGCCATTAAATACACTGTCCCAAGCTTATGAAAGGAAAGGTGCG	712
Db	704	CATCCCACTTTTGGAGGCCATTAAATACACTGTCCCAAGCTTATGAAAGGAAAGGTGCG	763
QY	713	AACAGGACAAAGTGTAAATTAACAGAGCTCATTCAGACATTCAAGCGAATCATTAAGTTGACA	772
Db	764	AACAGGACAAAGTGTAAATTAACAGAGCTCATTCAGACATTCAAGCGAATCATTAAGTTGACA	823
QY	773	TTGATTCAGTCAAGAGGTGTAGTTTACATCAAAAGCTCCCAAGATGTTGCTCTCTCT	832
Db	824	TTGATTCAGTCAAGAGGTGTAGTTTACATCAAAAGCTCCCAAGATGTTGCTCTCTCT	883
QY	833	CTTCAAGCTGTTTCTCACTGTACCTTCGGGTAATCGGAAAGAGCTTCAACTCTGTCTC	892
Db	884	CTTCAAGCTGTTTCTCACTGTACTCTCGGGTAATCGGAAAGAGCTTCAACTCTGTCTC	943
QY	893	ACCTGCTTGCAGGTGGGTTTGCTGAGTCTCTCGTTGTTTCCCTGGCCTCTGTGAAGAA	952
Db	944	ACCTGCTTGCAGGTGGGTTTGCTGAGTCTCTCGTTGTTTCCCTGGCCTCTGTGAAGAA	1003
QY	953	AATCACTCTAGTCCCTACTGCAATTTCTAGCCTTGCTTACTGTTGCCAATATGGGC	1012
Db	1004	AATCACTCTAGTCCCTACTGCAATTTCTAGCCTTGCTTACTGTTGCCAATATGGGC	1063
QY	1013	CAACCCGAATCTTCCCAATCTTATATCTTGGCTGCAGCGAGATGTCCTCAACAAAGAGC	1072
Db	1064	CAACCCGAATCTTCCCAATCTTATATCTTGGCTGCAGCGAGATGTCCTCAACAAAGAGC	1123
QY	1073	TGATACAGCAGAAATGGAAATGTGTTATGTGTTAAATGCCAGCTATACCTGTCCAAAGCTG	1132
Db	1124	TGATACAGCAGAAATGGAAATGTGTTATGTGTTAAATGCCAGCTATACCTGTCCAAAGCTG	1183
QY	1133	ACTTATATCCCGAATCTCATTTTCTGTGGTGTGCTGTGATATGACAGCTTTTGTGAGAAA	1192
Db	1184	ACTTATATCCCGAATCTCATTTTCTGTGGTGTGCTGTGATATGACAGCTTTTGTGAGAAA	1243

QY 1193 TTTTCCGCGTGGTGGACAAATCAGTAGATTTCATTGGAAGCAAAAGCCTCCATGGAT 1252
Db 1244 TTTTCCGCGTGGTGGACAAATCAGTAGATTTCATTGGAAGCAAAAGCCTCCATGGAT 1303
QY 1253 GTGTTCTAGTGCATGTTTAGCTGGGATCTCCGCTCCGCAACCATGCTATGCGCTTACA 1312
Db 1304 GTGTTCTAGTGCATGTTTAGCTGGGATCTCCGCTCCGCAACCATGCTATGCGCTTACA 1363
QY 1313 TCATGAAAGAGATGAGCATGCTTTTAGATGAGATGATACAGATTGTGAAAGAAAGAAC 1372
Db 1364 TCATGAAAGAGATGAGCATGCTTTTAGATGAGATGATGAGATTGTGAAAGAAAGAAC 1423
QY 1373 CTACTATATCTCCAAACTTCAATTTTCTGGGCCCACTCTCTGAGCTATGAGAAAGATTA 1432
Db 1424 CTACTATATCTCCAAACTTCAATTTTCTGGGCCCACTCTCTGAGCTATGAGAAAGATTA 1483
QY 1433 AGAAGCAGACTGAGAGATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAAC 1492
Db 1484 AGAAGCAGACTGAGAGATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACCTGGAGAAC 1543
QY 1493 CAAATGAACCTGTCCCTGTGTCTCAGAGGGTGGACAGAAAAGCAGAGAGCCCTCAGTC 1552
Db 1544 CAAATGAACCTGTCCCTGTGTCTCAGAGGGTGGACAGAAAAGCAGAGAGCCCTCAGTC 1603
QY 1553 CACCCTGTGCCCATCTGTCTACTCTCAGAGCAGCAGAGCAAAAAGCCCTGTCATCCCGCA 1612
Db 1604 CACCCTGTGCCCATCTGTCTACTCTCAGAGCAGCAGAGCAAAAAGCCCTGTCATCCCGCA 1663
QY 1613 GCGTGCCACGCGTCCAGCAGCTGCAGCCGTCGTGTAGAGGACGCCCGCTGGTACAGG 1672
Db 1664 GCGTGCCACGCGTCCAGCAGCTGCAGCCGTCGTGTAGAGGACGCCCGCTGGTACAGG 1723
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Db 1724 CGCTCAGTGGGCTGCACCTGTCCGAGAGAGGCTGGAGAGCAATAGCTCAAGCCTT 1783
QY 1733 CCTTCTCTGAGATTCATCAATCAGTTTCAATTTCAGCCAGCATGCGACATCTTACATG 1792
Db 1784 CCTTCTCTGAGATTCATCAATCAGTTTCAATTTCAGCCAGCATGCGACATCTTACATG 1843
QY 1793 GCTTCTCTCATCAGAAAGATGCTTTGGAATCTAACAACTTCCACTCTCTGATGGGA 1852
Db 1844 GCTTCTCTCATCAGAAAGATGCTTTGGAATCTAACAACTTCCACTCTCTGATGGGA 1903
QY 1853 CCAAGAGCTATGCGAGTTCTCCCTGTTCAAGAACTATCGAGAGCATCCCGAAACCA 1912
Db 1904 CCAAGAGCTATGCGAGTTCTCCCTGTTCAAGAACTATCGAGAGCATCCCGAAACCA 1963
QY 1913 GTCTGATTAAGGAGAGCAGCATCCCAAGAGCTGCAGACCGCCAGGCTTCAAGCA 1972
Db 1964 GTCTGATTAAGGAGAGCAGCATCCCAAGAGCTGCAGACCGCCAGGCTTCAAGCA 2023
QY 1973 GCCAGAGAGAGGATTTGCAATTCGCTCAGAACCAAGAGCATGCGCCAGAGGTCCTC 2032
Db 2024 GCCAGAGAGAGGATTTGCAATTCGCTCAGAACCAAGAGCATGCGCCAGAGGTCCTC 2083
QY 2033 TTTTATCTCCACTGATGAGATGAGAGGCTGGAGAGCAATTAACAACAAGCTTCTT 2092
Db 2084 TTTTATCTCCACTGATGAGATGAGAGGCTGGAGAGCAATTAACAACAAGCTTCTT 2143
QY 2093 TCGGACCTTTCACAGCAGCAGAGCACTCAAGAGTCTGCTGCGCTGGGCTTAAAGGCT 2152
Db 2144 TCGGACCTTTCACAGCAGCAGAGCACTCAAGAGTCTGCTGCGCTGGGCTTAAAGGCT 2203
QY 2153 GGCAGCTGGGATATTTGGGCCCCCAGAACCTTCACTCCCTTCCCTGAGCAGAGCTGTATT 2212
Db 2204 GGCAGCTGGGATATTTGGGCCCCCAGAACCTTCACTCCCTTCCCTGAGCAGAGCTGTATT 2263
QY 2213 TTGCGACAGAGTCTCTCACTTTCACTGTGCTCAGCAGCATCTACGAGAGAGGCTCAAGT 2272
Db 2264 TTGCGACAGAGTCTCTCACTTTCACTGTGCTCAGCAGCATCTACGAGAGAGGCTCAAGT 2323
QY 2273 ACTCTGCTTACAGCTGAGCGCAGCTGCGCACTTCCGAGAGCAAACTATTTCTGTGCGCA 2332

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QY 2333 GCGCGCAGAGCCAAAGTGAAGAGCTGACTGCGCGGAGAGCTGAGCATGGAAGAGCCCT 2392
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Db 2564 TGAATATCATTTAGAGTCTCTGAGAGAAAGACATTTGTGACTTATAGACAATTTT 2622
QY 2573 TTTTCTGTTCACAAAAAATTCCTGTGTAATCTGAAATATATATATATATATATATAT 2632
Db 2623 TTTTCTGTTCACAAAAAATTCCTGTGTAATCTGAAATATATATATATATATATATAT 2682
QY 2633 TATTTTGGAAAAATGAGCTATGTTGTAAGAAAGCAAGGTGATCAACCAAGTTGTTACT 2692
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QY 2693 CTCTTAACATCTGATTTGAGAGATCAGCTAATATCTTCTCAACAAAAATGGAAGGGCA 2752
Db 2743 CTCTTAACATCTGATTTGAGAGATCAGCTAATATCTTCTCAACAAAAATGGAAGGGCA 2802
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Db 2803 GATGCTGAATCCCGCTTACAGGAGAGAAACCAATTTATTCAGTGAATTAACATCCGC 2862
QY 2813 TTGTTCTTAAAAAAGCAAGTGTCTTTGTGTGAGAGCAAAATCCCTACATTTTCA 2872
Db 2863 TTGTTCTTAAAAAAGCAAGTGTCTTTGTGTGAGAGCAAAATCCCTACATTTTCA 2922
QY 2873 GTTGTGATCTAAGATCTCAAAATTTAGTCTTTTCCGAGCCCTTCCATATGACACT 2932
Db 2923 GTTGTGATCTAAGATCTCAAAATTTAGTCTTTTCCGAGCCCTTCCATATGACACT 2982
QY 2933 TAGCGCTGAGACTGAGCCAGCTTGGGGGTCAAGTATGAGACCTGTTAGGAGAGAGCC 2992
Db 2983 TAGCGCTGAGACTGAGCCAGCTTGGGGGTCAAGTATGAGACCTGTTAGGAGAGAGCC 3042
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QY 3053 TGAAGCCGAGGAGACAGAGCATCTGCTGAGAGAGCACTTATGAGGGGCTTGGCAAG 3112
Db 3103 TGAAGCCGAGGAGACAGAGCATCTGCTGAGAGAGCACTTATGAGGGGCTTGGCAAG 3162
QY 3113 TCTACCTTAAGCAAAACCCAGTACTCAGACAGAAAGTGGGGCTTGGACCACTAACAT 3172
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Db 3343 CTTCAGCTTTATGAGAGAGAGGAACTGTCTTATGAGATTGAGCTGAAACCAAGAGAAC 3402
QY 3353 TGGCAACATCAAGATTTAAGTGTGAGAGGCTTACAGGTACTCTCTTTGTGA 3412

Db	3403	GGGCAACATACGATTTAAGCTAAGGTTGGAGGCTAAAGACTACCTCCTCTTTGTA	3463
Qy	3413	AATCAAGAATTTGTTAAATGGATGGATTCCTTTAAATAAAGATGAATTGGTTTC	3472
Db	3463	AATCAAAATAATTGTTAAATGGGATTTGTCAATCTTTAAATAAAGATGAATTGGTTTC	3522
Qy	3473	AAGCCAAATNGAATTTAATTTGGGTTGGTAGAGACAGACGACCTTCAAAATTCGACG	3533
Db	3523	AAGCCAAATNGAATTTAATTTGGGTTGGTAGAGACAGACGACCTTCAAAATTCGACG	3583
Qy	3533	CAAGACATGTTTTTGGCCTTTCGTCTTCACTGCATGGATPACATTTGGTAAATGTAT	3592
Db	3583	CBAAGCAATGTTTTTGGCCTTTCGTCTTCACTGCATGGATPACATTTGGTAAATGTAT	3642
Qy	3593	AATATGCGAATTTTATATAGAACTTCCTAGGAGGTAAATATATAGGAAGATTAGAA	3653
Db	3643	AATATGCGAATTTTATATAGAACTTCCTAGGAGGTAAATATATAGGAAGATTAGAA	3702
Qy	3653	GGTACAAATTTGCTGAGGAGAACAGAGAAACCTGTTTCTTATGAGCTTTATCCCTCGG	3712
Db	3703	GGTACAAATTTGCTGAGGAGAACAGAGAAACCTGTTTCTTATGAGCTTTATCCCTCGG	3762
Qy	3713	CATGCGATGGGGCTATGTTTCTATGATGCGCTCAGACCTTTCACATTTACTAGTGGGCT	3772
Db	3763	CATGCGATGGGGCTATGTTTCTATGATGCGCTCAGACCTTTCACATTTACTAGTGGGCT	3822
Qy	3773	GAGAGAGGCTTTAGTAGAGAAAGAAATATTCAGATATAAACGGTTGAGAAAGCTGAGAA	3833
Db	3823	GAGAGAGGCTTTAGTAGAGAAAGAAATATTCAGATATAAACGGTTGAGAAAGCTGAGAA	3883
Qy	3833	CCATTGAGTTTGTATCAGTTGTGAATAGATGTCAAAGCCATGCGCAGCTGTTTTGGA	3892
Db	3883	CCATTGAGTTTGTATCAGTTGTGAATAGATGTCAAAGCCATGCGCAGCTGTTTTGGA	3942
Qy	3893	ACGCTGGCGGGGTCTTCAGTGGGAAAAAGCAATTCAAATNGAGCGAGGCAAAAGGGG	3953
Db	3943	ACGCTGGCGGGGTCTTCAGTGGGAAAAAGCAATTCAAATNGAGCGAGGCAAAAGGGG	4002
Qy	3953	GGTCCCTCAGTCCCTCAACCTTACATCAGTATGAGATCGGTCTTGGCAGCTGAACATAGG	4012
Db	4003	GGTCCCTCAGTCCCTCAACCTTACATCAGTATGAGATCGGTCTTGGCAGCTGAACATAGG	4062
Qy	4013	AGGTCACTGGAACAAAGTATATGTCAGATTTGGCTTTCAACATCCTCTGCGCTGAGTTT	4072
Db	4063	AGGTCACTGGAACAAAGTATATGTCAGATTTGGCTTTCAACATCCTCTGCGCTGAGTTT	4122
Qy	4073	TATACAGCTACAAATGTGGGTCTCTTTTGAAGCCTTAATTCACACAGACGTTTTTGGGG	4132
Db	4123	TATACAGCTACAAATGTGGGTCTCTTTTGAAGCCTTAATTCACACAGACGTTTTTGGGG	4182
Qy	4133	GTGGGGCTGGGCGGGGTGTGTCAATTGTTCTTTCCTTCCGTAAAGTGCAGTATGTG	4192
Db	4183	GTGGGGCTGGGCGGGGTGTGTCAATTGTTCTTTCCTTCCGTAAAGTGCAGTATGTG	4242
Qy	4193	CCTCGTATCTCAGGTTTTTCTCTGTTTTTGAAGAAATGACAGTTTTTGTACACAGATGTG	4252
Db	4243	CCTCGTATCTCAGGTTTTTCTCTGTTTTTGAAGAAATGACAGTTTTTGTACACAGATGTG	4302
Qy	4253	ACTTCATGTTCCTATATGCTGACTTTTAAACACGACACAGAAATGATATCTTCAACACGA	4312
Db	4303	ACTTCATGTTCCTATATGCTGACTTTTAAACACGACACAGAAATGATATCTTCAACACGA	4362
Qy	4313	CCGACCTTGTTATGAGGAGATGATAGACCGCACAGACTTCACTAATGTTGTCACAAAATATGT	4372
Db	4363	CCGACCTTGTTATGAGGAGATGATAGACCGCACAGACTTCACTAATGTTGTCACAAAATATGT	4422
Qy	4373	GCTATGATGGGGTGTAAAGTGAAGGACAGAAAGGGTCAAGCCGATTTGTATGATATCTGGG	4432
Db	4423	GCTATGATGGGGTGTAAAGTGAAGGACAGAAAGGGTCAAGCCGATTTGTATGATATCTGGG	4482
Qy	4433	AAAGTGTGTGTCAACGATTTTGAATTTAGTTTAAATATACATGAAATCTTTATCAGAC	4492
Db	4483	AAAGTGTGTGTCAACGATTTTGAATTTAGTTTAAATATACATGAAATCTTTATCAGAC	4542

QY	4493	ATTCGAGTTTCCACAGTGTGTTTGAATGTATGTAACACACACCAAAATGTATAACA	4553
Db	4543	ATTCGAGTTTCCACAGTGTGTTTGAATGTATGTAACACACACCAAAATGTATAACA	4603
QY	4553	GTTCAACCACTTCCAGAGTGTGTGTCAATGCCAAAATGTTTAAGAAAGAAAGCAGTAGC	4613
Db	4603	GTTCAACCACTTCCAGAGTGTGTGTCAATGCCAAAATGTTTAAGAAAGAAAGCAGTAGC	4663
QY	4613	TCCTTGCTTAACGATGTTTCAGAGAGTTTGGGGCACTTGTTTAATAGCTTCTCATTT	4673
Db	4663	TCCTTGCTTAACGATGTTTCAGAGAGTTTGGGGCACTTGTTTAATAGCTTCTCATTT	4723
QY	4673	TAGGGCTTCTCTGGGCCATATGGTCCCTTCTCTTGGAACGTGATGTATGTCATCTCAAT	4733
Db	4723	TAGGGCTTCTCTGGGCCATATGGTCCCTTCTCTTGGAACGTGATGTATGTCATCTCAAT	4783
QY	4733	AGCCTTAAGTCTGTGTTTCACTAGTGTCAATATCAATTCAGTTCTTGGAATCGAAGCTCCGTG	4793
Db	4783	AGCCTTAAGTCTGTGTTTCACTAGTGTCAATATCAATTCAGTTCTTGGAATCGAAGCTCCGTG	4843
QY	4843	GCGAAGGGGTGTGCTTCGAGAGCAGGCTCTGAGCTGCTTGATGTCTTTAAGTGGGGTGG	4853
Db	4893	GCGAAGGGGTGTGCTTCGAGAGCAGGCTCTGAGCTGCTTGATGTCTTTAAGTGGGGTGG	4903
QY	4853	TGGGCTGG 4859	
Db	4903	TGGGCTGG 4909	
RESULT 13			
US-10-357-930-27149			
; Sequence 27149, Application US/10357930			
; Publication No. US20040259086A1			
; GENERAL INFORMATION:			
; APPLICANT: Schlegel, Robert			
; APPLICANT: Endege, Wilson			
; APPLICANT: Monahan, John			
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR			
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF			
; FILE REFERENCE: MRI-007BCN			
; CURRENT APPLICATION NUMBER: US/10/357, 930			
; PRIOR FILING DATE: 2003-02-04			
; PRIOR APPLICATION NUMBER: 09/785, 276			
; PRIOR FILING DATE: 2003-02-16			
; PRIOR APPLICATION NUMBER: 60/183, 319			
; PRIOR FILING DATE: 2000-02-17			
; PRIOR APPLICATION NUMBER: 60/189, 862			
; PRIOR FILING DATE: 2000-03-16			
; PRIOR APPLICATION NUMBER: 60/207, 454			
; PRIOR FILING DATE: 2000-05-25			
; PRIOR APPLICATION NUMBER: 60/211, 314			
; PRIOR FILING DATE: 2000-06-09			
; PRIOR APPLICATION NUMBER: 60/219, 007			
; PRIOR FILING DATE: 2000-07-18			
; PRIOR APPLICATION NUMBER: 60/255, 281			
; PRIOR FILING DATE: 2000-12-13			
; NUMBER OF SEQ ID NOS: 62232			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 27149			
; LENGTH: 5145			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc feature			
; LOCATION: 1, 5144, 5145			
; OTHER INFORMATION: n = A,T,C or G			
US-10-357-930-27149			
Query Match			
Best Local Similarity 81.0%; Score 4413; DB 18; Length 5145;			
Matches 4683; Conservative 0; Mismatches 3; Indels 1; Gaps 1;			

QY 173 GCTTTCAGTCCAGTGTAAAGCTGTTGAGCGCGGAGCAAAAGGTAAGATGATGTAATG 232
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QY 233 CGCTGCGTCTCCAAAGCATCTTTTGTGTGAATGTTATTCAGTCACTCTCTTATGA 292
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QY 293 ATCAATGTAGAGGCGCTGTTGTGAGCGAGTCTTTGCAAGACATCAACGGGAAA 352
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QY 353 GAGAAAGAGCATTTCACTTGTGAGGCGCTCTTGTGAAATGGGTTTAACTCTCTTTTGGC 412
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QY 473 ACACACCATTAATCATCATGCTGSCAAATTAAGAAAGAGTGGGAAAAGAGACTTAATG 532
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QY 533 TTGTCAATGCGCCATGATGATGATGAACTCAATTTGTTAATGAGAGTGTGGCTTGC 592
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Db 704 CATCCACATTTTGGAAAGCATTAATCACTGCTCCAGCTTAATGAGAGAGTGGTGC 763
QY 713 AACAGAGCAAGTGTAAATTAATACAGAGCTCATCAGATTCAGCGAAACATAAGTTGACA 772
Db 764 AACAGAGCAAGTGTAAATTAATACAGAGCTCATCAGATTCAGCGAAACATAAGTTGACA 823
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Db 944 AACTGCTTGCAGAGGTTGCTGATCTCTCGTTGTTTCCCTGGCTCTGTGAGAGAA 1003
QY 953 AATTCACCTAGTCCCTACCTGCACTTCTCAGCCCTTGTACTCTGTGCAAACTTGGGC 1012
Db 1004 AATTCACCTAGTCCCTACCTGCACTTCTCAGCCCTTGTACTCTGTGCAAACTTGGGC 1063
QY 1013 CAACCCGAATCTTCCCAATCTTTATCTTGTGCTGCAGCGAGATGTCTTCAACAAGAGC 1072
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QY 1853 CCAACAAAGCTATGCGAGTTCTCCCTGTTTCAAGAACTATCGAGAGCACTCCGAAACCA 1912
Db 1904 CCAACAAAGCTATGCGAGTTCTCCCTGTTTCAAGAACTATCGAGAGCACTCCGAAACCA 1963
QY 1913 GTCCTGATTAAGAGGAGAGCAAGATCCCAAGAGCTGAGACCCGAGGCTTTCAGACA 1972
Db 1964 GTCCTGATTAAGAGGAGAGCAAGATCCCAAGAGCTGAGACCCGAGGCTTTCAGACA 2023
QY 1973 GCCAGAGCAAGCGATTTGATTCGATCAGAACAGAGAGAGTGGCACCCGCCAGAGTCCC 2032
Db 2024 GCCAGAGCAAGCGATTTGATTCGATCAGAACAGAGAGAGTGGCACCCGCCAGAGTCCC 2083
QY 2033 TTTTATCTCACAATGATTCGAATGGGAGGCTGAGAGCAATTTACACACAGCTTCTTT 2092
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QY 2093 TCGGCTTTTCCACAGCCAGCAGCACTTCAAGAGTGTGAGGCTTGAAGGCT 2152
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2384 GCCTGAGAGCAAGTGAAGAGCTGACTCGCGGAGCTGAGATGAAGAGACCCCT 2443
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2444 TTGAAGAAGTTTAAACGAGAGCTGCAATTTGAAGAGAGCATCATGTGAG 2503
2453 AGAAGAGTCAAGGAGAGAGTGGGAAAGTGGGAGTCACTGAGCTTTTGGGAGCA 2512
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2873 GTTGTGCTAAGAGATCTCAATATTAATAGTCTTGTGCGAACCCCTCATAGTACCT 2932
2923 GTTGTGCTAAGAGATCTCAATATTAATAGTCTTGTGCGAACCCCTCATAGTACCT 2982
2933 TAGGCTAAGATGAGCCAGCTTGGGGGTCAAGTATGATGAGCCCTGTTAGGAGAGAGC 2992
2983 TAGGCTAAGATGAGCCAGCTTGGGGGTCAAGTATGATGAGCCCTGTTAGGAGAGAGC 3042
2993 TAGGCTAAGATGAGCCAGCTTGGGGGTCAAGTATGATGAGCCCTGTTAGGAGAGAGC 3052
3043 TAGGCTAAGATGAGCCAGCTTGGGGGTCAAGTATGATGAGCCCTGTTAGGAGAGAGC 3102
3053 TGAAGAGAGAGAGAGAGAGATCTGCTGAGAGAGCACTTGAAGGAGCTTGGCAAG 3112
3103 TGAAGAGAGAGAGAGAGAGATCTGCTGAGAGAGCACTTGAAGGAGCTTGGCAAG 3162
3113 TCTAATCTTAAGAGAAACCAAGTACTCAGAGAGAGAAAGTGGGAGCTTTGACATACAT 3172
3163 TCTAATCTTAAGAGAAACCAAGTACTCAGAGAGAGAAAGTGGGAGCTTTGACATACAT 3222
3173 ATCTGATGAGCCATTTTCTAGGATTTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 3232
3223 ATCTGATGAGCCATTTTCTAGGATTTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 3282
3233 CCAATTTAAACTGTCTATGACAAATTCCTGAGGAGCTGATGAGAGTAAATTTT 3292
3283 CCAATTTAAACTGTCTATGACAAATTCCTGAGGAGCTGATGAGAGTAAATTTT 3342
3293 CTCTCACTTTTATGAAGAGAGAGAGAGTCTGATGAGTAAAGTAAAGTAAAGTAAAGT 3352
3343 CTCTCACTTTTATGAAGAGAGAGAGAGTCTGATGAGTAAAGTAAAGTAAAGTAAAGT 3402
3353 TGGCAACATCAAGATTTAAGCTAAGTGGAGGCTAAGCTAAGCTAAGCTAAGCTAAGCT 3412
3403 TGGCAACATCAAGATTTAAGCTAAGTGGAGGCTAAGCTAAGCTAAGCTAAGCTAAGCT 3462
3413 AATCAAGAAATTTTAAATGAGTGTGATCTTTAAATTAAGATGAATCTTGTGTTTC 3472

3463 AATCAAGAAATTTTAAATGAGTGTGATCTTTAAATTAAGATGAATCTTGTGTTTC 3522
3473 AAGCCAAATGTAATTTATTTGGGTTGGTAGAGAGAGAGACCTTCAATTCACG 3532
3523 AAGCCAAATGTAATTTATTTGGGTTGGTAGAGAGAGAGACCTTCAATTCACG 3582
3533 CAAGCAGATGTTTTTGGCTTTCTGCTTCACTGATGATACAGTGGTAAATGTAT 3592
3583 CAAGCAGATGTTTTTGGCTTTCTGCTTCACTGATGATACAGTGGTAAATGTAT 3642
3593 AATATGCAAAATTTTATGAAGAACTTCTGAAGAGTAAATTAATGGAAGTTAAGAA 3652
3643 AATATGCAAAATTTTATGAAGAACTTCTGAAGAGTAAATTAATGGAAGTTAAGAA 3702
3653 GGTAAATTTGCTGAG 3712
3703 GGTAAATTTGCTGAG 3762
3713 CATGAGTGGGAGTATGTTTCTATGATTTGCTCAGACTTTCACATTTACTAGTGGCT 3772
3763 CATGAGTGGGAGTATGTTTCTATGATTTGCTCAGACTTTCACATTTACTAGTGGCT 3822
3773 GAGAGAGCTTTAGTGAAGAGAGATTAATCAAGATTAACGTTGAGAGAGCTGAGAA 3832
3823 GAGAGAGCTTTAGTGAAGAGAGATTAATCAAGATTAACGTTGAGAGAGCTGAGAA 3882
3833 CCATTAAGTTTATGATCAATTTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3892
3883 CCATTAAGTTTATGATCAATTTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3942
3893 AAGCTGGGAGGAGTGTCTTCAAGTGAAGAAACCAATCAAAATGAGAGAGAGAGAG 3952
3943 AAGCTGGGAGGAGTGTCTTCAAGTGAAGAAACCAATCAAAATGAGAGAGAGAGAG 4002
3953 GGTCTCAAGTCTCAACCTCAATCACTGATGAAGTGGTCTTGGAGCTGAAATGAG 4012
4003 GGTCTCAAGTCTCAACCTCAATCACTGATGAAGTGGTCTTGGAGCTGAAATGAG 4062
4013 AGGTCACTGGAACAAGTATAGTGAAGTGGCTTTCAAAATCTCTGGCTTGAAGTT 4072
4063 AGGTCACTGGAACAAGTATAGTGAAGTGGCTTTCAAAATCTCTGGCTTGAAGTT 4122
4073 TATCAGCTAAGATGAGGAGTCTCTTTGAAGCTTAAATCAACAGAGAGCTTTTGGAG 4132
4123 TATCAGCTAAGATGAGGAGTCTCTTTGAAGCTTAAATCAACAGAGAGCTTTTGGAG 4182
4133 GTGGGAGTGGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4192
4183 GTGGGAGTGGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4242
4193 CCTGATCTCAAGTTTCTCTGTTTGAAGAAATGAGAGAGAGAGAGAGAGAGAGAG 4252
4243 CCTGATCTCAAGTTTCTCTGTTTGAAGAAATGAGAGAGAGAGAGAGAGAGAGAG 4302
4253 ACTTCATGTTTCTATGAGTGACTTCTAAGACAGAGAGAGAGAGAGAGAGAGAGAG 4312
4303 ACTTCATGTTTCTATGAGTGACTTCTAAGACAGAGAGAGAGAGAGAGAGAGAGAG 4362
4313 CCGACTTGGTATGAGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4372
4363 CCGACTTGGTATGAGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4422
4373 GCTATGATGGGAGTGAAG 4432
4423 GCTATGATGGGAGTGAAG 4482
4433 AAGAGTGTGATCAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATG 4492
4483 AAGAGTGTGATCAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATG 4542
4493 ATTCTCAAGTTTCAACAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 4552
4543 ATTCTCAAGTTTCAACAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 4602

QY 4553 GTTCACCACTTCAGAGTGTGTCATGCCAAAACATGTTTAAAGAAAGAGAGATAGC 4612
Db 4603 GTTCACCACTTCAGAGTGTGTCATGCCAAAACATGTTTAAAGAAAGAGAGATAGC 4662
QY 4613 TCCTTGCTAACGATGTTTTCAGAGAGTTTGAGGAGCATTTGTTTAAAGAGCTTCGTCAAT 4672
Db 4663 TCCTTGCTAACGATGTTTTCAGAGAGTTTGAGGAGCATTTGTTTAAAGAGCTTCGTCAAT 4722
QY 4673 TAGGGCTTCCTTGAGGAGCATGTCCTTCCTTGAGAACGATGATATAGTCAATCTTAC 4732
Db 4723 TAGGGCTTCCTTGAGGAGCATGTCCTTCCTTGAGAACGATGATATAGTCAATCTTAC 4782
QY 4733 AGCCTTTAGTGTGTTTCACTAGTGTCAATATCAATTCAGTTCTTGAAATCAGACTGCGGAG 4792
Db 4783 AGCCTTTAGTGTGTTTCACTAGTGTCAATATCAATTCAGTTCTTGAAATCAGACTGCGGAG 4842
QY 4793 GCGAAGGGGTGCTGCGAGAGCGGCTTGAGAGCTTGATGTCTTTAGGTGAGGTG 4852
Db 4843 GCGAAGGGGTGCTGCGAGAGCGGCTTGAGAGCTTGATGTCTTTAGGTGAGGTG 4902
QY 4853 TGAGCTG 4859
Db 4903 TGAGCTG 4909

RESULT 14
US-10-357-930-28675
; Sequence 28675, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: HUMAN PROSTATE CANCER
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28675
; LENGTH: 5145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 5144, 5145
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-28675

Query Match 81.0%; Score 4413; DB 18; Length 5145;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4683; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 173 GCTTTCAGTCCAGTGTAAAGCTGTGAGCGCGGAGCAAAAGTTAAAGATGATGATG 232
Db 224 GCTTTCAGTCCAGTGTAAAGCTGTGAGCGCGGAGCAAAAGTTAAAGATGATGATG 283

QY 233 CGCTGCTGCTCCAAAGCATCTTTGTTGTGGAATGGTTATTCAGTCACTCTTTATGA 292
Db 284 CGCTGCTGCTCCAAAGCATCTTTGTTGTGGAATGGTTATTCAGTCACTCTTTATGA 343
QY 293 ATCAATGTGAGGGGCTGCTTGTGAGCGAGTCTTTGCAAGAGCAATCAAGGGGAAA 352
Db 344 ATCAATGTGAGGGGCTGCTTGTGAGCGAGTCTTTGCAAGAGCAATCAAGGGGAAA 403
QY 353 GAGAAAGACATTCATCTTGAGAGGCTTTGCTGAAAATGGGTTTAACTCTCTTTGGC 412
Db 404 GAGAAAGACATTCATCTTGAGAGGCTTTGCTGAAAATGGGTTTAACTCTCTTTGGC 463
QY 413 AGTACCAACGAGCTGAGCTTCACTTTTATGATCAATGAGTGTGAGCTTTGAGC 472
Db 464 AGTACCAACGAGCTTCACTTTTATGATCAATGAGTGTGAGCTTTGAGC 523
QY 473 AACACCACTTATCATCTGTCGCAATTTAAAGAAAGAGTGGGAAAAGGACTTATG 532
Db 524 AACACCACTTATCATCTGTCGCAATTTAAAGAAAGAGTGGGAAAAGGACTTATG 583
QY 533 TTGTATGCGCCATGAGATGATGGAATCTCAATTTGTACTGAGAGTGTGCTTGC 592
Db 584 TTGTATGCGCCATGAGATGATGGAATCTCAATTTGTACTGAGAGTGTGCTTGC 643
QY 593 TGGAAAGTGGAAAGGAAAGTGTGCTAATTTGATAGCCGCAATTTGTGGAATCAATA 652
Db 644 TGGAAAGTGGAAAGGAAAGTGTGCTAATTTGATAGCCGCAATTTGTGGAATCAATA 703
QY 653 CATCCACATTTTGAAGCCATTAATATCACTGCTCAAGCTTTATGAGCGAAGGTGC 712
Db 704 CATCCACATTTTGAAGCCATTAATATCACTGCTCAAGCTTTATGAGCGAAGGTGC 763
QY 713 AACGAGCAAAAGTTAATTAACAGAGCTCATCAGCAATTCAGGAAACATAGGTTGAC 772
Db 764 AACGAGCAAAAGTTAATTAACAGAGCTCATCAGCAATTCAGGAAACATAGGTTGAC 823
QY 773 TTGATTCAGTCAAGAGTGTGATTTAAGATCAAGAGCTCCCAAGATGTGCTCTCT 832
Db 824 TTGATTCAGTCAAGAGTGTGATTTAAGATCAAGAGCTCCCAAGATGTGCTCTCT 883
QY 833 CTTCAAGCTGTTTTCATCTGATCTTCTGAGTAACTGAGAAAGAGCTTCACTGTTTC 892
Db 884 CTTCAAGCTGTTTTCATCTGATCTTCTGAGTAACTGAGAAAGAGCTTCACTGTTTC 943
QY 893 ACCGTGTCGAGGTGGTGTGCTGAGTCTCTGCTGTTTCTCTGAGCTCTGTGAAGAA 952
Db 944 ACCGTGTCGAGGTGGTGTGCTGAGTCTCTGCTGTTTCTCTGAGCTCTGTGAAGAA 1003
QY 953 AATCACTAGTCCCTCACTGATTTCTCAGAGCTTCACTGTTGCAACATTTGGGC 1012
Db 1004 AATCACTAGTCCCTCACTGATTTCTCAGAGCTTCACTGTTGCAACATTTGGGC 1063
QY 1013 CAACCCGAATTTCTCCCAATCTTTATCTTGCTGCCAGGAGATGCTTCAACAAAGAGC 1072
Db 1064 CAACCCGAATTTCTCCCAATCTTTATCTTGCTGCCAGGAGATGCTTCAACAAAGAGC 1123
QY 1073 TGAATCAGCAGAGATGGGATTTGTTATGTTAATGCCAGCTAATCTGCAAGGCTTG 1132
Db 1124 TGAATCAGCAGAGATGGGATTTGTTATGTTAATGCCAGCAATCTGTCAAAGGCTTG 1183
QY 1133 ACTTTATCCCGAGTCTCAATTTCTGCGTGTGCTGTGAATGACAGCTTTGTGAGAAA 1192
Db 1184 ACTTTATCCCGAGTCTCAATTTCTGCGTGTGCTGTGAATGACAGCTTTGTGAGAAA 1243
QY 1193 TTTTGGCGGTGTGAGCAAAATGATGATTTTCAATTTGAAGAAAGCAAGCTTCAATGGAT 1252
Db 1244 TTTTGGCGGTGTGAGCAAAATGATGATTTTCAATTTGAAGAAAGCAAGCTTCAATGGAT 1303
QY 1253 GTGTTCTAGTGACATGTTTATGCTGGGATCTCCGCTCGCCACCATGCTATTCGCTACA 1312
Db 1304 GTGTTCTAGTGACATGTTTATGCTGGGATCTCCGCTCGCCACCATGCTATTCGCTACA 1363

QY	1313	TCATGAAAGAGATGGACATGCTCTTAAGATGAAGCTTACAGATTTTGTGAAAAGAAAAGAC	1317
Db	1364	TCATGAAAGAGATGGACATGCTCTTAAGATGAAGCTTACAGATTTTGTGAAAAGAAAAGAC	1422
QY	1373	CTACTATATCTCCAACTTCAATTTTCTGGGGCAACTCTGTGACATATGAGAAAGATTA	1433
Db	1444	CTACTATATCTCCAACTTCAATTTTCTGGGGCAACTCTGTGACATATGAGAAAGATTA	1488
QY	1433	AGAACCAAGCTGGAGCATCAGGGGCAAAAGACAACTCAGAGCTGTGCACTGGAGAGC	1492
Db	1484	AGAACCAAGCTGGAGCATCAGGGGCAAAAGACAACTCAGAGCTGTGCACTGGAGAGC	1543
QY	1493	CAAAATGAACCTGTCCCTGTGTCTCAGAGGGTGTGACAGAAAAAGCAGACGCCCTCACTC	1552
Db	1544	CAAAATGAACCTGTCCCTGTGTCTCAGAGGGTGTGACAGAAAAAGCAGACGCCCTCACTC	1603
QY	1553	CACCCCTGGCGCACTCTGTCTACTCAGAGGGCAGCAGCAAAAGGCGGTGCATCCCGGCA	1612
Db	1604	CACCCCTGGCGCACTCTGTCTACTCAGAGGGCAGCAGCAAAAGGCGGTGCATCCCGGCA	1663
QY	1613	GCGTGCCCAAGCGGTGCCAGCGGTGCAGCCGTGCTGTATGAGGACAGCCCGCTGTATCAGG	1672
Db	1664	GCGTGCCCAAGCGGTGCCAGCGGTGCAGCCGTGCTGTATGAGGACAGCCCGCTGTATCAGG	1723
QY	1673	CGCTCAGTGGGCTGCACCTGTTCGCGACACAGGCTGGAGACAGCATATTAAGCTAACGCTT	1733
Db	1724	CGCTCAGTGGGCTGCACCTGTTCGCGACACAGGCTGGAGACAGCATATTAAGCTAACGCTT	1783
QY	1733	CCTTCTCTGTGGATATCAAAATCAGTTATATATTCAGCGCAGATGGCAGCATCTTCAATG	1792
Db	1784	CCTTCTCTGTGGATATCAAAATCAGTTATATATTCAGCGCAGATGGCAGCATCTTCAATG	1843
QY	1793	GCTTCTCTCTCATCAGAAAGATGCTTTGGAATATCTAACAACTTTCACATCTCTGTATGGGA	1852
Db	1844	GCTTCTCTCTCATCAGAAAGATGCTTTGGAATATCTAACAACTTTCACATCTCTGTATGGGA	1903
QY	1853	CCAAACAGCTATGCCAGATTTCTCCCTGTTCAGAAATATCGAGCAGACTCCGAAACCA	1912
Db	1904	CCAAACAGCTATGCCAGATTTCTCCCTGTTCAGAAATATCGAGCAGACTCCGCAACCA	1963
QY	1913	GTCCTGATTAAGAGGAGAACCGAGCATCCCAAGAAAGCTGCACACGCGCAGGCGCTTCAGCA	1972
Db	1964	GTCCTGATTAAGAGGAGAACCGAGCATCCCAAGAAAGCTGCACACGCGCAGGCGCTTCAGCA	2023
QY	1973	GCCAGAGCAAGCGATTTGCAATTCGATTCAGAAACCAAGCAGAGAGTGGACCGCCAGAGAGTCCC	2032
Db	2024	GCCAGAGCAAGCGATTTGCAATTCGATTCAGAAACCAAGCAGAGAGTGGACCGCCAGAGAGTCCC	2083
QY	2033	TTTTATCTCCACTGATCGAAGTGGAGCGTGGAGGACAAATTAACACACAGCTTCTTT	2092
Db	2084	TTTTATCTCCACTGATCGAAGTGGAGCGTGGAGGACAAATTAACACACAGCTTCTTT	2143
QY	2093	TGCGGCTTTTCCACCAAGCGCAGAGACCTTCAGAAAGTCTGCGCTGGGCGCTTAAAGGCGCT	2152
Db	2144	TGCGGCTTTTCCACCAAGCGCAGAGACCTTCAGAAAGTCTGCGCGCTTAAAGGCGCT	2203
QY	2153	GGCACTCGGATATCTTTGGCCCCCCCCAGACCTTCACCCCTTCCCTGACACGACAGCTGTAT	2212
Db	2204	GGCACTCGGATATCTTTGGCCCCCCCCAGACCTTCACCCCTTCCCTGACACGACAGCTGTAT	2263
QY	2213	TTTGCCACAGAGTCTGCACATTTCTACTGTGCGCTGAGCCATCTTACGGAGGCAAGTGCAGTT	2272
Db	2264	TTTGCCACAGAGTCTGCACATTTCTACTGTGCGCTGAGCCATCTTACGGAGGCAAGTGCAGTT	2323
QY	2273	ACTCTGCGCTAAGCTGTGAGCCAGCTGCCCATCTTGGGAGACCAAACTCTAATTTCTGTGGCA	2332
Db	2324	ACTCTGCGCTAAGCTGTGAGCCAGCTGCCCATCTTGGGAGACCAAACTCTAATTTCTGTGGCA	2383
QY	2333	GGCGGCAAAAGCAAGTACAGAGCTGTACTCGCGCGAGAGCTGGCATTAAGAGAGCCCT	2392
Db	2384	GGCGGCAAAAGCAAGTACAGAGCTGTACTCGCGCGAGAGCTGGCATTAAGAGAGCCCT	2443
QY	2393	TTGAAAGCAGTTTAAACGACAGAGCTGCCAAATGAATTTTGGAGAGAGCATCATGTACAG	2452

[illegible]

Db 3523 AAGCCAAATGTAATTAATTTGGGTGGTAGCAGAGCAGCAGCCTTCAATTCACAG 3582
Qy 3533 CAAGCAGATGTTTGGCCCTTCTGCTCAGTCAGTGAATAAGTTGGTAATAT 3592
Db 3583 CAAGCAGATGTTTGGCCCTTCTGCTCAGTCAGTGAATAAGTTGGTAATAT 3642
Qy 3593 AATATGGCAGAAATTTATAGAAATCTTCAGGAGGTAATATATGGAAGATTAGAA 3652
Db 3643 AATATGGCAGAAATTTATAGAAATCTTCAGGAGGTAATATATGGAAGATTAGAA 3702
Qy 3653 GGTACAAATGCTGAGAGAGAGAGAAACCTGTCTTCTAGTGGCTTTTATCCCTCG 3712
Db 3703 GGTACAAATGCTGAGAGAGAGAGAAACCTGTCTTCTAGTGGCTTTTATCCCTCG 3762
Qy 3713 CATGCATGGGGCTGATGTTCTATGATTCCTCAGACTTTTCACTTTAATAATGAGGT 3772
Db 3763 CATGCATGGGGCTGATGTTCTATGATTCCTCAGACTTTTCACTTTAATAATGAGGT 3822
Qy 3773 GAGAGAGCTTTATAGAGAGAGAAATATTCAGAATAAAAGGTTGAGAAAGCTGAGAGA 3832
Db 3823 GAGAGAGCTTTATAGAGAGAGAAATATTCAGAATAAAAGGTTGAGAAAGCTGAGAGA 3882
Qy 3833 CCATTGATGTTGATGATGTTGGAATAGAGTGAAGCCATGCGCAAGCTTTTGGAA 3892
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Qy 3893 AGCGTGGCCGGCGTGTCTTCACTGAGAAAAGCAATCAAAATGAGCGAGACCAAGGGG 3952
Db 3943 AGCGTGGCCGGCGTGTCTTCACTGAGAAAAGCAATCAAAATGAGCGAGACCAAGGGG 4002
Qy 3953 GGTCTCAGTCTCTCAACCTACATCACTGTATGAAATGGTCTTGGCAGCTGAACATAG 4012
Db 4003 GGTCTCAGTCTCTCAACCTACATCACTGTATGAAATGGTCTTGGCAGCTGAACATAG 4062
Qy 4013 AGGTCACTGGAACAAGTGAATGAGCAGATGCTTCAACATCTCTCGGTGATGAGTT 4072
Db 4063 AGGTCACTGGAACAAGTGAATGAGCAGATGCTTCAACATCTCTCGGTGATGAGTT 4122
Qy 4073 TATCAGCTACATGTTGGGTCTCTTTTGAAGCTTAATTCACACAGCAGCTTTTGGGG 4132
Db 4123 TATCAGCTACATGTTGGGTCTCTTTTGAAGCTTAATTCACACAGCAGCTTTTGGGG 4182
Qy 4133 GTGGGGCTGGGGGGGTGTCATGTTCTTCCCTTCTGTAAGTGTCCGTAAGTGTG 4192
Db 4183 GTGGGGCTGGGGGGGTGTCATGTTCTTCCCTTCTGTAAGTGTCCGTAAGTGTG 4242
Qy 4193 CCTGCTATCTCAGGTTTCTCTGTTTGAAGAAATGACAGGTTTGGACAGAGATG 4252
Db 4243 CCTGCTATCTCAGGTTTCTCTGTTTGAAGAAATGACAGGTTTGGACAGAGATG 4302
Qy 4253 ACTTCATGTTTCTATGTTGCTTAAACACAGCAGAAATGATGACTCAACAGAG 4312
Db 4303 ACTTCATGTTTCTATGTTGCTTAAACACAGCAGAAATGATGACTCAACAGAG 4362
Qy 4313 CCGACTTGGTATGAGGAGTGAATGAGCCGACAGACTTCATGTTGTCACAAATATGT 4372
Db 4363 CCGACTTGGTATGAGGAGTGAATGAGCCGACAGACTTCATGTTGTCACAAATATGT 4422
Qy 4373 GCTATGATGGGGGTGAAGTGAAGCAGAAAGGGTCAAGCCGACTTGTATGATCTGGG 4432
Db 4423 GCTATGATGGGGGTGAAGTGAAGCAGAAAGGGTCAAGCCGACTTGTATGATCTGGG 4482
Qy 4433 AAAAGTGTGTCACAGATTTGATTTTGAATATACATTTGAAATCTTTAATCAGAC 4492
Db 4483 AAAAGTGTGTCACAGATTTGATTTTGAATATACATTTGAAATCTTTAATCAGAC 4542
Qy 4493 ATTCTCAAGTTTCAACAGATTTTGAATTTGATGACACACACCAATGTGTACA 4552
Db 4543 ATTCTCAAGTTTCAACAGATTTTGAATTTGATGACACACACCAATGTGTACA 4602
Qy 4553 GTTCAACATTTCCAGAGTGTGTCATGCCAAAACATGTTTAAAGAAAGAGAGTACG 4612
Db 4603 GTTCAACATTTCCAGAGTGTGTCATGCCAAAACATGTTTAAAGAAAGAGAGTACG 4662

Qy 4613 TCCTTGCTAAGATGTTTCAGAGAGTTGGGGCAGCTTGTTTAATAGCTTCTGTCA 4672
Db 4663 TCCTTGCTAAGATGTTTCAGAGAGTTGGGGCAGCTTGTTTAATAGCTTCTGTCA 4722
Qy 4673 TAGGGCTCTCTGGCCATGATGCCCTTCTCTGGAACGTGTATGATCAATCCCTAC 4732
Db 4723 TAGGGCTCTCTGGCCATGATGCCCTTCTCTGGAACGTGTATGATCAATCCCTAC 4782
Qy 4733 AGCCTTAGTCTGGTTCATGATGTCAGATTAATCAATCAATGGAATCGAGACTGCCGTG 4792
Db 4783 AGCCTTAGTCTGGTTCATGATGTCAGATTAATCAATCAATGGAATCGAGACTGCCGTG 4842
Qy 4793 GCGAAGGGGTGGCCTCGAGAGCAGGCTCTGAGACTCTTGATGTTTAAAGTGGGTGG 4852
Db 4843 GCGAAGGGGTGGCCTCGAGAGCAGGCTCTGAGACTCTTGATGTTTAAAGTGGGTGG 4902
Qy 4853 TGGCTGG 4859
Db 4903 TGGCTGG 4909

RESULT 15
US-10-648-593-115
; Sequence 115, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 115
; LENGTH: 4790
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-648-593-115

Query Match 78.2%; Score 4262; DB 18; Length 4790;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4782; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 355 GAAAGAGACATTCATTGGAAGGGCTTGTGCTGAAAATGGGTTTAATCTCTCTTTGGCCAG 414
Db 1 GAAAGAGACATTCATTGGAAGGGCTTGTGCTGAAAATGGGTTTAATCTCTCTTTGGCCAG 60
Qy 415 TCACCAACGAGCTGAGCTCATACATTTTAATGTAATGAGATGAGTGGCTGAGCCTTTGAGCAG 474
Db 61 TCACCAACGAGCTGAGCTCATACATTTTAATGTAATGAGATGAGTGGCTGAGCCTTTGAGCAG 120
Qy 475 ACCACATTAATCATCTGTGCAAAATTAAGAAGAGGTGGGAAAAGAGGACTTAATGTT 534
Db 121 ACCACATTAATCATCTGTGCAAAATTAAGAAGAGGTGGGAAAAGAGGACTTAATGTT 180
Qy 121 ACCACATTAATCATCTGTGCAAAATTAAGAAGAGGTGGGAAAAGAGGACTTAATGTT 180
Qy 535 GTCATGGCCCATGAGATGATGAACTCAATTTGTTACTGAGAGGTGGTGGCTCTGCTG 594
Db 181 GTCATGGCCCATGAGATGATGAACTCAATTTGTTACTGAGAGGTGGTGGCTCTGCTG 240
Qy 595 GAAAGTGAACGGAAGAAAGTGTGCTAATGTAATGATACCGGCCATTTGTGGAATACATCA 654
Db 241 GAAAGTGAACGGAAGAAAGTGTGCTAATGTAATGATACCGGCCATTTGTGGAATACATCA 300
Qy 655 TCCCAATTTTGAAGCCATTATATCAACTGCTCAAGCTTATGAAGGAGGTTGGCA 714
Db 301 TCCCAATTTTGAAGCCATTATATCAACTGCTCAAGCTTATGAAGGAGGTTGGCA 360
Qy 715 CAGAGCAAAAGTGTTAATTAACAGAGCTCATCCAGCATTCAGCGAAAACATTAAGTTGACATT 774

Db 361 CAGGCAAAAGTGTAAATTAACAGAGCTCAATCCAGACTTCAAGGCAAAACATTAAGTTGACATT 420
Qy 775 GATTGACATGCAAGAGTGTATGTTTAACATCAAACTCCCAAGAGTTGGCTCTCTCT 834
Db 421 GATTGACATGCAAGAGTGTATGTTTAACATCAAACTCCCAAGAGTTGGCTCTCTCTCT 480
Qy 835 TCAGACTGTTTCTCACTGTAATCTTGGGTAAACGTGAAGAGAGCTTCAACTCTGTAC 894
Db 481 TCAGACTGTTTCTCACTGTAATCTTGGGTAAACGTGAAGAGAGCTTCAACTCTGTAC 540
Qy 895 CTGCTTGACAGGTGGGTTTGTCTGAGTTCTCTGTTTCCCTGGCTCTGTGAAGAAAA 954
Db 541 CTGCTTGACAGGTGGGTTTGTCTGAGTTCTCTGTTTCCCTGGCTCTGTGAAGAAAA 600
Qy 955 TCCACTCAAGTCCCACTGCAATTTCTGACCTTGGCTTACCTGTTGCCAATTTGGGCA 1014
Db 601 TCCACTCAAGTCCCACTGCAATTTCTGACCTTGGCTTACCTGTTGCCAATTTGGGCA 660
Qy 1015 ACCGGAATTTCTTCCCAATCTTATCTTGGCTGCGAGAGATGTCCTCAACAGAGGCTG 1074
Db 661 ACCGGAATTTCTTCCCAATCTTATCTTGGCTGCGAGAGATGTCCTCAACAGAGGCTG 720
Qy 1075 ATACAGCAGAAATGGGATTTGTTATGTTAAATGCGACCTATACCTGTCAAAGCTGAC 1134
Db 721 ATACAGCAGAAATGGGATTTGTTATGTTAAATGCGACCAATACCTGTCAAAGCTGAC 780
Qy 1135 TTTATCCCGAGTCTCATTTCTGCTGCTGCTGCTGAATGACAGTTTGTGAAGAAATT 1194
Db 781 TTTATCCCGAGTCTCATTTCTGCTGCTGCTGCTGAATGACAGTTTGTGAAGAAATT 840
Qy 1195 TTGCGGTGTTGGAACAATCAATAGATTTCAATTGGAAGAAAAAGCTCCAAATGATGT 1254
Db 841 TTGCGGTGTTGGAACAATCAATAGATTTCAATTGGAAGAAAAAGCTCCAAATGATGT 900
Qy 1255 GTTCTAGTGAATGTTTATGCTGGAATCTCCGCTCCGACACATGCTATGCTTACATC 1314
Db 901 GTTCTAGTGAATGTTTATGCTGGAATCTCCGCTCCGACACATGCTATGCTTACATC 960
Qy 1315 ATGAAGAGATGACATGCTTTTATGATGAATGACATTTGTAAGAAAAAGAAAGACT 1374
Db 961 ATGAAGAGATGACATGCTTTTATGATGAATGACATTTGTAAGAAAAAGAAAGACT 1020
Qy 1375 ACTATATCTCCAACTTCAATTTTCTGGGCAACCTCGAATGAGAAAGATTAG 1434
Db 1021 ACTATATCTCCAACTTCAATTTTCTGGGCAACCTCGAATGAGAAAGATTAG 1080
Qy 1435 AACGAGCTGAGCATCAAGGCAAAAGAGCAAACTCAAGCTGTGCACTGAGAGCA 1494
Db 1081 AACGAGCTGAGCATCAAGGCAAAAGAGCAAACTCAAGCTGTGCACTGAGAGCA 1140
Qy 1495 AATGAACCTGTCCCTGCTGTCTCAGAGGTGAGCAAGAAAGAGAGAGCCCTCTAGTCA 1554
Db 1141 AATGAACCTGTCCCTGCTGTCTCAGAGGTGAGCAAGAAAGAGAGAGCCCTCTAGTCA 1200
Qy 1555 CCTGTGCGGACTGTGCTCACTCAAGGCAAGAGCAAAAGCCCGTCACTCCGCGACG 1614
Db 1201 CCTGTGCGGACTGTGCTCACTCAAGGCAAGAGCAAAAGCCCGTCACTCCGCGACG 1260
Qy 1615 GTGCGCAGCGTCCAGCGTCAAGCCGTGCTGTAGAGAGCAAGCCCGCTGTACAGCG 1674
Db 1261 GTGCGCAGCGTCCAGCGTCAAGCCGTGCTGTAGAGAGCAAGCCCGCTGTACAGCG 1320
Qy 1675 CTCAAGTGGGCTGCACTGTCCGAGACAGGCTGGAAGACAGCAATTAAGCTCAAGGCTTC 1734
Db 1321 CTCAAGTGGGCTGCACTGTCCGAGACAGGCTGGAAGACAGCAATTAAGCTCAAGGCTTC 1380
Qy 1735 TTTCTCTCGAATCAATCAAGTTTCAATTCAAGCAGACATGAGAGCATCTCTACATGAGC 1794
Db 1381 TTTCTCTCGAATCAATCAAGTTTCAATTCAAGCAGACATGAGAGCATCTCTACATGAGC 1440
Qy 1795 TTTCTCTCATGAGAGATGCTTTGGAATCAAAACCTTCACTTCTGATGGAGC 1854

Db 1441 TTTCTCTCATGAGAGATGCTTTGGAATCAAAACCTTCACTTCTGATGGAGC 1500
Qy 1855 AACAGATGATGCAAGTTCTCCCTGTTGAGGAATGATGAGAGAGACTCCGAACAGT 1914
Db 1501 AACAGATGATGCAAGTTCTCCCTGTTGAGGAATGATGAGAGAGACTCCGAACAGT 1560
Qy 1915 CCTGATTAAGAGAGAGCAGCATCCCAAGAGCTGACAGCCGACGCTTACAGAGC 1974
Db 1561 CCTGATTAAGAGAGAGCAGCATCCCAAGAGCTGACAGCCGACGCTTACAGAGC 1620
Qy 1975 CAGAGCAAGCATTTGATTCGCTGAGAACAGCAGAGTGGACCCGCAAGGCTCTT 2034
Db 1621 CAGAGCAAGCATTTGATTCGCTGAGAACAGCAGAGTGGACCCGCAAGGCTCTT 1680
Qy 2035 TTTATCTCACTGCAATGCAAGTGGAGGCTGAGAGCAATTCACACAGGCTCTTTC 2094
Db 1681 TTTATCTCACTGCAATGCAAGTGGAGGCTGAGAGCAATTCACACAGGCTCTTTC 1740
Qy 2095 GGCCCTTTCACACAGCAGACACACTCAAGAGTCTGCTGACCTTGAAGGCTG 2154
Db 1741 GGCCCTTTCACACAGCAGACACACTCAAGAGTCTGCTGACCTTGAAGGCTG 1800
Qy 2155 CACTCGAATATCTTGGCCCCCAGACCTTACCTTACCTTCCCTGACAGAGCTGTATTT 2214
Db 1801 CACTCGAATATCTTGGCCCCCAGACCTTACCTTACCTTCCCTGACAGAGCTGTATTT 1860
Qy 2215 GCGACAGATGCTCAACTTCTACCTGACGCAATCTTACGAGAGGAGGAGGCACTTAC 2274
Db 1861 GCGACAGATGCTCAACTTCTACCTGACGCAATCTTACGAGAGGAGGAGGCACTTAC 1920
Qy 2275 TCTGCTTACAGCTCAGCAGACCTCCCACTTGGAGAGCAAGCTTATCTGTGCGCAG 2334
Db 1921 TCTGCTTACAGCTCAGCAGACCTCCCACTTGGAGAGCAAGCTTATCTGTGCGCAG 1980
Qy 2335 CGGAGAGGCCAAGTGAAGAGTGAATCTCGGCGAGAGCTGGCATGAAGAGGCCCTTT 2394
Db 1981 CGGAGAGGCCAAGTGAAGAGTGAATCTCGGCGAGAGCTGGCATGAAGAGGCCCTTT 2040
Qy 2395 GAAGAAGCTTTAAACCGAGAGAGTCCCAATGGAATTTGAGAGAGCATGTCAGAG 2454
Db 2041 GAAGAAGCTTTAAACCGAGAGAGTCCCAATGGAATTTGAGAGAGCATGTCAGAG 2100
Qy 2455 AACAGTCAAGGAGAGAGCTGGGAAAGTGGGCACTGCTTATCTTCCGCGACAGT 2514
Db 2101 AACAGTCAAGGAGAGAGCTGGGAAAGTGGGCACTGCTTATCTTCCGCGACAGT 2160
Qy 2515 GAATCAATGAGTCTCTGAGAGAGAAAGCACTTGTGACTTATAGCAATTTT 2574
Db 2161 GAATCAATGAGTCTCTGAGAGAGAAAGCACTTGTGACTTATAGCAAA - TTTT 2219
Qy 2575 TTTCTTGTTCACAAAAAATTCCTGTGTAATCTGAAATTAATATGTAATATATATA 2634
Db 2220 TTTCTTGTTCACAAAAAATTCCTGTGTAATCTGAAATTAATATGTAATATATA 2279
Qy 2635 TTTTGGAAAAATGAGCTATGTTGTAAGAGCAAGGAGTCAACCCAGTTGTACTCT 2694
Db 2280 TTTTGGAAAAATGAGCTATGTTGTAAGAGCAAGGAGTCAACCCAGTTGTACTCT 2339
Qy 2695 CTTAACATCTGCAATTTGAGAGATCAGCTAATCTTCTCAACAAAAATGAGAGGCA 2754
Db 2340 CTTAACATCTGCAATTTGAGAGATCAGCTAATCTTCTCAACAAAAATGAGAGGCA 2399
Qy 2755 TGCTAAGATCCCTCTGAGAGAGAAACCAATTTATTCAGTGAATTAACATCTCTT 2814
Db 2400 TGCTAAGATCCCTCTGAGAGAGAAACCAATTTATTCAGTGAATTAACATCTCTT 2459
Qy 2815 GTTCTTAAAAAAGCAAGTCTTGTGTTGTTGAGAGCAAAATCCCTACATTTTCAAGT 2874
Db 2460 GTTCTTAAAAAAGCAAGTCTTGTGTTGTTGAGAGCAAAATCCCTACATTTTCAAGT 2519
Qy 2875 TGCTCTACTAAGAGATCTCAAAATTAATGATCTTTGTCCGAGCCCTTCATATGACCTTA 2934
Db 2520 TGCTCTACTAAGAGATCTCAAAATTAATGATCTTTGTCCGAGCCCTTCATATGACCTTA 2579

[illegible]

QY	4015	GTCACTGGAA	CAAGTATAGTGAATGG	CGTTTGAACATCCTCGCTGGAGTTT	4074
Db	3660	GTCACTGGAA	CAAGTATAGTGAATGG	CGTTTGAACATCCTCGCTGGAGTTT	3719
QY	4075	TCAAGCTA	CAATGTGGGTCTCTTTTGAAGCCTTAA	TTCAACAAGCAGACTTTTGGGGGT	4134
Db	3720	TCAAGCTA	CAAGTGTGGGTCTCTTTTGAAGCCTTAA	TTCAACAAGCAGACTTTTGGGGGT	3779
QY	4135	GGGGCTGGGG	CGGGTGTGTGCATTTGTTCTTTCCCTTCTGTAAAGTGCCTAAGTTGCTGCC	4194	
Db	3780	GGGGCTGGGG	CGGGTGTGTGCATTTGTTCTTTCCCTTCTGTAAAGTGCCTAAGTTGCTGCC	3839	
QY	4195	TGCTATCT	CAGGTTTTCTCTGTTTTTGAAGAAATGGA	CAGTTTTTTTGAACAAGATGTGAC	4254
Db	3840	TGCTATCT	CAGGTTTTTCTCTGTTTTTGAAGAAATGGA	CAGTTTTTTTGAACAAGATGTGAC	3889
QY	4255	TTTCAATGTTT	CTTATGTGTACTTTAAACACAGACAGAA	TATGATCTCAACACAGACC	4314
Db	3900	TTTCAATGTTT	CTTATGTGTACTTTAAACACAGACAGAA	TATGATCTCAACACAGACC	3959
QY	4315	GACTTGTTAT	GGGATGATGAGCGCGACACACCTCACTAGTTTGTGACAAATATATGTGC	4374	
Db	3960	GACTTGTTAT	GGGATGATGAGCGCGACACACCTCACTAGTTTGTGACAAATATATGTGC	4019	
QY	4375	TATGATGGGG	TGTAAAGTGAAGGACAGAGAGGTCA	CGCGATGTATATATCTGGGAA	4434
Db	4020	TATGATGGGG	TGTAAAGTGAAGGACAGAGAGGTCA	CGCGATGTATATATCTGGGAA	4079
QY	4435	AAGTGTGTGT	CAACGATTTGAATGTTTTTATGATATACATTTGAATCTTTATATCAACAT	4494	
Db	4080	AAGTGTGTGT	CAACGATTTGAATGTTTTTATGATATACATTTGAATCTTTATATCAACAT	4139	
QY	4495	TCTCAAGTTT	CACACAGTATGTTTGAATGTTATGTACACACACCAATAGTGTAA	CAGT	4554
Db	4140	TCTCAAGTTT	CACACAGTATGTTTGAATGTTATGTACACACACCAATAGTGTAA	CAGT	4199
QY	4555	TCACCACTT	CCAGAGTGTGTCATGCCCAAAACATGTTTAAAGAAAGAAAGCAGTAGCTC	4614	
Db	4200	TCACCACTT	CCAGAGTGTGTCATGCCCAAAACATGTTTAAAGAAAGAAAGCAGTAGCTC	4259	
QY	4615	CTTGTCTAAC	ATGTTTCAAGAGTTTGGGGGACCTGTGTTTATATGAGCTTCTGTCA	TTTA	4674
Db	4260	CTTGTCTAAC	ATGTTTCAAGAGTTTGGGGGACCTGTGTTTATATGAGCTTCTGTCA	TTTA	4319
QY	4675	GGGCTTCT	CTTGGCCATGATCCCTTCTCTTCTGGAACGTGATGTACATCTCA	CAG	4734
Db	4320	GGGCTTCT	CTTGGCCATGATCCCTTCTCTTCTGGAACGTGATGTACATCTCA	CAG	4379
QY	4735	CGTTAATGT	CGGTTCCTAGTGTCAATATATAGTTCTTTGGAATGGAACCTGCCGTGC	4794	
Db	4380	CGTTAATGT	CGGTTCCTAGTGTCAATATATAGTTCTTTGGAATGGAACCTGCCGTGC	4439	
QY	4795	GAAAGGGT	TGGCTTCGAGAGCAGGCTCTGGAGCGTCTGGAATGCTTTAGTGGGGTGGTG	4854	
Db	4440	GAAAGGGT	TGGCTTCGAGAGCAGGCTCTGGAGCGTCTGGAATGCTTTAGTGGGGTGGTG	4499	
QY	4855	GCTGGCTCT	TTCAAGCATGTAAATTTGGGGAAACCTTCGCGTCTACTAGGGGTGATACAGAT	4914	
Db	4500	GCTGGCTCT	TTCAAGCATGTAAATTTGGGGAAACCTTCGCGTCTACTAGGGGTGATACAGAT	4559	
QY	4915	GGTATATTTT	AAAGCAAACTAAGCTTCTATATGGAAGTGCCTGGAAATATGATTTAGGA	4974	
Db	4560	GGTATATTTT	AAAGCAAACTAAGCTTCTATATGGAAGTGCCTGGAAATATGATTTAGGA	4619	
QY	4975	CATGTGTAA	AGTTAGATGGAAGACTGTAAATGTTTAAATATGAAATATAGTGTCTTTTGA	5034	
Db	4620	CATGTGTAA	AGTTAGATGGAAGACTGTAAATGTTTAAATATGAAATATAGTGTCTTTTGA	4679	
QY	5035	AGTAAAGCC	CAGCGTGTGAACCGTTAACTGTGCATTTCTCATTTTGAATGTGTCAATGATG	5094	
Db	4680	AGTAAAGCC	CAGCGTGTGAACCGTGTAACTGTGCATTTCTCATTTTGAATGTGTCAATGATG	4739	
QY	5095	TTTATGTATGA	ATATGATTTAAATATCAAACTGATGCTCTGTTTATATCAT	5145	

Db 1392 CAATTTCTGGGCAACTCTGGACTATGAGAAATTAAGAACCAAGCTGAGATC 1451
QY 1452 AGGGCCAAAGAGCAATCTCAAGCTGCTGCACTGGAGAGCCAAATGAACCTGTCCCTGC 1511
Db 1452 AGGGCCAAAGAGCAATCTCAAGCTGCTGCACTGGAGAGCCAAATGAACCTGTCCCTGC 1511
QY 1512 TGTCTCAGAGGGTGGACAGAAAAAGCAGAGCCCTCAGTCCACCCCTGTGGCGAATCTGCG 1571
Db 1512 TGTCTCAGAGGGTGGACAGAAAAAGCAGAGCCCTCAGTCCACCCCTGTGGCGAATCTGCG 1571
QY 1572 TACCTCAGAGGGCAGCAGAGCAAAAGGCCGTGCAATCCCGCAGCGTCCAGCGCTGCCAG 1631
Db 1572 TACCTCAGAGGGCAGCAGAGCAAAAGGCCGTGCAATCCCGCAGCGTCCAGCGCTGCCAG 1631
QY 1632 CGTGCAGCCGTGCTGTGTAAGAGCAGCCCGCTGTGATCCCGCAGCGTCCAGCGCTGCCAG 1691
Db 1632 CGTGCAGCCGTGCTGTGTAAGAGCAGCCCGCTGTGATCCCGCAGCGTCCAGCGCTGCCAG 1691
QY 1692 GTCCGAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTTCCTTCTCTGGAATATCA 1751
Db 1692 GTCCGAGACAGGCTGGAAGACAGCAATAAGCTCAAGCGTTCCTTCTCTGGAATATCA 1751
QY 1752 ATCAGTTTCAATTCAGCCAGCATGGCAGCATCTTACATGGCTTCTCTCATCAGAGA 1811
Db 1752 ATCAGTTTCAATTCAGCCAGCATGGCAGCATCTTACATGGCTTCTCTCATCAGAGA 1811
QY 1812 TGTCTTGAATATCTACAAACCTTCCATCTGTAAGAGGACCAACAGCTATGCAATG 1871
Db 1812 TGTCTTGAATATCTACAAACCTTCCATCTGTAAGAGGACCAACAGCTATGCAATG 1871
QY 1872 CTCCTCTGTTGAGAACTATTCGAGAGCAGCTCCGAAACCAAGTCTGATTAAGAGAGAGC 1931
Db 1872 CTCCTCTGTTGAGAACTATTCGAGAGCAGCTCCGAAACCAAGTCTGATTAAGAGAGAGC 1931
QY 1932 CAGCATTCCTCCAGAAAGCTGCAACACCGCCAGGCTTCAAGACCCAGAGAGCCGATTGCA 1991
Db 1932 CAGCATTCCTCCAGAAAGCTGCAACACCGCCAGGCTTCAAGACCCAGAGAGCCGATTGCA 1991
QY 1992 TTCCGCTCAGAAACCAAGAGTGGACACCGCCAGAGAGTCCCTTTATCTCCACATGCAATG 2051
Db 1992 TTCCGCTCAGAAACCAAGAGTGGACACCGCCAGAGAGTCCCTTTATCTCCACATGCAATG 2051
QY 2052 AAGTGGAGCGTGGAGGACAAATTAACACACAGCTTCTTTTCGGCTTTTCACACAGCA 2111
Db 2052 AAGTGGAGCGTGGAGGACAAATTAACACACAGCTTCTTTTCGGCTTTTCACACAGCA 2111
QY 2112 GCAGCAGCTCAAGAGTCTGCGCTGGGCTTAAAGGCTGGCACTGGATATCTTGGC 2171
Db 2112 GCAGCAGCTCAAGAGTCTGCGCTGGGCTTAAAGGCTGGCACTGGATATCTTGGC 2171
QY 2172 CCCCCAGACCTTAACCCCTTCCCTGACCAAGCAGCTGGATTTTTCACAGAGTCTTCA 2231
Db 2172 CCCCCAGACCTTAACCCCTTCCCTGACCAAGCAGCTGGATTTTTCACAGAGTCTTCA 2231
QY 2232 CTTCTAATCTTCCCTCAGCATCTTAAGAGGAGTGGCAGTTACTCTGCTTACAGCTGAG 2291
Db 2232 CTTCTAATCTTCCCTCAGCATCTTAAGAGGAGTGGCAGTTACTCTGCTTACAGCTGAG 2291
QY 2292 CCAGCTGCCCACTGGCGAGACCAAGTCTATTCTGTGCGCAGAGGGGAGAGAACCAATGA 2351
Db 2292 CCAGCTGCCCACTGGCGAGACCAAGTCTATTCTGTGCGCAGAGGGGAGAGAACCAATGA 2351
QY 2352 CAGAGCTGACTCGCGGCGAGACTGGCATGAAGAGGCCCTTTGAAAGAGTTTAAACG 2411
Db 2352 CAGAGCTGACTCGCGGCGAGACTGGCATGAAGAGGCCCTTTGAAAGAGTTTAAACG 2411
QY 2412 CAGAGCTGCAAAATGAAATTTTGAAGAGCATATGTCAGAGAACCGTTCACGGGAGAG 2471
Db 2412 CAGAGCTGCAAAATGAAATTTTGAAGAGCATATGTCAGAGAACCGTTCACGGGAGAG 2471
QY 2472 GCTGGGAAAAGTGGGAGTCACTGCTTTTCGGGAGCATGAAATCATTAAGGCTC 2531
Db 2472 GCTGGGAAAAGTGGGAGTCACTGCTTTTCGGGAGCATGAAATCATTAAGGCTC 2531

Db 2472 GCTGGGAAAAGTGGGAGTCACTGCTTTTCGGGAGCATGAAATCATTAAGGCTC 2531
QY 2532 CTGAGAGAAAAGACATTTGATCTTATTAACAATTTTTTTCTGTTCACAAAAAA 2591
Db 2532 CTGAGAGAAAAGACATTTGATCTTATTAACA- TTTTTTTTCTGTTCACAAAAAA 2590
QY 2592 ATTCCTCTAATATCGAAAT 2651
Db 2591 ATTCCTCTAATATCGAAAT 2650
QY 2652 TATGATGTAAGAAAGCAACAGTGAATCAACCCAGTTGATCTCTTAACATCTGCAATTTG 2711
Db 2651 TATGATGTAAGAAAGCAACAGTGAATCAACCCAGTTGATCTCTTAACATCTGCAATTTG 2710
QY 2712 AGAGATCAGTAAATATCTTCTCAACAAAAATGGAAGGAGAGATGATGATCCCTCTA 2771
Db 2711 AGAGATCAGTAAATATCTTCTCAACAAAAATGGAAGGAGAGATGATGATCCCTCTA 2770
QY 2772 GACGAGGAAAACCATTTTATTCAGTGAATTAACATCTCTTGTCTTAAAAAGCAG 2831
Db 2771 GACGAGGAAAACCATTTTATTCAGTGAATTAACATCTCTTGTCTTAAAAAGCAG 2830
QY 2832 TGTCTTTGTGTTGAGAGCAAAATCCCTACCATTTTCAAGTTGCTTAAGAGATC 2891
Db 2831 TGTCTTTGTGTTGAGAGCAAAATCCCTACCATTTTCAAGTTGCTTAAGAGATC 2890
QY 2892 TCAAATTTATGCTTTTGTCCGACCTTCCATATGATACCTTAAGCGCTGAGACTAGCCA 2951
Db 2891 TCAAATTTATGCTTTTGTCCGACCTTCCATATGATACCTTAAGCGCTGAGACTAGCCA 2950
QY 2952 GCTTGGGGGTCAAGTATGAGACCTGTTAAGGACAGAGCTGATGTAATCCAGAGAG 3011
Db 2951 GCTTGGGGGTCAAGTATGAGACCTGTTAAGGACAGAGCTGATGTAATCCAGAGAG 3010
QY 3012 AATGATCTATCCAAAGCTGATTCACAAACCCAGCTCACTGACAGCCGAGGAGACGA 3071
Db 3011 AATGATCTATCCAAAGCTGATTCACAAACCCAGCTCACTGACAGCCGAGGAGACGA 3070
QY 3072 GCATCATCTGCTGAGAGCACTTAAAGGCGCTTGGCAAGGTATACCTTAAGAGCAACC 3131
Db 3071 GCATCATCTGCTGAGAGCACTTAAAGGCGCTTGGCAAGGTATACCTTAAGAGCAACC 3130
QY 3132 AGTACCTCAGACAGAAAGTCCGGGCTTTGACACATCAATCATCTGAGCCCATTTTC 3191
Db 3131 AGTACCTCAGACAGAAAGTCCGGGCTTTGACACATCAATCATCTGAGCCCATTTTC 3190
QY 3192 AGGCATTTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3251
Db 3191 AGGCATTTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3250
QY 3252 CACAAAATCCCGTGGGCTTAATGAGATGAGATATTTTTTTTCTCTCAGCTTTAAGAGA 3311
Db 3251 CACAAAATCCCGTGGGCTTAATGAGATGAGATATTTTTTTTCTCTCAGCTTTAAGAGA 3310
QY 3312 GAAAGGAAAATGCTAGATTCAGTGAACCAACAGAACTGGCAACATCAGATTTAA 3371
Db 3311 GAAAGGAAAATGCTAGATTCAGTGAACCAACAGAACTGGCAACATCAGATTTAA 3370
QY 3372 GCTAAGTTGGAGAGCTTAAAGTCTACCTCTCTTGTAAATCAAGAAATGTTTAA 3431
Db 3371 GCTAAGTTGGAGAGCTTAAAGTCTACCTCTCTTGTAAATCAAGAAATGTTTAA 3430
QY 3432 ATGGGATGTCATCTTTTAAATTAAGATGAACCTTGTTTCAAGCAATGGAATTTAT 3491
Db 3431 ATGGGATGTCATCTTTTAAATTAAGATGAACCTTGTTTCAAGCAATGGAATTTAT 3490
QY 3492 TTGGGTTGTAGCAGAGCAGCAGCCTTCAAAATCTGACCAAAAGCAGATGTTTTGCC 3551
Db 3491 TTGGGTTGTAGCAGAGCAGCAGCCTTCAAAATCTGACCAAAAGCAGATGTTTTGCC 3550
QY 3552 CTTTCTGCTTCACTGATGATATGATGATGATGATGATGATGATGATGATGATGATGAT 3611
Db 3551 CTTTCTGCTTCACTGATGATATGATGATGATGATGATGATGATGATGATGATGATGAT 3610

Dp	586	CCATACACTTTTAGTACAAATGGAGTGGCTGAGCCTTTGAGCACACCAATTAATCAATC	645
Qy	492	GTGCGAAATTAAAGAGAGGTGGGAAAAGAGACTTATTTGTTCTATGGCCCATGAGAT	551
Dp	646	GTGGCAAAATTAAAGAGAGGTGGGAAAAGAGACTTATTTGTTCTATGGCCCATGAGAT	705
Qy	552	GATTGAACTCAAAATTGTTACTGAGAGGTGGTGGCTGCTGCGTGGAAAGTGGAAACGGAAA	611
Dp	706	GATTGAACTCAAAATTGTTACTGAGAGGTGGTGGCTGCTGCGTGGAAAGTGGAAACGGAAA	765
Qy	612	AGTCGCTGAAATTGATATAGCCGGCCATTTGTGGAAATACATACATCCACATTTTGGAAAGC	671
Dp	766	AGTCGCTGAAATTGATATAGCCGGCCATTTGTGGAAATACATACATCCACATTTTGGAAAGC	825
Qy	672	CATTAAATATCAACTGCTCCAAAGCTTATAGGGAAGTTGCAACAGACAAAGTGTAAAT	731
Dp	826	CATTAAATATCAACTGCTCCAAAGCTTATAGGGAAGTTGCAACAGACAAAGTGTAAAT	885
Qy	732	TACAGAGCTCAATCCAGACTTACAGGGAACATTAAGGTTGACATTAATGATGAGTCAAGAGT	791
Dp	886	TACAGAGCTCAATCCAGACTTACAGGGAACATTAAGGTTGACATTAATGATGAGTCAAGAGT	945
Qy	792	TGTAATTTACAGTCAAAAGCTCCAAAGATGTTGGCCTCTCTCTTACAGACTGTTTCTCAC	851
Dp	946	TGTAATTTACAGTCAAAAGCTCCAAAGATGTTGGCCTCTCTCTTACAGACTGTTTCTCAC	1000
Qy	852	TGTACTCTGGGTAACCTGAGAGAGAGCTTCAACTCTGTCACTGCTTGCAGGTGGGTT	911
Dp	1006	TGTACTCTGGGTAACCTGAGAGAGAGCTTCAACTCTGTCACTGCTTGCAGGTGGGTT	1066
Qy	912	TGCTGAGTTCTCTGCTGTTTTCCTGGGCTCTGTGAAGAAAATCCACTCTATGTCCTTAC	971
Dp	1066	TGCTGAGTTCTCTGCTGTTTTCCTGGGCTCTGTGAAGAAAATCCACTCTATGTCCTTAC	1122
Qy	972	CTGCAATTTCTCAGCCTTGCTTAACCTGTTGCCCAACTTGGGCAACCCGAATTTCTTCCCA	1033
Dp	1126	CTGCAATTTCTCAGCCTTGCTTAACCTGTTGCCCAACTTGGGCAACCCGAATTTCTTCCCA	1188
Qy	1032	TCTTATCTTGAGCTGCGACGAGATGTCTCAACAAGAGCTGATACAGCAAGATGGAT	1093
Dp	1186	TCTTATCTTGAGCTGCGACGAGATGTCTCAACAAGAGCTGATACAGCAAGATGGAT	1244
Qy	1092	TGGTATATGTGTTAAATGCGACGATATACCTGTGCCAAAGCTGTATATCCCGAGTCTCA	1155
Dp	1246	TGGTATATGTGTTAAATGCGACGATATACCTGTGCCAAAGCTGTATATCCCGAGTCTCA	1308
Qy	1152	TTTCCGCGTGGTGGCTGTGAATGACAGCTTTTGTGAAGAAAATTTGGCCGTGTGGACAA	1213
Dp	1306	TTTCCGCGTGGTGGCTGTGAATGACAGCTTTTGTGAAGAAAATTTGGCCGTGTGGACAA	1366
Qy	1212	ATCAGTATATTTCAATTTAGAGAAAGCAAAAGCCTCAATGATGATGTGTTCTTAGTGCATCTGTT	1272
Dp	1366	ATCAGTATATTTCAATTTAGAGAAAGCAAAAGCCTCAATGATGATGTGTTCTTAGTGCATCTGTT	1422
Qy	1272	AGCTGGAGTCTCCGCTCCGCCACCAATCGTATGCTATCATCATGAAGAGATGACAT	1333
Dp	1426	AGCTGGAGTCTCCGCTCCGCCACCAATCGTATGCTATCATCATGAAGAGATGACAT	1488
Qy	1332	GTCCTTATATGAAGCTTACAGATTTGTGAAGAAAAGAAAGCCTACTATATCTCCAAACTT	1399
Dp	1486	GTCCTTATATGAAGCTTACAGATTTGTGAAGAAAAGAAAGCCTACTATATCTCCAAACTT	1544
Qy	1392	CAATTTTCTGGGCAACTCTCGGACTATAGAGAAAGATTAAGAACCAAGCTGAGACATC	1455
Dp	1546	CAATTTTCTGGGCAACTCTCGGACTATAGAGAAAGATTAAGAACCAAGCTGAGACATC	1600
Qy	1452	AGGGCCAAAGAGCAAACTCAAGCTGCTGACCTGGAAGAGCCAAATGAACCTGCTCCGTC	1511
Dp	1606	AGGGCCAAAGAGCAAACTCAAGCTGCTGACCTGGAAGAGCCAAATGAACCTGCTCCGTC	1665
Qy	1512	TGCTCAAGAGGTGAGCAAGAAACCGAGAACCCCTCATGCTCAACCCTGTGCGCAATCTGCG	1577
Dp	1666	TGCTCAAGAGGTGAGCAAGAAACCGAGAACCCCTCATGCTCAACCCTGTGCGCAATCTGCG	1722

QY 1572 TACCTCAGAGGACAGAGCAAAAGGCCGTCATCCCGCAGGCGCCAGCGGTGCCAG 1631
| | | | |
Db 1726 TACTCAGAGGACAGAGCAAAAGGCCGTCATCCCGCAGGCGCCAGCGGTGCCAG 1785
| | | | |
QY 1632 CGTGCAGCGGTGCTGTTAGAGGACAGCGCCGCTGTATCAGAGCGCTCATGTGGCTGCACCT 1691
| | | | |
Db 1786 CGTGCAGCGGTGCTGTTAGAGGACAGCGCCGCTGTATCAGAGCGCTCATGTGGCTGCACCT 1845
| | | | |
QY 1692 GTCGAGACAGGCTGGAGAGACAGCAATATGCTCAAGCGCTCTTCTCTGTGATATCA 1751
| | | | |
Db 1846 GTCGAGACAGGCTGGAGAGACAGCAATATGCTCAAGCGCTCTTCTCTGTGATATCA 1905
| | | | |
QY 1752 ATCAGTTTCAATTTACGCCAGCAGATGCGATCTTACATGCTTCTCTCATCAGAGA 1811
| | | | |
Db 1906 ATCAGTTTCAATTTACGCCAGCAGATGCGATCTTACATGCTTCTCTCATCAGAGA 1965
| | | | |
QY 1812 TGTCTTGGAAATTAATAAACTTTCCATCTCTGATGTGGACCAACAGCTATGCCAGTT 1871
| | | | |
Db 1966 TGTCTTGGAAATTAATAAACTTTCCATCTCTGATGTGGACCAACAGCTATGCCAGTT 2025
| | | | |
QY 1872 CTCCTCTGTTACGAACTATCGGAGGAGCTCCCGAAACAGTCTCTGATATGAGAGAAC 1931
| | | | |
Db 2026 CTCCTCTGTTACGAACTATCGGAGGAGCTCCCGAAACAGTCTCTGATATGAGAGAAC 2085
| | | | |
QY 1932 CAGCATCCCAAGAGCTGACAGCCGCTTACAGACAGCCAGAGCAAGCATTTGCA 1991
| | | | |
Db 2086 CAGCATCCCAAGAGCTGACAGCCGCTTACAGACAGCCAGAGCAAGCATTTGCA 2145
| | | | |
QY 1992 TTCCGTCAGAACACAGAGAGAGTGCACCGCCAGAGGTCTCTTTATCTCCACTGCATCG 2051
| | | | |
Db 2146 TTCCGTCAGAACACAGAGAGAGTGCACCGCCAGAGGTCTCTTTATCTCCACTGCATCG 2205
| | | | |
QY 2052 AAGTGGAGCGCTGAGAGCAATTAACAACAGCTTCTTTGCGGCTTTCCACGAGCA 2111
| | | | |
Db 2206 AAGTGGAGCGCTGAGAGCAATTAACAACAGCTTCTTTGCGGCTTTCCACGAGCA 2265
| | | | |
QY 2112 GAGACACTCAGCAAGTCTGCTGCGCTTGAAGGCTGCGCATCGATATCTTGGC 2171
| | | | |
Db 2266 GAGACACTCAGCAAGTCTGCTGCGCTTGAAGGCTGCGCATCGATATCTTGGC 2325
| | | | |
QY 2172 CCCCAGACCTTACCCCTTCCCTGACAGCAGCTGTGATTTTGGCAGAGTCTTCA 2231
| | | | |
Db 2326 CCCCAGACCTTACCCCTTCCCTGACAGCAGCTGTGATTTTGGCAGAGTCTTCA 2385
| | | | |
QY 2232 CTCTACTCTGCTCAGCATCTACGAGGAGTCCAGTTACTCTGCTTCAAGCTGAG 2291
| | | | |
Db 2386 CTCTACTCTGCTCAGCATCTACGAGGAGTCCAGTTACTCTGCTTCAAGCTGAG 2445
| | | | |
QY 2292 CCAAGTCCCACTTGGCGAGACCAAGTCTATTTCTGTGCGCAGCGCGAGAACCAAGTGA 2351
| | | | |
Db 2446 CCAAGTCCCACTTGGCGAGACCAAGTCTATTTCTGTGCGCAGCGCGAGAACCAAGTGA 2505
| | | | |
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Db 2506 CAGAGCTGACTCGCGCGAGCTGGCATGAGAGAGCCCTTTGAAAAGAGTTTAAAG 2565
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QY 2412 CAGAACTGCCAAATGGAATTTGAGAGAGCATCATGTCAAGAGAACAGTCAACGAGAGA 2471
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QY 2472 GCTGGGGAAAGATTGGGCACTCATGCTTTTGGGCGAGCATGGAATCATTTAGGTCTC 2531
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QY 2832 TGTCTTGGTGTGAGAGACAAATCCCTACATTTTTCAGTTGCTGTGCTCTAGAGATC 2891
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Db 2985 TGTCTTGGTGTGAGAGACAAATCCCTACATTTTTCAGTTGCTGTGCTCTAGAGATC 3044
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QY 3252 CACAAAATTCGGTGGGCTGATGATGAGATATTTTTTTCTTCTCAGCTTTATGAGA 3311
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Db 3585 ATGGATTTGTCAATCTTTTAAATTAAGATGAATCTTGTTTC 3625
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RESULT 18
US-09-964-277-1
? Sequence 1, Application US/09964277
? Patent No. US20020137170A1
? GENERAL INFORMATION:
? APPLICANT: Lucbe, Ralf M.
? APPLICANT: Wei, Bo
? TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
? FILE REFERENCE: 200125.434
? CURRENT APPLICATION NUMBER: US/09/964,277
? NUMBER OF SEQ ID NOS: 22
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 1
? LENGTH: 3496
? TYPE: DNA

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QY 2172 CCCCCAGACTCTAATCCCTTCCCTGACAGAGCTGTGATTTTGGCCACAGAGTCTTACA 2231
DB 2196 CCCCCAGACTCTAATCCCTTCCCTGACAGAGCTGTGATTTTGGCCACAGAGTCTTACA 2255
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DB 2256 CTTTACTCTGCTCAGCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2315
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DB 2376 CAGAGCTGACTCGCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2435
QY 2412 CAGAGCTGCAATGGAATTTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2471
DB 2436 CAGAGCTGCAATGGAATTTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2495
QY 2472 GCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2531
DB 2496 GCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2555
QY 2532 CTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2591
DB 2556 CTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2614
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DB 2615 ATTCCCTGTAATCTGAAT 2674
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DB 2795 GACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2854
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DB 2855 TGTCTTGT 2914
QY 2891 CTCAAAAT 2950
DB 2915 CTCAAAAT 2974
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DB 3095 AGCATCACTCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3154
QY 3131 CAGTACCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3190
DB 3155 CAGTACCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3214

QY 3191 TAGCATTTGTGAATAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 3250
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DB 3455 AATGGATTGTCAATCTTTTAAATTAAGATGAAGATTGGTTTC 3496

RESULT 19
US-09-816-494-1
; Sequence 1, Application US/09816494
; Patent No. US20020034807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; FILE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-03002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589) ... (2583)
US-09-816-494-1

Query Match 56.5%; Score 3079; DB 9; Length 3544;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3299; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 173 GCTTTCAGTCCAGGTGAAGCTGTGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 232
DB 224 GCTTTCAGTCCAGGTGAAGCTGTGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 283
QY 233 CGGTGCTCTCCAAAGCATCTTTGT 292
DB 284 CGGTGCTCTCCAAAGCATCTTTGT 343
QY 293 ATCAATGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 352
DB 344 ATCAATGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 403
QY 353 GAGAAAGAGCATTTCACTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 412
DB 404 GAGAAAGAGCATTTCACTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 463
QY 413 AGTCAACCAAGCTGAGCTCTATCACTTTTGAATGAATGAATGAATGAATGAATGAATGAATGA 472
DB 464 AGTCAACCAAGCTGAGCTCTATCACTTTTGAATGAATGAATGAATGAATGAATGAATGAATGA 523
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Qy 713 AACAGCAAAAGTGTAAATTAACAGAGCTCATCCAGCATTCAGCCGAAACATAAGTTGACA 772
Db 764 AACAGCAAAAGTGTAAATTAACAGAGCTCATCCAGCATTCAGCCGAAACATAAGTTGACA 823
Qy 773 TTGATTCAGATCAGAGGTTGATGTTTACATCAAAAGCTCCGAAAGTTGGCTCTCTCT 832
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Qy 1373 CTACTATATCTTCAAACTTCAATTTTCTGGGCCAACTCTGACATGAGAAAGAAATTA 1432
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Qy 1433 AGAAGCAGATGAGAGATCAGGGCCAAAGAGCAAACTCAAGCTGTGACCTGAGAGAGC 1492
Db 1484 AGAAGCAGATGAGAGATCAGGGCCAAAGAGCAAACTCAAGCTGTGACCTGAGAGAGC 1543
Qy 1493 CAATGAACTGCTGCTGCTCTCAGAGGGTGAACAGAAAAGGAGAGAGCCCTCAGTC 1552
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Db 1724 CGCTCATGCGGCTCACACTGCTCCGACAGAGGCTGGAAAGACAAATTAAGCTCAAGCTT 1783
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Qy	3353	TGGCAACATCAGATTTAAAGCTTAGTGGAGGCTTACGAGTCTACCTCTTTTGA	3412
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Qy	3413	AATCAAGAATGTTTAAATGGGATGTGCAATCCTTTAAATGAAGTGAACCTTGTTTC	3472
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Db	3523	AA 3524	

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; CURRENT APPLICATION NUMBER: US/10/377,072
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895,860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/843,297
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; PRIOR FILING DATE: 2001-03-22
; Remaining Prior Application data removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589) ... (2586)
; US-10-377-072-25

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Query Match	56.5%	Score 3079;	DB 17;	Length 3544;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 3299; Conservative	0;	Mismatches 2;	Indels 1;	Gaps 1;

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QY	233	CGCTGCTGCTCCAAAGCATCTTTTGTGTGGAATGTAATCCAGATCATCTTTATGA	29
Db	284	CGCTGCTGCTCCAAAGCATCTTTTGTGTGGAATGTAATTCAGATCATCTTTATGA	34
QY	293	ATCAAAATGTAAGGGGCTGCTTTGTGAGACGAGTCCCTTTGCAAGACACATCAACGGGAAA	35
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QY	353	GAGAAAGACATTCATCTTGAGAGGCTCTGCTGAAAAATGGTTTAACTCTCTTTGGC	41
Db	404	GAGAAAGACATTCATCTTGAGAGGCTCTGCTGAAAAATGGTTTAACTCTCTTTGGC	46
QY	413	AGTCACACACAGCTTGAACCTCAATACCTTTTAGTCAATGAGATGCTGAGCCTTTGAGC	47
Db	464	AGTCACACACAGCTTGAACCTCAATACCTTTTAGTCAATGAGATGCTGAGCCTTTGAGC	52
QY	473	ACACACACATTCATCATCTGTGGCAAAATTAAGAAGAGAGTGGGAAAAAGAGACTTATG	53
Db	524	ACACACACATTCATCATCTGTGGCAAAATTAAGAAGAGAGTGGGAAAAAGAGACTTATG	58
QY	533	TTGTCAATGGCCATGAGATGATTTGGAACCTCAATTTGTTACTGAGAGTTGGTGGCTTGC	59
Db	584	TTGTCAATGGCCATGAGATGATTTGGAACCTCAATTTGTTACTGAGAGTTGGTGGCTTGC	64
QY	593	TGGAAGTGGAAACGGAAAAAGTGCCTAATTTGATGACCGGCCCATTTGTGGAAATACATA	65
Db	644	TGGAAGTGGAAACGGAAAAAGTGCCTAATTTGATGACCGGCCCATTTGTGGAAATACATA	70
QY	653	CATCCCACTTTTGGAAAGCATTATATCACTGCTCCAAAGCTTATGAGAGGAAGTTGC	71
Db	704	CATCCCACTTTTGGAAAGCATTATATCACTGCTCCAAAGCTTATGAGAGGAAGTTGC	76

QY	713	AACAGAGCAAAAGTGTAAATTA	CAGAGCTCATCCAGATTA	CACGAGAAACAATAAGTTGACA	772
Db	764	AACAGAGCAAAAGTGTAAATTA	CAGAGCTCATCCAGATTA	CACGAGAAACAATAAGTTGACA	823
QY	773	TTGATTGCAGTCAGAAAGGTT	GTAGTTTACGATCAAAAGCTCC	GAAAGTGTGCCTCTCTCT	832
Db	824	TTGATTGCAGTCAGAAAGGTT	GTAGTTTACGATCAAAAGCTCC	GAAAGTGTGCCTCTCTCT	883
QY	833	CTTCAGACTGTTTTCTCACTG	TAACTTCTGGGTTAACTGGAA	GAAGCTTCAACTCTGTTC	892
Db	884	CTTCAGACTGTTTTCTCACTG	TAACTTCTGGGTTAACTGGAA	GAAGCTTCAACTCTGTTC	943
QY	893	ACCTGCTTGACAGTGGGTTG	CTGAGTTCTCGTGTGTTTCC	CTGGCCCTCTGTGAAGAA	952
Db	944	ACCTGCTTGACAGTGGGTTG	CTGAGTTCTCGTGTGTTTCC	CTGGCCCTCTGTGAAGAA	1001
QY	953	AATCCACTCTAGTCCCTTAC	CTGCAATTTCTCAGCCTTGCT	TACTGTGTGCAACATTGGGC	1011
Db	1004	AATCCACTCTAGTCCCTTAC	CTGCAATTTCTCAGCCTTGCT	TACTGTGTGCAACATTGGGC	1061
QY	1013	CAACCCGAATCTTCCCAATCT	TTAATCTTGAGTCAGGAGAA	TGTCCTCAACAAGAGAC	1077
Db	1064	CAACCCGAATCTTCCCAATCT	TTAATCTTGAGTCAGGAGAA	TGTCCTCAACAAGAGAC	1122
QY	1073	TGATACAGCAGAAATGGGAT	TTGGTTATGTGTAAATGCCAG	CTATACCTGTCCAAAGCCTG	1133
Db	1124	TGATACAGCAGAAATGGGAT	TTGGTTATGTGTAAATGCCAG	CTATACCTGTCCAAAGCCTG	1188
QY	1133	ACTTATATCCCGAGCTCAT	TATTTCCCTGCTGTGCTGTGA	TACAGCTTTTGTGAGAAA	1197
Db	1184	ACTTATATCCCGAGCTCAT	TATTTCCCTGCTGTGCTGTGA	TACAGCTTTTGTGAGAAA	1243
QY	1193	TTTGGCCGTGGTTGAGCAAA	TACAGTAGATTTCAATGAGAA	ACAAAGCCCTCAATGAT	1251
Db	1244	TTTGGCCGTGGTTGAGCAAA	TACAGTAGATTTCAATGAGAA	ACAAAGCCCTCAATGAT	1301
QY	1253	GTGTTCTTAGTGACACTGTT	TAGCTGGGATCTCCGCTCGGC	CAATCGTATGCGCTTACA	1311
Db	1304	GTGTTCTTAGTGACACTGTT	TAGCTGGGATCTCCGCTCGGC	CAATCGTATGCGCTTACA	1361
QY	1313	TCATGAAAGAGATGGACAN	TGTCTTAAGATGAAGCTTACA	GATTTGTGAAAGAAAAGAC	1377
Db	1364	TCATGAAAGAGATGGACAN	TGTCTTAAGATGAAGCTTACA	GATTTGTGAAAGAAAAGAC	1422
QY	1373	CTACTATATCTCCAAACTT	CAATTTTCTGGGCCCAACTCC	CTGGACTATGAGAAAGATT	1433
Db	1424	CTACTATATCTCCAAACTT	CAATTTTCTGGGCCCAACTCC	CTGGACTATGAGAAAGATT	1483
QY	1433	AGAACACAGACTGGAGACT	CAAGGGCCAAAGACAACTCA	AGCTGCTGCACTTGAAGAGC	1497
Db	1484	AGAACACAGACTGGAGACT	CAAGGGCCAAAGACAACTCA	AGCTGCTGCACTTGAAGAGC	1544
QY	1493	CAAAATGAACCTGTCCCTG	CTGTGCTCAGAGGGTGGACA	GAGAAAAGCGACGCCCTCAGTC	1551
Db	1544	CAAAATGAACCTGTCCCTG	CTGTGCTCAGAGGGTGGACA	GAGAAAAGCGACGCCCTCAGTC	1601
QY	1553	CACCTGTGCGCACTCTGCT	ACTCAGAGGACAGACGACAA	AGAGCCCGCTGCACTCCGCCA	1612
Db	1604	CACCTGTGCGCACTCTGCT	ACTCAGAGGACAGACGACAA	AGAGCCCGCTGCACTCCGCCA	1663
QY	1613	GCGTGGCCAGAGGTGGCCAG	CGCGGACCGCTGTGTAGAGGA	CAGCCCGCTGGTTACAGG	1677
Db	1664	GCGTGGCCAGAGGTGGCCAG	CGCGGACCGCTGTGTAGAGGA	CAGCCCGCTGGTTACAGG	1722
QY	1673	CGCTCAGTGGGCTGCACTGT	TCGCGACAGAGCTGGAAGACA	GACATATAGACTCAAGCGTT	1733
Db	1724	CGCTCAGTGGGCTGCACTGT	TCGCGACAGAGCTGGAAGACA	GACATATAGACTCAAGCGTT	1783
QY	1733	CGTTCTCTCTGGATATCAAT	ATCAAGTTTCAATTTACAGCC	AGCATGGCAGATCTCTTAACATG	1797
Db	1784	CGTTCTCTCTGGATATCAAT	ATCAAGTTTCAATTTACAGCC	AGCATGGCAGATCTCTTAACATG	1843

QY	1793	GCTTCTCTCAATCAGAAAGATGCTTTGGAAATCTCAAAACCTTCCACTACTCTGGATGGGA	1852
Db	1844	GCTTCTCTCAATCAGAAAGATGCTTTGGAAATCTCAAAACCTTCCACTACTCTGGATGGGA	1903
QY	1853	CCAAACAAGCTATGCGAGTCTCCCTGTTCAGAACTATCGSAGCAGACTCCGAAACCA	1912
Db	1904	CCAAACAAGCTATGCGAGTCTCCCTGTTCAGAACTATCGSAGCAGACTCCGAAACCA	1963
QY	1913	GTCTGTATTAAGAGAGAAAGCCAGCATCCCCAAAGAGCTGCAGACCGCCAGCTTCAAGCA	1972
Db	1964	GTCTGTATTAAGAGAGAAAGCCAGCATCCCCAAAGAGCTGCAGACCGCCAGCTTCAAGCA	2023
QY	1973	GCCAGACGAAGCGATTCGATTCGGTTCAGAAACCGACACAGTGGGACCGCCAGAGGTCCC	2032
Db	2024	GCCAGACGAAGCGATTCGATTCGGTTCAGAAACCGACACAGTGGGACCGCCAGAGGTCCC	2083
QY	2033	TTTATATCTCCACTCATTCGAAGTGGAGCGTGGAGAGCAATTACACACAGCTTCTCTT	2092
Db	2084	TTTATATCTCCACTCATTCGAAGTGGAGCGTGGAGAGCAATTACACACAGCTTCTCTT	2143
QY	2093	TCGGACCTTTCCACGAGCCAGACGACCTCAAGAAGTCTGCGCTGGCCCTTAAGGGCT	2152
Db	2144	TCGGACCTTTCCACGAGCCAGACGACCTCAAGAAGTCTGCGCTGGCCCTTAAGGGCT	2203
QY	2153	GGCACCTGGGATATCTTTGGCCCCCAGACCTCTACACCTTCCCTGACACGACGCTGTAT	2212
Db	2204	GGCACCTGGGATATCTTTGGCCCCCAGACCTCTACACCTTCCCTGACACGACGCTGTAT	2263
QY	2213	TTTGCACAGAGTCTCTCACTTCTACCTGTGCTCAGCATCTTACGAGAGGCGATGSCAGTT	2272
Db	2264	TTTGCACAGAGTCTCTCACTTCTACCTGTGCTCAGCATCTTACGAGAGGCGATGSCAGTT	2323
QY	2273	ACTCTGCTCACAGCTGCAGCCAGCTGCCCACTTGCAGAGACCAAGTCTATCTGTGCGCA	2332
Db	2324	ACTCTGCTCACAGCTGCAGCCAGCTGCCCACTTGCAGAGACCAAGTCTATCTGTGCGCA	2383
QY	2333	GGCGGCGAAGGCCCAAGTGAAGAAGCTACTCTGCGCGGAGAGTGGCATGMAAGAGCCCC	2392
Db	2384	GGCGGCGAAGGCCCAAGTGAAGAAGCTACTCTGCGCGGAGAGTGGCATGMAAGAGCCCC	2443
QY	2393	TTGAAAAGCATTTTAAACGACGAAGCTGCCAAATGSAATTGGAGAGAGCATCATGTCAG	2452
Db	2444	TTGAAAAGCATTTTAAACGACGAAGCTGCCAAATGSAATTGGAGAGAGCATCATGTCAG	2503
QY	2453	AGAACAGGTCAACGGAAGAGCTGCGGGAAGTGGCACTCAGTCTTTCGGGCGACA	2512
Db	2504	AGAACAGGTCAACGGAAGAGCTGCGGGAAGTGGCACTCAGTCTTTCGGGCGACA	2563
QY	2513	TGGAATCATTTAGAGTCTCTGAGAGAAAGACACTTGTGACTTCTATPAGCAATTTTTT	2572
Db	2564	TGGAATCATTTAGAGTCTCTGAGAGAAAGACACTTGTGACTTCTATPAGCAAA-TTTTT	2622
QY	2573	TTTTTCTGTTCACAAAAAATTCCTCTGTAAATCTGAAATATATATATATGTACATPACATTA	2632
Db	2623	TTTTTCTGTTCACAAAAAATTCCTCTGTAAATCTGAAATATATATATATGTACATPACATTA	2682
QY	2633	TATTTTGGAAAAATGAGACTATGGTGTGTAAGCAACAGGTGATCAACCAAGTGTACT	2692
Db	2683	TATTTTGGAAAAATGAGACTATGGTGTGTAAGCAACAGGTGATCAACCAAGTGTACT	2742
QY	2693	CTCTTAAACATCTGCATTTGAGAGATCAGCTATATCTTCTCAACAAAAATGGAAGGCA	2752
Db	2743	CTCTTAAACATCTGCATTTGAGAGATCAGCTATATCTTCTCAACAAAAATGGAAGGCA	2802
QY	2753	GATGCTAGAAATCCCCCTTACACGGAAGAAAACCTTTATATTCAGTGAATTACACATCTCTC	2812
Db	2803	GATGCTAGAAATCCCCCTTACACGGAAGAAAACCTTTATATTCAGTGAATTACACATCTCTC	2862
QY	2813	TTGTCTTAAAAAAGCAAGTGTCTTTGGTGTGGAAGACAAAATCCCTACCAATTTTCAC	2872
Db	2863	TTGTCTTAAAAAAGCAAGTGTCTTTGGTGTGGAAGACAAAATCCCTACCAATTTTCAC	2922
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Db 2923 GTTGTGCTACTAAGAGATCTCAATATTTAGCTTTTGTCCGAGACCTTCCATAGTACACCT 2982
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Db 2983 TAGCGCTGAGACTGAGCAGCTTGGGGGTGAGGTAGGTATGACCTTTTGGGACAGAGCC 3042
Qy 2993 TAGGTGTAATCCAGAGAAATGATCTATCCAAAGCTGATTCAGAAACCAAGCTCAGC 3052
Db 3043 TAGGTGTAATCCAGAGAAATGATCTATCCAAAGCTGATTCAGAAACCAAGCTCAGC 3102
Qy 3053 TGACAGCCGAGGAGACAGAGCACTCTGCTGTGAGACCATTTAGGGGCTTGGCCAGG 3112
Db 3103 TGACAGCCGAGGAGACAGAGCACTCTGCTGTGAGACCATTTAGGGGCTTGGCCAGG 3162
Qy 3113 TCTACCTTAGAGCAAAACCAAGTACTCAGACAGAGAAAGTCGGGGCTTTGACACATACAT 3172
Db 3163 TCTACCTTAGAGCAAAACCAAGTACTCAGACAGAGAAAGTCGGGGCTTTGACACATACAT 3222
Qy 3173 ATCTGGTAGCCATTTTCTAGAGCATTTGTGAATAGTAGTAGTCACTTTCAGAG 3232
Db 3223 ATCTGGTAGCCATTTTCTAGAGCATTTGTGAATAGTAGTAGTCACTTTCAGAG 3282
Qy 3233 CCAATTCAACTGTCTATGACAGAAATTTCCCGTGGGCTTGAATGAGATATTTTTCCT 3292
Db 3283 CCAATTCAACTGTCTATGACAGAAATTTCCCGTGGGCTTGAATGAGATATTTTTCCT 3342
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Db 3343 CTCTCAGCTTTATGAGAGAGAGGAACTGTCTAGAGATTCAGTGAACCAACAGAGAAC 3402
Qy 3353 TGGCAACATCAGATTTTAAAGCTTAAAGTGGAGGCTTAAAGAGTCTACCTCCCTTTTGA 3412
Db 3403 TGGCAACATCAGATTTTAAAGCTTAAAGTGGAGGCTTAAAGAGTCTACCTCCCTTTTGA 3462
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Qy 3473 AA 3474
Db 3523 AA 3524

RESULT 21
US-10-377-072-25
; Sequence 25, Application US/10377072
; Publication No. US20040157221A9
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Miyoung
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; FILE REFERENCE: MP103-0180NMIM
; CURRENT APPLICATION NUMBER: US/10/377,072
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895,860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/843,297

; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; PRIOR FILING DATE: 2001-03-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)...(2586)
US-10-377-072-25

Query Match 56.5%; Score 3079; DB 18; Length 3544;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3299; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 173 GCTTTCAGTCCAGTGTAAAGCTGTGGAGCGCGAGCAAAAGTAAAGATGTAAATG 232
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Db 464 AGTCAACACAGCGCTGACCTCATACCTTTTATGATCAATGAGTGGCTGAGCCTTTGAGC 523
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Qy 533 TTGTCAATGCCATGAGATGATGAACTCAATTTGTTCTGAGAGTGGCTGCTGCG 592
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Qy 713 AACAGGACAAAGTAAATTAACAGAGCTATCCACATTCAGCCGAAACATTAAGTTGCA 772
Db 764 AACAGGACAAAGTAAATTAACAGAGCTATCCACATTCAGCCGAAACATTAAGTTGCA 823
Qy 773 TTGATTCAGTCAAGAGTTGATTTAGATCAATCAAGCTCCCAAGATTTGCTCTCTCT 832
Db 824 TTGATTCAGTCAAGAGTTGATTTAGATCAATCAAGCTCCCAAGATTTGCTCTCTCT 883
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Db 884 CTTCACTGTTTCTCACTGTACTTCTGGGTAACTGGAGAAAGCTTCAACTCTGTTTC 943
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Db 1544 CAATGAACTGTCCCTGCTGTCTCAGAGGGTGGACAGAAAAGCGAGAGCCCTCAGTC 1603
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Qy 1853 CCAACAGCTATGACGATTTCCCTGTTCAAGAACTATCGAGAGAGATCCCGAAACCA 1912
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Qy 1913 GTCTGTATAGAGAGAGCCAGCATCCCAAGAGCTGCAAGCCGACAGGCTTTCAGCA 1972
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Qy 1973 GCACAGACAGATGTCATTCGGTCAAGAACAGACAGATGGACCCGCGCAAGAGTCC 2032
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QY 3473 AA 3474
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Db 3523 AA 3524
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RESULT 22
; US-10-370-715B-261
; Sequence 261, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 261
; LENGTH: 3521
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-370-715B-261
Query Match 56.3%; Score 3069; DB 18; Length 3521;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3459; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

Db 158 CGTTTCCCTCTGAGGAAATTGGAGCTGCGGCCCCCAAAAGCTTTCACTGAGTGTAA 217
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|
QY 192 GCTGTGAGGCGCGGAGCAAAAGTAAAGAAATGATGTAATGCGTGTGCTCCAAAGCA 251
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|
|
Db 218 GCTGTGAGGCGCGGAGCAAAAGTAAAGAAATGATGTAATGCACTGCGTGTCCAAAGCA 277
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|
QY 252 TCTTTTGTGGAATGTTTATTCAGATCACTCTTTATATGAATCAAAATGAGGGGCTGC 311
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|
|
Db 278 TCTTTTGTGGAATGTTTATTCAGATCACTCTTTATATGAATCAAAATGAGGGGCTGC 337
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|
|
QY 312 TTTTGAACGAGATCTTTGCAAGACATCAACGGGAAAGAAAGAGACATTCCTACTT 371
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|
|
Db 338 TTTTGAACGAGATCTTTGCAAGACATCAACGGGAAAGAAAGAGACATTCCTACTT 397
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|
QY 372 GAGGGGCTTGTGCTGAAAATGGTTTAACTCTCTTTTGCAGTACCAACAGCTGACC 431
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Db 398 GAGGGGCTTGTGCTGAAAATGGTTTAACTCTCTTTTGCAGTACCAACAGCTGACC 457
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|
QY 432 TCATACACTTTTATGATGAATGGAGTGGCTGAGGCTTTGAGCACCAACCATTAATCATC 491
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|
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Db 458 TCATACACTTTTATGATGAATGGAGTGGCTGAGGCTTTGAGCACCAACCATTAATCATC 517
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QY 492 GTGGCAATTTAAAGAGAGGTGGGAAAGAGACATTAATGTTGTCAATGAGCCCATGAGAT 551
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|
|
Db 518 GTGGCAATTTAAAGAGAGGTGGGAAAGAGACATTAATGTTGTCAATGAGCCCATGAGAT 577
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|
QY 552 GATTGGAATCTCAATTTGTACTAGAGAGTTGTGTGCTCTGCTGAAAATGAGAAACGAAAA 611
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|
|
Db 578 GATTGGAATCTCAATTTGTACTAGAGAGTTGTGTGCTCTGCTGAAAATGAGAAACGAAAA 637
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|
|
QY 612 AGTGTCTAATGATGATGAGCGGCAATTTGTGAATCAATATCATCCCATTTTGGAGC 671
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|
Db 638 AGTGTCTAATGATGATGAGCGGCAATTTGTGAATCAATATCATCCCATTTTGGAGC 697
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|
QY 672 CATTAATATCACTGCTCCAAAGCTTATGAAGAGAGGTGCAACAGACAAAGTGTAAAT 731
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|
|
Db 698 CATTAATATCACTGCTCCAAAGCTTATGAAGAGAGGTGCAACAGACAAAGTGTAAAT 757
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|
|
QY 732 TACAGAGCTCATCAGATTCAGCGAAACATAAGTTGATGATTTGACAGTCAGAGAT 791
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|
Db 758 TACAGAGCTCATCAGATTCAGCGAAACATAAGTTGATGATTTGACAGTCAGAGAT 817
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|
QY 792 TGTAGTTTACATCAAAAGCTCCCAAGATGTGCTCTCTCTTCAAGCTGTTTCTCAC 851
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|
|
Db 818 TGTAGTTTACATCAAAAGCTCCCAAGATGTGCTCTCTCTTCAAGCTGTTTCTCAC 877
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QY 852 TGTACTTCTGGGTAAACTGGAAGAGCTTCAACTGTTCACCTGTTCAGAGTGGGTT 911
|
|
|
Db 878 TGTACTTCTGGGTAAACTGGAAGAGCTTCAACTGTTCACCTGTTCAGAGTGGGTT 937
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|
QY 912 TGTGAGTCTCTCGTTGTTTCCCTGCGCTCTGTGAAGGAAATCCACTGTAGTCCCTAC 971
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|
|
Db 938 TGTGAGTCTCTCGTTGTTTCCCTGCGCTCTGTGAAGGAAATCCACTGTAGTCCCTAC 997
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|
QY 972 CTGCAATTTCAAGCTTGTCTTACCTGTTCACCAATTTGGGCCAACCCGAATTTCCCA 1031
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|
Db 998 CTGCAATTTCAAGCTTGTCTTACCTGTTCACCAATTTGGGCCAACCCGAATTTCCCA 1057
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|
QY 1032 TCTTTATCTTGGCTGCGACGAGATGTCTCAACAAAGAGCTGATACAGCAGATGGGAT 1091
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Db 1058 TCTTTATCTTGGCTGCGACGAGATGTCTCAACAAAGAGCTGATACAGCAGATGGGAT 1117
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QY 1092 TGGTTATGTGTTAAATGACAGCTATACGTGTCAAAAGCTGACTTATCCCGAGATCTCA 1151
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|
|
Db 1118 TGGTTATGTGTTAAATGACAGCTATACGTGTCAAAAGCTGACTTATCCCGAGATCTCA 1177
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|
QY 1152 TTTCTGCGTGTGCTGTGATATGACAGCTTTTGTGAAGAAATTTTGCCTGTGTGACAA 1211
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|
|
Db 1178 TTTCTGCGTGTGCTGTGATATGACAGCTTTTGTGAAGAAATTTTGCCTGTGTGACAA 1237
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|
QY 1212 ATCAGTAGATTCATTTGAGAAAGCAAAAGCTCCGAATGATGTCTTATGAGCACTGTTT 1271
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|
|
Db 1238 ATCAGTAGATTCATTTGAGAAAGCAAAAGCTCCGAATGATGTCTTATGAGCACTGTTT 1297
|
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|

Db 3457 AATGGATGTGCAATCCTTTAAATAAGATGAACCTTGTTCAA 3500

RESULT 23

US-10-257-026-1
; Sequence 1, Application US/10257026
; Publication No. US20040086859A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: New dual specificity phosphatase
; FILE REFERENCE: DUSP10KDM5
; CURRENT APPLICATION NUMBER: US/10/257,026
; CURRENT FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3059
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (127)..(2121)
US-10-257-026-1

Query Match 52.1%; Score 2837; DB 17; Length 3059;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3057; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 412 CAGTACCCACCGCCGACCTCATACCTTTAATGATGAGATGAGCCCTTTGAG 471
Db 1 CAGTACCCACCGCCGACCTCATACCTTTAATGATGAGATGAGCCCTTTGAG 60
QY 472 CACACCCACCATTAATCATCTGTGCAAAATTAAGAAAGAGTGGGAAAAAGAGACTTAAT 531
Db 61 CACACCCACCATTAATCATCTGTGCAAAATTAAGAAAGAGTGGGAAAAAGAGACTTAAT 120
QY 532 GTTGTTCATGCGCCATGAGATGATTTGGAATCAATCAATTTGTTACTGAGAGGTTGTGCTCTG 591
Db 121 GTTGTTCATGCGCCATGAGATGATTTGGAATCAATCAATTTGTTACTGAGAGGTTGTGCTCTG 180
QY 592 CTGGAAGTGAAGGAAAGGAAAGTGTGCTTAATGATGAGCCGCTTTGTTGAAATACAT 651
Db 181 CTGGAAGTGAAGGAAAGGAAAGTGTGCTTAATGATGAGCCGCTTTGTTGAAATACAT 240
QY 652 ACATCCCAATTTTGAAGCCATTAATATCACTGCTCCAACTTATGAGCGAAGTTG 711
Db 241 ACATCCCAATTTTGAAGCCATTAATATCACTGCTCCAACTTATGAGCGAAGTTG 300
QY 712 CAAAGGACAAAGTGTAAATTAAGAGCTCATCCAGATTGAGCGAAACATPAAGTTGAC 771
Db 301 CAAAGGACAAAGTGTAAATTAAGAGCTCATCCAGATTGAGCGAAACATPAAGTTGAC 360
QY 772 ATTGATTCAGTCAAGAGGTTGATGTTAAGATCAAAAGCTCCAAAGANTGGCTCTCTC 831
Db 361 ATTGATTCAGTCAAGAGGTTGATGTTAAGATCAAAAGCTCCAAAGANTGGCTCTCTC 420
QY 832 TCTTCAAGCTGTTTCTCACTGTAATCTTGAGTAACTGAGAAAGCTTCAACTCTGTT 891
Db 421 TCTTCAAGCTGTTTCTCACTGTAATCTTGAGTAACTGAGAAAGCTTCAACTCTGTT 480
QY 892 CACCTGCTGAGAGTGGTGTGCTGAGATGTTCTGCTGTTTCCCTGGCTCTGTGAAGGA 951
Db 481 CACCTGCTGAGAGTGGTGTGCTGAGATGTTCTGCTGTTTCCCTGGCTCTGTGAAGGA 540
QY 952 AAATCACTCTAGTCCCTACCTGCAATTTCTCAGGCTTGCTTACCTGTTGCAACATTTGG 1011
Db 541 AAATCACTCTAGTCCCTACCTGCAATTTCTCAGGCTTGCTTACCTGTTGCAACATTTGG 600
QY 1012 CCAACCCGAATTTTCCCAATCTTTATCTTGAGTCCAGCGAGATGTCTCAACAGAG 1071
Db 601 CCAACCCGAATTTTCCCAATCTTTATCTTGAGTCCAGCGAGATGTCTCAACAGAG 660

QY 1072 CTGATACAGCAAGATGGGATTTGTTAATGTTAAATGCGACATACCTGTCCAAAGCCT 1131
Db 661 CTGATACAGCAAGATGGGATTTGTTAATGTTAAATGCGACATACCTGTCCAAAGCCT 720
QY 1132 GACTTTATCCCGAGTCTCATTTTCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1191
Db 721 GACTTTATCCCGAGTCTCATTTTCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 1192 ATTTTGGCGTGTGAGCAAAATCAAGTATGATTTCAATGAAAGCAAAAGCCTCAATGGA 1251
Db 781 ATTTTGGCGTGTGAGCAAAATCAAGTATGATTTCAATGAAAGCAAAAGCCTCAATGGA 840
QY 1252 TGTGTTCTAGTCACTGTTTGTAGCTGGGATCCCGCTCCGCAACATCCGATGCGCTAC 1311
Db 841 TGTGTTCTAGTCACTGTTTGTAGCTGGGATCCCGCTCCGCAACATCCGATGCGCTAC 900
QY 1312 ATCATGAAGAGATGACATGCTTTAGATGATGATGATGATGATGATGATGATGATGATGAT 1371
Db 901 ATCATGAAGAGATGACATGCTTTAGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 1372 CCTACTATATCTCCAACTTCAATTTTCTGGGCCAATCTCTGCACTATGAGAGAGATT 1431
Db 961 CCTACTATATCTCCAACTTCAATTTTCTGGGCCAATCTCTGCACTATGAGAGAGATT 1020
QY 1432 AAGAACCAGACTGAGGATGAGGAGGCAAGAGCAAACTCAAGCTGTGCACTGAGAGAG 1491
Db 1021 AAGAACCAGACTGAGGATGAGGAGGCAAGAGCAAACTCAAGCTGTGCACTGAGAGAG 1080
QY 1492 CCAATGAACCTGTCCCTGCTGTCTCAGAGAGGTGAGCAAGAAAGCGAGAGCGCCCTCAGT 1551
Db 1081 CCAATGAACCTGTCCCTGCTGTCTCAGAGAGGTGAGCAAGAAAGCGAGAGCGCCCTCAGT 1140
QY 1552 CCACCTGTGCGCACTGCTGTACCTGAGAGAGGAGAGCAAGAAAGCGCCCTGCACTCCCGC 1611
Db 1141 CCACCTGTGCGCACTGCTGTACCTGAGAGAGGAGAGCAAGAAAGCGCCCTGCACTCCCGC 1200
QY 1612 AGCGTGCCAGCGTGCCAGCGTGCAAGCGTCCCTGTTAGAGAGAGCGCGCTGATACAG 1671
Db 1201 AGCGTGCCAGCGTGCCAGCGTGCAAGCGTCCCTGTTAGAGAGAGCGCGCTGATACAG 1260
QY 1672 GCGCTCAGTGGGCTGCACTGTCCGAGACAGGCTGGAAGACAGCAATPAAGCTCAAGCGT 1731
Db 1261 GCGCTCAGTGGGCTGCACTGTCCGAGACAGGCTGGAAGACAGCAATPAAGCTCAAGCGT 1320
QY 1732 TCCCTGCTGGAATTCAAATGATTTGATTTTCCAGAGAGTGGACATCTTCAAT 1791
Db 1321 TCCCTGCTGGAATTCAAATGATTTGATTTTCCAGAGAGTGGACATCTTCAAT 1380
QY 1792 GCGTTCCTCATCAGAAAGTGTGGAATACTAACAACCTTCCACTCTGATGAGG 1851
Db 1381 GCGTTCCTCATCAGAAAGTGTGGAATACTAACAACCTTCCACTCTGATGAGG 1440
QY 1852 ACCAACAAGTATGCGAGTTCCTCCCTGTTCAAGAACTATGAGAGACCTCCGAAC 1911
Db 1441 ACCAACAAGTATGCGAGTTCCTCCCTGTTCAAGAACTATGAGAGACCTCCGAAC 1500
QY 1912 AGTCTGATTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1971
Db 1501 AGTCTGATTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560
QY 1972 AGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2031
Db 1561 AGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1620
QY 2032 CTTTATCTCCACTGATGAGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2091
Db 1621 CTTTATCTCCACTGATGAGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1680
QY 2092 TTGCGCTTTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2151
Db 1681 TTGCGCTTTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1740
QY 2152 TGGCACTGGGATATCTTGCGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2211

Db 1741 TGGCACTGGAGATATCTTGGCCCCCGAGACTCTACCCCTTCCCTACCGCAGCGCTGGTAT 1800
Qy 2212 TTGGCAGAGATCCCTACACTTCTACTGCTCAGACCATCTAGAGGAGCGAGT 2271
Db 1801 TTGGCAGAGATCCCTACACTTCTACTGCTCAGACCATCTAGAGGAGCGAGT 1860
Qy 2272 TACTGCTCAGCTCAGCGAGCGAGTCCCACTTCCGAGACCAAGTCAATCTGCGGC 2331
Db 1861 TACTGCTCAGCTCAGCGAGCGAGTCCCACTTCCGAGACCAAGTCAATCTGCGGC 1920
Qy 2332 AGCGCGCAGAGCCCAAGTGCAGAGCTGACTGCGCGAGAGTGCATGAGAGAGCCCC 2391
Db 1921 AGCGCGCAGAGCCCAAGTGCAGAGCTGACTGCGCGAGAGTGCATGAGAGAGCCCC 1980
Qy 2392 TTTGAAAAGCATTTAAACGAGAGCTGCCAAATGGAATTTGGAGAGAGCATCTATGCA 2451
Db 1981 TTTGAAAAGCATTTAAACGAGAGCTGCCAAATGGAATTTGGAGAGAGCATCTATGCA 2040
Qy 2452 GAGAACAGATCAGCGGAGAGAGCTGGGAGAAAGTGGCAGTCAAGTCTTCTGCGCAGC 2511
Db 2041 GAGAACAGATCAGCGGAGAGAGCTGGGAGAAAGTGGCAGTCAAGTCTTCTGCGCAGC 2100
Qy 2512 ATGGAATCATTTAGAGTCTCTGAGAGAGAGACATTTGTCATTTAGACAAATTTT 2571
Db 2101 ATGGAATCATTTAGAGTCTCTGAGAGAGAGACATTTGTCATTTAGACAAATTTT 2159
Qy 2572 TTTTCTGCTCAGAAAAAATCCCTGTAATCTGAAATATATATATATATATATATAT 2631
Db 2160 TTTTCTGCTCAGAAAAAATCCCTGTAATCTGAAATATATATATATATATATATAT 2219
Qy 2632 ATATTTTGGAAAAATGAGAGCTAGTGTATGTAAGCAACAGTGCATCAACCCAGTTGTAC 2691
Db 2220 ATATTTTGGAAAAATGAGAGCTAGTGTATGTAAGCAACAGTGCATCAACCCAGTTGTAC 2279
Qy 2692 TCTCTTAAATCTGCTGATTTGAGAGTCACTAATCTTCTCAACAAATTTGAGAGGC 2751
Db 2280 TCTCTTAAATCTGCTGATTTGAGAGTCACTAATCTTCTCAACAAATTTGAGAGGC 2339
Qy 2752 AGATGCTGAATCCCTCTTAAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2811
Db 2340 AGATGCTGAATCCCTCTTAAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2399
Qy 2812 CTGTTCTTAAAGAGAGAGTCTTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2871
Db 2400 CTGTTCTTAAAGAGAGAGTCTTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2459
Qy 2872 CGTGTGCTACTAAGAGATCTCAATATATATCTTGTCCGAGCCCTTCAATAGTACAC 2931
Db 2460 CGTGTGCTACTAAGAGATCTCAATATATATCTTGTCCGAGCCCTTCAATAGTACAC 2519
Qy 2932 TTAGAGCTGAGACCTGAGCGAGCTGGGGGTCAAGTATGACCTGTTAGGAGAGAGC 2991
Db 2520 TTAGAGCTGAGACCTGAGCGAGCTGGGGGTCAAGTATGACCTGTTAGGAGAGAGC 2579
Qy 2992 CTAGTGTGAATCCAGAGAGAGATGATCTATCCAAAGCTGATTCACAAACCCAGCTAC 3051
Db 2580 CTAGTGTGAATCCAGAGAGAGATGATCTATCCAAAGCTGATTCACAAACCCAGCTAC 2639
Qy 3052 CTGACAGCGAGAGAGACAGAGATCACTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 3111
Db 2640 CTGACAGCGAGAGAGACAGAGATCACTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 2699
Qy 3112 GTCTACTTAAAGCAATCCAGTATCTCAGACAGAGAGAGAGAGAGAGAGAGAGAG 3171
Db 2700 GTCTACTTAAAGCAATCCAGTATCTCAGACAGAGAGAGAGAGAGAGAGAGAGAG 2759
Qy 3172 TATCTGTAGAGCCATTTCTAGGAGATGTAATAGTATGATGATGATGATGATGATGAT 3231
Db 2760 TATCTGTAGAGCCATTTCTAGGAGATGTAATAGTATGATGATGATGATGATGATGAT 2819
Qy 3232 ACAAATTCAACTGTCTATGACAAATTTCCGTGGGCTAGATGAGATATTTTTTTT 3291

Db 2820 ACAAATTCAACTGTCTATGACAAATTTCCGTGGGCTAGATGAGATATTTTTTTT 2879
Qy 3292 TCTTCTGAGCTTTTAAAG 3351
Db 2880 TCTTCTGAGCTTTTAAAG 2939
Qy 3352 CTGGCAATCATCAGATTTTAACTAAGTGGAGGCTAAGAGATCTACCTCCCTTTGT 3411
Db 2940 CTGGCAATCATCAGATTTTAACTAAGTGGAGGCTAAGAGATCTACCTCCCTTTGT 2999
Qy 3412 AATATCAAGAGATTTTAAATGGATTTGATCTCTTAAATTAAGATGAATTTGTTT 3471
Db 3000 AATATCAAGAGATTTTAAATGGATTTGATCTCTTAAATTAAGATGAATTTGTTT 3059

RESULT 24
US-10-296-115-520
; Sequence 520, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hysag Inc
; TITLE OF INVENTION: NO. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 520
; LENGTH: 2966
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2966)
; OTHER INFORMATION: n = a,t,c or g
US-10-296-115-520

Query Match 48.1%; Score 2624; DB 17; Length 2966;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2844; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 582 GGTGGCTCTGCTGGAAGAGTGAACGAGAAAGTGTGTAATGATATACCGGCAATTTGT 641
Db 67 GTGGCTCTGCTGGAAGAGTGAACGAGAAAGTGTGTAATGATATACCGGCAATTTGT 126
Qy 642 GGAATACAT 701
Db 127 GGAATACAT 186
Qy 702 GCGAAGTTGCAAGAGCAAAAGTGTATATATATATATATATATATATATATATATAT 761
Db 187 GCGAAGTTGCAAGAGCAAAAGTGTATATATATATATATATATATATATATATATAT 246
Qy 762 TAAAGTGAAT 821
Db 247 TAAAGTGAAT 306
Qy 822 TGGCTCTCTCTCAGAGCTGTTTCTCACTGATCTTGGGTAACTGAGAGAGAGCTT 881
Db 307 TGGCTCTCTCTCAGAGCTGTTTCTCACTGATCTTGGGTAACTGAGAGAGAGCTT 366
Qy 882 CAATCTGTTCACTGCTTGGAGAGTGGTGTGCTAGATCTCTGTTTCCCTGGGCT 941
Db 367 CAATCTGTTCACTGCTTGGAGAGTGGTGTGCTAGATCTCTGTTTCCCTGGGCT 426
Qy 942 CTGTGAAG 1001
Db 427 CTGTGAAG 486
Qy 1002 CAACATTTGGGCAACCGGAATTTTCCCAATCTTATCTTGGCTGACAGAGATGTCT 1061

Db 487 CAACATTGGGCAACCCGGAATTCCTCCAAFCCTTATCTTGCGTGCAGGAGATGTCCT 546
Qy 1062 CAACAAGAGCTGTATACAGCAAGATGGGATTTGGTTATGTGTAAATGCCAGTAACTGG 1121
Db 547 CAACAAGAGCTGTATACAGCAAGATGGGATTTGGTTATGTGTAAATGCCAGCAATACCTG 606
Qy 1122 TCCAAAGCTGACCTTTATCCCGAGTCTCATTTTCGCGGTGTCGTGAAATGACGCTT 1181
Db 607 TCCAAAGCTGACCTTTATCCCGAGTCTCATTTTCGCGGTGTCGTGAAATGACGCTT 666
Qy 1182 TTGTGAGAAAATTTTGGCCGTGGTTGGAACAATCAGTAGATTTTCATTGAGAAAGCAAAAGC 1241
Db 667 TTGTGAGAAAATTTTGGCCGTGGTTGGAACAATCAGTAGATTTTCATTGAGAAAGCAAAAGC 726
Qy 1242 CTCGAATGAGTGTGTTCTAGTGACATGTTTAAAGTGGGATCTCCCGTCCGCCACCATGCG 1301
Db 727 CTCGAATGAGTGTGTTCTAGTGACATGTTTAAAGTGGGATCTCCCGTCCGCCACCATGCG 786
Qy 1302 TATGCGCTACATCATGATGAGATGAGACATGCTTTAGATGAACTTACAGATTTGTGAA 1361
Db 787 TATGCGCTACATCATGATGAGATGAGACATGCTTTAGATGAACTTACAGATTTGTGAA 846
Qy 1362 AGAAAAAAGACCTACTATATCTTCAAACCTTCAATTTTGGGCGCAACTCTGGACTATGA 1421
Db 847 AGAAAAAAGACCTACTATATCTTCAAACCTTCAATTTTGGGCGCAACTCTGGACTATGA 906
Qy 1422 GAAGAAGATTAAGAACAGACCTGAGACATCAGGGCCCAAGAGCAAACTCAACTCTGGA 1481
Db 907 GAAGAAGATTAAGAACAGACCTGAGACATCAGGGCCCAAGAGCAAACTCAACTCTGGA 966
Qy 1482 CCTGGAAGAACCAATGAACTGTCTCTGCTGTCTCAAGAGGTGACAGAAAAGGAGAC 1541
Db 967 CCTGGAAGAACCAATGAACTGTCTCTGCTGTCTCAAGAGGTGACAGAAAAGGAGAC 1026
Qy 1542 GCGCCCTCAGTCCACCTGTGCGGACCTCTGCTCAAGAGGTGACAGAAAAGGAGAC 1601
Db 1027 GCGCCCTCAGTCCACCTGTGCGGACCTCTGCTCAAGAGGTGACAGAAAAGGAGAC 1086
Qy 1602 GCATCCCGCAGACGTCGCCAGGCTGCCAGCGTGCAGCGCTGTTAGAGAACAGGCC 1661
Db 1087 GCATCCCGCAGACGTCGCCAGGCTGCCAGCGTGCAGCGCTGTTAGAGAACAGGCC 1146
Qy 1662 GCTGGTACAGGCGCTCAAGTGGGCTGACCTGTCCGACAGACAGGCTGAAAGACAGCATTA 1721
Db 1147 GCTGGTACAGGCGCTCAAGTGGGCTGACCTGTCCGACAGACAGGCTGAAAGACAGCATTA 1266
Qy 1722 GCTCAAGGCTCTCTCTCTGGAATGAAATCAGTTTCATTTACAGCAGCATGGCAGC 1781
Db 1207 GCTCAAGGCTCTCTCTCTGGAATGAAATCAGTTTCATTTACAGCAGCATGGCAGC 1266
Qy 1782 ATCTTACATGAGCTTCTCTCATCAGAAATGCTTTGGAATATCAAACTTCCACTAC 1841
Db 1267 ATCTTACATGAGCTTCTCTCATCAGAAATGCTTTGGAATATCAAACTTCCACTAC 1326
Qy 1842 TCTGATAGGACCAACAAGCTATGCGAGTTCTCCCTGTTCAAGAACTATGAGACAGAC 1901
Db 1327 TCTGATAGGACCAACAAGCTATGCGAGTTCTCCCTGTTCAAGAACTATGAGACAGAC 1386
Qy 1902 TCCGGAACCAAGTCTGTATAGAGAGAGAGACAGCATCCCAAGAGCTGCAAGCCGCAAG 1961
Db 1387 TCCGGAACCAAGTCTGTATAGAGAGAGAGAGACAGCATCCCAAGAGCTGCAAGCCGCAAG 1446
Qy 1962 GCCTTACAGCAGCAGCAAGCAAGATTTGCTATGCGTCAAGACAGCAGCAGTGGCAGCG 2021
Db 1447 GCCTTACAGCAGCAGCAGCAAGCAAGATTTGCTATGCGTCAAGACAGCAGCAGTGGCAGCG 1506
Qy 2022 CCAAGAGTCCCTTTTATCTCACTGCAATCAAGTGGAGAGGCTGGAGACAATTAACAAC 2081
Db 1507 CCAAGAGTCCCTTTTATCTCACTGCAATCAAGTGGAGAGGCTGGAGACAATTAACAAC 1566
Qy 2082 CAGCTTCTTTTGGGCTTTTCAACAGCAGCAGCAGCAGTCAAGAAATGCTGGCCGCGG 2141
Db 1567 CAGCTTCTTTTGGGCTTTTCAACAGCAGCAGCAGCAGTCAAGAAATGCTGGCCGCGG 1626
Qy 2142 CCTTAAAGGCTGGCACTCGATATCTTTGGCCCCCAGACCTTACCCCTTCCCTGACAG 2201
Db 1627 CCTTAAAGGCTGGCACTCGATATCTTTGGCCCCCAGACCTTACCCCTTCCCTGACAG 1686
Qy 2202 CAGCTGATATTTTGGCAAGAGTCTCTCACTTTACTCTGCTGAGCATTAACGAGG 2261
Db 1687 CAGCTGATATTTTGGCAAGAGTCTCTCACTTTACTCTGCTGAGCATTAACGAGG 1746
Qy 2262 CAGTCCAGTTACTCTGCTCAGCTGAGCAGCTGCGCCACTTGGCGGAGCAAGTCTA 2321
Db 1747 CAGTCCAGTTACTCTGCTCAGCTGAGCAGCTGCGCCACTTGGCGGAGCAAGTCTA 1806
Qy 2322 TTCTGTGCGCAGGCGGCAAGGCCAAGTGAAGAGCTGAAGCTGCGGCGGAGCTGAGTGA 2381
Db 1807 TTCTGTGCGCAGGCGGCAAGGCCAAGTGAAGAGCTGAAGCTGCGGCGGAGCTGAGTGA 1866
Qy 2382 AGAGAGCCCTTTTAAAGCAGTTTAAACGAGAGCTGCAATGGAATTTGAGAGAG 2441
Db 1867 AGAGAGCCCTTTTAAAGCAGTTTAAACGAGAGCTGCAATGGAATTTGAGAGAG 1926
Qy 2442 CATCATGTCAAGAGACAGTCAAGGAGAGCTGGGGAAGAGTGGGCACTGAGCTTACCTT 2501
Db 1927 CATCATGTCAAGAGACAGTCAAGGAGAGCTGGGGAAGAGTGGGCACTGAGCTTACCTT 1986
Qy 2502 TTGCGGCAAGTGAATCATTTGAGTCTCTGAGAAAGAACACTTGTGACTTCTATA 2561
Db 1987 TTGCGGCAAGTGAATCATTTGAGTCTCTGAGAAAGAACACTTGTGACTTCTATA 2046
Qy 2562 GACATTTTTTTTTTCTGTTTCAAAAAAATCCCTGTAAATCTGAAATATATATATGT 2621
Db 2047 GACAA-TTTTTTTTTCTGTTTCAAAAAAATCCCTGTAAATCTGAAATATATATATGT 2105
Qy 2622 ACATACATATATATTTTTTGGAAAAATGAGCTATGATGTAAGCAACAGGTGATCAAC 2681
Db 2106 ACATACATATATATTTTTTGGAAAAATGAGCTATGATGTAAGCAACAGGTGATCAAC 2165
Qy 2682 CAGTTTACTCTCTTAAACATCTGCAATTTGAGAGATCAGTAACTCTTCTCAAAAA 2741
Db 2166 CAGTTTACTCTCTTAAACATCTGCAATTTGAGAGATCAGTAACTCTTCTCAAAAA 2225
Qy 2742 ATGGAAGGAGATGCTAAGATCCCCCTTGAAGAGAGAAACATTTTATCAGTAAT 2801
Db 2226 ATGGAAGGAGATGCTAAGATCCCCCTTGAAGAGAGAAACATTTTATCAGTAAT 2285
Qy 2802 TACATCTCTCTTGTCTTAAAAAGCAAGTCTTGTGTGTGAGAACAAATCCCT 2861
Db 2286 TACATCTCTCTTGTCTTAAAAAGCAAGTCTTGTGTGTGAGAACAAATCCCT 2345
Qy 2862 ACCATTTTACAGTTGCTATAGAGATCTGAAATATAGCTTTGTCGGAACCTTCC 2921
Db 2346 ACCATTTTACAGTTGCTATAGAGATCTGAAATATAGCTTTGTCGGAACCTTCC 2405
Qy 2922 ATAGTACACCTTACGCTGAGACTGAGCAGCTTGGGGCTCAGTATGATGAGACCTGTTA 2981
Db 2406 ATAGTACACCTTACGCTGAGACTGAGCAGCTTGGGGCTCAGTATGATGAGACCTGTTA 2465
Qy 2982 GGGACAGACCTTATGTTGTAATTCAGAGAAATGATCTTATCAAAAGCTGATTCACAA 3041
Db 2466 GGGACAGACCTTATGTTGTAATTCAGAGAAATGATCTTATCAAAAGCTGATTCACAA 2525
Qy 3042 CCAGCTCACTGACAGCAGCAGGAGCAAGAGATCACTGTGTGACGGAACAATTAGGGG 3101
Db 2526 CCAGCTCACTGACAGCAGCAGGAGCAAGAGATCACTGTGTGACGGAACAATTAGGGG 2585
Qy 3102 CCTTGCAGAGTCTACTTATAGCAAAACCAAGTACTTCAAGCAGGAAAGTGGGGCTTTG 3161
Db 2586 CCTTGCAGAGTCTACTTATAGCAAAACCAAGTACTTCAAGCAGGAAAGTGGGGCTTTG 2645
Qy 3162 ACCACTACCATATCTGATAGCCCAATTTTCTAGGCAATTTGATGATGATGATGATGCA 3221
Db 2646 ACCACTACCATATCTGATAGCCCAATTTTCTAGGCAATTTGATGATGATGATGATGCA 2705

Qy	3222	CACTTTTCAGACCAATTCAAATGTCCTTAAGCACAAAATTCGCCGAGGCTGATGAGAACT	3281
Db	2706	CACITTTCAAGCAAAATTCAAATGTCTTAAGCACAAAATTCGCCGTGGGCTTGATGAGAACT	2765
Qy	3282	AATTTTTTTTCTTCTCAGCTTTAAGAAGAGAGAAACTGTCTAGAAATTCAGCTGAAC	3341
Db	2766	AATTTTTTTTCTTCTCAGCTTTAAGAAGAGAGAAACTGTCTAGAAATTCAGCTGAAC	2822
Qy	3342	CACCAAGAACTGGCAACATCAACGATTTAAGCTAAGTTGGAGGCTAACGAGTCTACT	3401
Db	2826	CACCAAGAACTGGCAACATCAACGATTTAAGCTAAGTTGGAGGCTAACGAGTCTACT	2885
Qy	3402	CCCTCTTTGTAATCAAGAATTGTTT	3428
Db	2886	CCCTCTTTGTAATCAAGAATTGTTT	2912

RESULT 25
US-10-168-506-2

```

? Sequence 2, Application US/10168506
? Publication No. US2004005329A1
? GENERAL INFORMATION:
? APPLICANT: PLOWMAN, GREGORY D.
? APPLICANT: MARTINEZ, RICARDO
? APPLICANT: WHITE, DAVID
? APPLICANT: MANNING, GERRARD
? APPLICANT: SUDARSNAM, SUCHA
? APPLICANT: HILL, RON
? APPLICANT: FLANNAGAN, PETER
? TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASSES
? FILE REFERENCE: 038602/1351
? CURRENT APPLICATION NUMBER: US/10/168,506
? CURRENT FILING DATE: 2002-06-21
? PRIOR APPLICATION NUMBER: PCT/US00/34736
? PRIOR FILING DATE: 2000-12-21
? NUMBER OF SEQ ID NOS: 76
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 2
? LENGTH: 2732
? TYPE: DNA
? ORGANISM: Homo sapiens
? OS-10-168-506-2

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Query Match	45.1%	Score 2459;	DB 17;	Length 2732;
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 2729; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy	1	AAAAAAGAAAGACGAGAGGAGAGACGACGGGACGGGACGGGACGGGACGGGACGGC	60
Dp	1	GAHAAGAAAGACGAGAGGAGAGACGGGACGGGACGGGACGGGACGGGACGGC	60
Qy	61	TCGGCTCCGGCGCGCGCTCCGCAAGTCCGGGAGCGAGAGGGGGGCCCGAGGGGAGACGC	120
Dp	61	TCGGCTCCGGCGCGCGCTCCGCAAGTCCGGGAGCGAGAGGGGGGCCCGAGGGGAGACGC	120
Qy	121	GTGACACTTTGCTTCCCTCTGAGGGAATTGGAGGTCCGCGGCGCCCAAAAGCTTTCAG	180
Dp	121	GTGACAACTTTGCTTCCCTCTGAGGGAATTGGAGAGTCCGCGGCGCCCAAAAGCTTTCAG	180
Qy	181	TCCAGTGTAAAGCTGTGGAGCGCGGGAGCAAAAGTAAAGATGATGTATGCGCTGGCT	240
Dp	181	TCCAGTGTAAAGCTGTGGAGCGCGGGAGCAAAAGTAAAGATGATGTATGCGCTGGCT	240
Qy	241	GCTCCAAAGCATCTTTGTTGTGGAATGGTTATTCAGTCATCTCTTTATGATTCAAATG	300
Dp	241	GCTCCAAAGCATCTTTGTTGTGGAATGGTTATTCAGTCATCTCTTTATGATTCAAATG	300
Qy	301	TGAGGGGCTGCTTTGTGACGAGAGTCTTTGCAGAAGCATCAACGGGAAAGAGAAAG	360
Dp	301	TGAGGGGCTGCTTTGTGACGAGAGTCTTTGCAGAAGCATCAACGGGAAAGAGAAAG	360
Qy	361	GACATTCACCTGGAGGGCTCTTGCTGAATAAGGTTTAACTCTCTTTTGCAGTCACCA	420

Db	361	GACATTCAC	TGGAGGGCTCTTGC	GAAGAAATGGGTTAACTCTCTTTTGC	AAGTCACCA	420
Qy	421	CCAGCTGAC	CTCATACATTTT	AGTACAAATGAGTGGCTGAGCCTTTG	AAGACACACC	480
Db	421	CCAGCTGAC	CTCATACATTTT	AGTACAAATGAGTGGCTGAGCCTTTG	AAGACACACC	480
Qy	441	ATTACATCA	TGTGTGGCAATTTAA	AGAGAGTGGGAAAAGAGACTTAATGTTGT	CAATG	540
Db	481	ATTACATCA	TGTGTGGCAATTTAA	AGAGAGTGGGAAAAGAGACTTAATGTTGT	CAATG	540
Qy	541	GCCCATGAG	TGATTTGGAAC	CAATTTGTTACTGAGAGTTTGATGGCTCTGCTG	GAAGAGT	600
Db	541	GCCCATGAG	TGATTTGGAAC	CAATTTGTTACTGAGAGTTTGATGGCTCTGCTG	GAAGAGT	600
Qy	601	GGAACGGA	AAAAAGTCTGCTAA	TATGATAGCCGGCAATTTGTGGAATACATACAT	CCAC	660
Db	601	GGAACGGA	AAAAAGTCTGCTAA	TATGATAGCCGGCAATTTGTGGAATACATACAT	CCAC	660
Qy	661	ATTTTGGAA	GCCATTAAATACAT	CTGCTCCAAAGCTTATGAAAGCAAGTTTGCAACAGAC	720	
Db	661	ATTTTGGAA	GCCATTAAATACAT	CTGCTCCAAAGCTTATGAAAGCAAGTTTGCAACAGAC	720	
Qy	721	AAAGGTAA	TATACAGAGCTCAT	CAGACTCAGCGAAACATTAAGSTTGACATTAATGC	780	
Db	721	AAAGGTAA	TATACAGAGCTCAT	CAGACTCAGCGAAACATTAAGSTTGACATTAATGC	780	
Qy	781	AGTCAGAA	GGTGTGATTAACAT	CAATCAAGCTCCCAAGATGTTGCTCTCTCTCCACAG	840	
Db	781	AGTCAGAA	GGTGTGATTAACAT	CAATCAAGCTCCCAAGATGTTGCTCTCTCTCCACAG	840	
Qy	841	TGTTTTCT	CACGTATCTTCTG	GGTAAACTGAGAAAGACTTCAACTGTGTTCACTGCTT	900	
Db	841	TGTTTTCT	CACGTATCTTCTG	GGTAAACTGAGAAAGACTTCAACTGTGTTCACTGCTT	900	
Qy	901	GCAGTGG	STTTGCTGAGTTCT	CTCGTGTTTCCCTGGCCCTGTGAAAGAAATCCACT	960	
Db	901	GCAGTGG	STTTGCTGAGTTCT	CTCGTGTTTCCCTGGCCCTGTGAAAGAAATCCACT	960	
Qy	961	CTAGTCC	CTACCTGATTTCT	CAGCCTGCTTACCTGTGTCACATTTGGGCCAACCCGA	1020	
Db	961	CTAGTCC	CTACCTGATTTCT	CAGCCTGCTTACCTGTGTCACATTTGGGCCAACCCGA	1020	
Qy	1021	ATTCTTCC	CAATCTTTATCTT	GCTGCCAGAGATGTCCTCAACAGAGCTGATPACG	1080	
Db	1021	ATTCTTCC	CAATCTTTATCTT	GCTGCCAGAGATGTCCTCAACAGAGCTGATPACG	1080	
Qy	1081	CAGAA	TGGGATTTGGTATGT	GTAAATGCCAGCTATACCTGTCCAAAGCCTGACTTTATC	1140	
Db	1081	CAGAA	TGGGATTTGGTATGT	GTAAATGCCAGCTATACCTGTCCAAAGCCTGACTTTATC	1140	
Qy	1141	CCCGAGT	CTCATTTCCGCGT	GCATGCTGTGATGACACTTTTGTGAAGAAATTTTGC	1200	
Db	1141	CCCGAGT	CTCATTTCCGCGT	GCATGCTGTGATGACACTTTTGTGAAGAAATTTTGC	1200	
Qy	1201	TGTTTGA	CAAAATGATGATTT	CATTGAGAAAGCAAAAGCCTCCAAATGATGTGTCTA	1260	
Db	1201	TGTTTGA	CAAAATGATGATTT	CATTGAGAAAGCAAAAGCCTCCAAATGATGTGTCTA	1260	
Qy	1261	GTGCACT	GTTTAGCTGGGATTT	CCCGCTCCGCACACATCGCTATCGCTTAATCATGTAAG	1320	
Db	1261	GTGCACT	GTTTAGCTGGGATTT	CCCGCTCCGCACACATCGCTATCGCTTAATCATGTAAG	1320	
Qy	1321	AGAA	TGGAACATGCTTTA	AGATGAAAGCTTACAGATTTGTGAAAGAAAGAAAGCTATCTA	1380	
Db	1321	AGAA	TGGAACATGCTTTA	AGATGAAAGCTTACAGATTTGTGAAAGAAAGAAAGCTATCTA	1380	
Qy	1381	TCTCAAA	ACTTCAATTTTCTG	GGCCAACTCTGGAATATGAGAAAGATTTAAGAACG	1440	
Db	1381	TCTCAAA	ACTTCAATTTTCTG	GGCCAACTCTGGAATATGAGAAAGATTTAAGAACG	1440	
Qy	1441	ACTGAG	CATCAGGCAAGAG	CAAACTCAGCTGTGCACTTGAGAGCCCAATGAA	1500	
Db	1441	ACTGAG	CATCAGGCAAGAG	CAAACTCAGCTGTGCACTTGAGAGCCCAATGAA	1500	

Db 1441 ACTGGAGCATCAGGCGCCAAAGCAAACTCAGCTGTGACCTGGAGAGCCAAATGAA 1500
QY 1501 CCTGTCCCTCTGTCTCTCAGAGGGTGGACAGAAAAGGAGAGCGCCCTCAGTCCACCTCT 1560
Db 1501 CCGTCCCTCTGTCTCTCAGAGGGTGGACAGAAAAGGAGAGCGCCCTCAGTCCACCTCT 1560
QY 1561 GCCGACTGTGCTACTCTCAGAGGAGCAGAGCAAAAGGCCGTGATCCCGCAGCGTGGCC 1620
Db 1561 GCCGACTGTGCTACTCTCAGAGGAGCAGAGCAAAAGGCCGTGATCCCGCAGCGTGGCC 1620
QY 1621 AGGTCGCCAGCGCTGAGCGCGTGTGTAGAGAGCAGCCCGTGTGTAGAGCGCTCACT 1680
Db 1621 AGGTCGCCAGCGCTGAGCGCGTGTGTAGAGAGCAGCCCGTGTGTAGAGCGCTCACT 1680
QY 1681 GGGCTGCACCTGTCTCCGACAGAGGCTGAAAGCAGCAATAGCTCAAGGCTTCTCTCT 1740
Db 1681 GGGCTGCACCTGTCTCCGACAGAGGCTGAAAGCAGCAATAGCTCAAGGCTTCTCTCT 1740
QY 1741 CTGGATATCAATCACTTTCATATTCAGCCAGCATGGAGCATCTTTCATGGCTTCTCC 1800
Db 1741 CTGGATATCAATCACTTTCATATTCAGCCAGCATGGAGCATCTTTCATGGCTTCTCC 1800
QY 1801 TCATCAGAGATGCTTTGGAATTAATAAACCCTTCACTCTGATGGAGCACAAG 1860
Db 1801 TCATCAGAGATGCTTTGGAATTAATAAACCCTTCACTCTGATGGAGCACAAG 1860
QY 1861 CTATGCGAGTCTCTCCCTGTTCAGAGAACTATCGAGCAGACTCCGAAACAGTCTGAT 1920
Db 1861 CTATGCGAGTCTCTCCCTGTTCAGAGAACTATCGAGCAGACTCCGAAACAGTCTGAT 1920
QY 1921 AAGGAGAAAGCCAGCATCCCAAGAAAGCTGCAAGCCGCGGCTTTCAGAGCAGCAAGC 1980
Db 1921 AAGGAGAAAGCCAGCATCCCAAGAAAGCTGCAAGCCGCGGCTTTCAGAGCAGCAAGC 1980
QY 1981 AAGCATTTGCTTCCGTGAGAACTAGAGCAGTGGCAACGCCAGAGGCTTTCATCT 2040
Db 1981 AAGCATTTGCTTCCGTGAGAACTAGAGCAGTGGCAACGCCAGAGGCTTTCATCT 2040
QY 2041 CCAGTGCATCGAAGTGGAGCGTGGAGGACATTAACAACAAGCTTCTTTCGAGCTT 2100
Db 2041 CCAGTGCATCGAAGTGGAGCGTGGAGGACATTAACAACAAGCTTCTTTCGAGCTT 2100
QY 2101 TCCACAGCGAGACACCTCAAGAGTGTGTGCTGGGCTTTAAAGGCTGGCACTCG 2160
Db 2101 TCCACAGCGAGACACCTCAAGAGTGTGTGCTGGGCTTTAAAGGCTGGCACTCG 2160
QY 2161 GATATCTTGGCCCCCAGACCTCTACCCCTTCCGACAGAGAGTGTATTTTGGCA 2220
Db 2161 GATATCTTGGCCCCCAGACCTCTACCCCTTCCGACAGAGAGTGTATTTTGGCA 2220
QY 2221 GAGTCTCAACCTTCTACTGTGCTCAGCCATCTTACGAGGCAAGTCCAGTCTTCTGCC 2280
Db 2221 GAGTCTCAACCTTCTACTGTGCTCAGCCATCTTACGAGGCAAGTCTTCTGCC 2280
QY 2281 TACAGCTCAGCGAGCTGCCCACTTGGCGAGACCAAGCTTATCTGTGCGGAGCGGAG 2340
Db 2281 TACAGCTCAGCGAGCTGCCCACTTGGCGAGACCAAGCTTATCTGTGCGGAGCGGAG 2340
QY 2341 AAGCAAGTGAAGAGTGAAGTGTGAGAGGAGCTGAGCAAGAGAGAGCCCTTTGAAAG 2400
Db 2341 AAGCAAGTGAAGAGTGAAGTGTGAGAGGAGCTGAGCAAGAGAGAGCCCTTTGAAAG 2400
QY 2401 CAGTTTAAACGCAAGGCTGCAATGGAATTTGAGAGAGCATGTCAGAGAAAG 2460
Db 2401 CAGTTTAAACGCAAGGCTGCAATGGAATTTGAGAGAGCATGTCAGAGAAAG 2460
QY 2461 TCAAGGGAAGAGCTGGGGAAGTGGGAGTCAAGTCAAGTCTTTCGAGAGCAAGATC 2520
Db 2461 TCAAGGGAAGAGCTGGGGAAGTGGGAGTCAAGTCAAGTCTTTCGAGAGCAAGATC 2520
QY 2521 ATTGAGGTCTCTGAGAGAAAGACATTTGATCTTATAGCAATTTTTCCTTGG 2580
Db 2521 ATTGAGGTCTCTGAGAGAAAGACATTTGATCTTATAGCAATTTTTCCTTGG 2580

QY 2581 TTCACAAAAAATTCCTGTAAATCTGAAATATATATGATACATATATATTTTGG 2640
Db 2580 TTCACAAAAAATTCCTGTAAATCTGAAATATATATGATACATATATATTTTGG 2639
QY 2641 GAAATGAGCTATGATGTAAAGCAACAGGATGATCAACCACTGTGTTCTCTTAAAC 2700
Db 2640 GAAATGAGCTATGATGTAAAGCAACAGGATGATCAACCACTGTGTTCTCTTAAAC 2699
QY 2701 ATCTGCAATTTAGAGATCACTAATCTCTCT 2733
Db 2700 ATCTGCAATTTAGAGATCACTAATCTCTCT 2732

RESULT 26
US-09-964-277-20
; Sequence 20, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Lucbe, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 3332
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-277-20

Query Match 38.8%; Score 2117; DB 9; Length 3332;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2357; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1115 ATACCTGTCCAAAGCCGTGAATTTATCCCGAGCTCATTTTCCGCGTGGCCGTGAATG 1174
Db 975 ATACCTGTCCAAAGCCGTGAATTTATCCCGAGCTCATTTTCCGCGTGGCCGTGAATG 1034
QY 1175 ACAGCTTTGTGAGAAATTTTTCGCGTGTGGACAAATCAGTAGATTTTCATTGAGAAAG 1234
Db 1035 ACAGCTTTGTGAGAAATTTTTCGCGTGTGGACAAATCAGTAGATTTTCATTGAGAAAG 1094
QY 1235 CAAAGCCTCCATGATGTGTCTTATGTCAGCTGTTTACGTGGATCTCCCGCTCGGCA 1294
Db 1095 CAAAGCCTCCATGATGTGTCTTATGTCAGCTGTTTACGTGGATCTCCCGCTCGGCA 1154
QY 1295 CCATGCTATGCGCTCATCATGAAGAGATGAGACATGCTTTAGATGAAGCTTACAGAT 1354
Db 1155 CCATGCTATGCGCTCATCATGAAGAGATGAGACATGCTTTAGATGAAGCTTACAGAT 1214
QY 1355 TTGTGAAAGAAAAAGACCTACTATATCTCAAACTTCAATTTTCTGGCCAACTCTGG 1414
Db 1215 TTGTGAAAGAAAAAGACCTACTATATCTCAAACTTCAATTTTCTGGCCAACTCTGG 1274
QY 1415 ACTATGAGAAAGATTAAGAACAGACTGAGCATTCAGGCGCAAGAGCAAACTCAAGC 1474
Db 1275 ACTATGAGAAAGATTAAGAACAGACTGAGCATTCAGGCGCAAGAGCAAACTCAAGC 1334
QY 1475 TGCTGCACTGGAAGAGCAATGAACCTGTCCCTGTGTCTCAGAGGTTGAGCAAGAAA 1534
Db 1335 TGCTGCACTGGAAGAGCAATGAACCTGTCCCTGTGTCTCAGAGGTTGAGCAAGAAA 1394
QY 1535 GCGAGACGCGCTCTCAGTCACTGTGCGGACTGTGTAACCTCAGAGGCAAGCAAGAAA 1594
Db 1395 GCGAGACGCGCTCTCAGTCACTGTGCGGACTGTGTAACCTCAGAGGCAAGCAAGAAA 1454
QY 1595 GGCCTGTGATCCCGCAGCGTGGCCAGCGTCCAGAGGTGAGAGCGCTGCTGTGAAGG 1654
Db 1455 GGCCTGTGATCCCGCAGCGTGGCCAGCGTCCAGAGGTGAGAGCGCTGCTGTGAAGG 1514

Qy	1655	ACAGCCCGCTGGTATCAGGCGGCTCACTGAGGCTGCACTGTGCGCAGACAGAGGCTGGAAAGCA	171
Db	1515	ACAGCCCGCTGGTATCAGGCGGCTCACTGAGGCTGCACTGTGCGCAGACAGAGGCTGGAAAGCA	157
Qy	1715	GCAATTAAGCTCAAGCGTTCTTCTCTCGATGATCAAAATCAAGTTTCATATTCAGCCAGCA	1774
Db	1575	GCAATTAAGCTCAAGCGTTCTTCTCTCGATGATCAAAATCAAGTTTCATATTCAGCCAGCA	163
Qy	1775	TGGCAGCATTCCTTACATGGCTTCTCTCATCAGAAATGCTTGGAAATCTCAAACTT	183
Db	1635	TGGCAGCATTCCTTACATGGCTTCTCTCATCAGAAATGCTTGGAAATCTCAAACTT	1694
Qy	1835	CCACTACTGCGATGGGACAAACAAGCTATGCGACATCTCCCTGTACAGGAACATACGG	1894
Db	1685	CCACTACTCTGGATGGGACCAACAAGCTATGCGACATCTCCCTGTACAGGAACATACGG	175
Qy	1895	AGCAGACTCCCGAAACAGTCTCGATTAAGAGGAAGCCAGCATCCCGCAAGAAGCTGCAGA	195
Db	1755	AGCAGACTCCCGAAACAGTCTCGATTAAGAGGAAGCCAGCATCCCGCAAGAAGCTGCAGA	1814
Qy	1955	CCGCCAGGCTTCAGACAGCCAGCAAGCAAGCATTCGATTCGGTCAAAACAGCAGCAGTG	2014
Db	1815	CCGCCAGGCTTCAGACAGCCAGCAAGCAAGCATTCGATTCGGTCAAAACAGCAGCAGTG	1874
Qy	2015	GCACCGCCCAAGAGGCCCTTTTATCTCCATCGCATCGAAGTGGGAGCGGTGAGAGCAATT	2074
Db	1875	GCACCGCCCAAGAGGCCCTTTTATCTCCATCGCATCGAAGTGGGAGCGGTGAGAGCAATT	193
Qy	2075	ACCAACACAGCTTCCTTTGCGGCTTTCACACAGCCAGCAGAGCACTCAAGAACTGTGCTG	2134
Db	1935	ACCAACACAGCTTCCTTTGCGGCTTTCACACAGCCAGCAGAGCACTCAAGAACTGTGCTG	1994
Qy	2135	GCTTGGGCTTTAAGGGCTGGGCACTCGATATCTTGGGCCCCCGACACTTCACCCCTTCC	2194
Db	1995	GCTTGGGCTTTAAGGGCTGGGCACTCGATATCTTGGGCCCCCGACACTTCACCCCTTCC	2054
Qy	2195	TGACACAGAGCTGATATTTTGGCAAGAGTCTTCAACTTTCATCTTTCGCTCAAGCATCT	2254
Db	2055	TGACACAGAGCTGATATTTTGGCAAGAGTCTTCAACTTTCATCTTTCGCTCAAGCATCT	2114
Qy	2255	ACGAGGAGTGGSCAGTTACTCTGCGCTACAGCTGACGCGAGCTGCGCACTTGGCGGAGAC	2314
Db	2115	ACGAGGAGTGGSCAGTTACTCTGCGCTACAGCTGACGCGAGCTGCGCACTTGGCGGAGAC	2174
Qy	2315	AAGTCTATTTCTGTGGCAGCGCGGCGCAAGCCAAAGTGAAGACTGACGCGCGGAGCT	2374
Db	2175	AAGTCTATTTCTGTGGCAGCGCGGCGCAAGCCAAAGTGAAGACTGACGCGCGGAGCT	2234
Qy	2375	GGCATGAAAGAGAGCCCTTTGAAAAAGCAGTTTAAACGCAAGAGCTGCCAATGGAATTTG	2434
Db	2235	GGCATGAAAGAGAGCCCTTTGAAAAAGCAGTTTAAACGCAAGAGCTGCCAATGGAATTTG	2294
Qy	2435	GAGAGAGCATATGTCAGAGAACAGGTGACGCGGAAAGACCTGGGGGAAAGTGGGCACTCAGT	2494
Db	2295	GAGAGAGCATATGTCAGAGAACAGGTGACGCGGAAAGACCTGGGGGAAAGTGGGCACTCAGT	2354
Qy	2495	CTAGCTTTCCGGCAGCATGGAATCATTTGAAGTCTCCTGAGAGAAAGACACTTGTGAC	2554
Db	2355	CTAGCTTTCCGGGAGCATGGAATCATTTGAAGTCTCCTGAGAGAAAGACACTTGTGAC	2414
Qy	2555	TTCTATAGACAATTTTTTTTCTTGTTCACAAAAAAATTCCTGTAAATCTGAAATATA	2614
Db	2415	TTCTATATACAAA - TTTTCTTGTTCACAAAAAAATTCCTGTAAATCTGAAATATA	2474
Qy	2615	TATATGTATCATACATATATATTTTTTGGAAATGGAAGTATGCTGTAAAGCAACAGGTGG	2674
Db	2474	TATATGTATCATACATATATATTTTTTGGAAATGGAAGTATGCTGTAAAGCAACAGGTGG	2534
Qy	2675	ATCAACCCAGTTGTACTCTCTTAAACATCTGCATTTGAGAGTCACTAAATACCTCTCTC	2734
Db	2534	ATCAACCCAGTTGTACTCTCTTAAACATCTGCATTTGAGAGTCACTAAATACCTCTCTC	2594
Qy	2735	AACAAAAATGAAAGGCGAGATGCTAGAAATCCCCCTTACGAGGAGAAAAACATTTTATTC	2794

Db	2594	AACAAAATGGAAGGCGAGATGCTAGAAATCCCCCTAGACGGAGAAAACATTATATTC	2655
Oy	2795	AGTGAATTACACATCTCTTGTTCTTTAAAAAGCAAGTCTTTGGTTTGAGAGACAA	285
Db	2654	AGTAATATACATCTCTTGTTCTTTAAAAAGCAAGTCTTTGGTTTGAGAGACAA	2713
Oy	2855	ATCCCCCTACCATTTT - CACGTTTGCTACTTAAGATCTCAAATATTAGTCTTTGCCG	2913
Db	2714	ATCCCCCTACCATTTTTCACGTTTGCTACTTAAGATCTCAAATATTAGTCTTTGCCG	2773
Oy	2914	ACCCCTTCATAGTACACCTTAGGCGCTAGACTGAGCCAGCTTTGGGGGTCAGTATAGTATGA	2973
Db	2774	ACCCCTTCATAGTACACCTTAGGCGCTAGACTGAGCCAGCTTTGGGGGTCAGTATAGTATGA	2833
Oy	2974	CCCTGTTAGGGAGACAGACCTTAGTGTAAATCCAGAGAAATGATCTTATCCAAAGCTGAT	3033
Db	2834	CCCTGTTAGGGAGACAGACCTTAGTGTAAATCCAGAGAAATGATCTTATCCAAAGCTGAT	2893
Oy	3034	TCACAAACCCACGCTCACCTGACAGCCGAGGGACAGAGCATCTCTGCTGACGAGCC	3093
Db	2894	TCACAAACCCACGCTCACCTGACAGCCGAGGGACAGAGCATCTCTGCTGACGAGCC	2953
Oy	3094	ATTAGGGGCTTGGCAAGGTCTACCTTAGACAAACCCAGTACTCAGACAGGAAGTGC	3153
Db	2954	ATTAGGGGCTTGGCAAGGTCTACCTTAGACAAACCCAGTACTCAGACAGGAAGTGC	3013
Oy	3154	GGGCTTTGACACACATATCTGGTAGCCCATTTTCTAGGCAATTGGAATAGGATAGTAT	3213
Db	3014	GGGCTTTGACACACATATCTGGTAGCCCATTTTCTAGGCAATTGGAATAGGATAGTAT	3073
Oy	3214	GCTAGTCACATTTTTCAGACCAATTCAAACGTCTATGACAAAAATTCGCCGTGGGCTTAG	3273
Db	3074	GCTAGTCACATTTTTCAGACCAATTCAAACGTCTATGACAAAAATTCGCCGTGGGCTTAG	3133
Oy	3274	ATGAGATTAATTTTTTTTTCTTCTCAGCTTTATGAGAAAGGAAACTGTCTAGATTC	3333
Db	3134	ATGAGATTAATTTTTTTTTCTTCTCAGCTTTATGAGAAAGGAAACTGTCTAGATTC	3193
Oy	3334	AGCTGAACCAACAGAAACCTGGCAACATCACGATTTTAAGCTTAGGTTGGAGGCTTAACGA	3393
Db	3194	AGCTGAACCAACAGAAACCTGGCAACATCACGATTTTAAGCTTAGGTTGGAGGCTTAACGA	3253
Oy	3394	GTCATACCTCCCTCTTGTGAATCAAAAGATTTGTTAAATGGAGTTGTCATCTCTTAA	3453
Db	3354	GTCATACCTCCCTCTTGTGAATCAAAAGATTTGTTAAATGGAGTTGTCATCTCTTAA	3313
Oy	3454	TAAAGATGAACCTTGTTTC 3472	
Db	3314	TAAAGATGAACCTTGTTTC 3332	

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RESULT 27
US-10-104-047-1750
; Sequence: 1750, Application US/10104047
; Publication NO. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1750
; LENGTH: 2558
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1750

Query Match          38.5%, Score 2098, DB 17, Length 2558

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Oy	4732	CAGCCTTAGGCTGGCTCACTAGGTGAGAATAACATTTTGGAAATCGAGACTCCGT	4791
Dd	2161	CAGCCTTAGGCTGGCTCACTAGGTGAGAATAACATTTTGGAAATCGAGACTCCGT	2220
Oy	4792	GCGCAGAGGGTGCCCTCGAGGCAGACGCTGGAGCTGGTGGATTCCTTAAGTGGGGTG	4851
Dd	2221	GCGCAGAGGGTGCCCTCGAGGCAGACGCTGGAGCTGGTGGATTCCTTAAGTGGGGTG	2280
Oy	4852	GTGGCTGGCTCTCTTCAGCATGTATTGGGGAAAACCTTCGGCTCTAATGAGGGGTATCA	4911
Dd	2281	GTGGCTGGCTCTCTTCAGCATGTATTGGGGAAAACCTTCGGCTCTAATGAGGGGTATCA	2340
Oy	4912	GATGGTGAATTTTAAAGACAACAACTAGACTTATGTAGAGAAGTCTGGAAAATGATTTA	4971
Dd	2341	GATGGTGAATTTTAAAGACAACAACTAGACTTATGTAGAGAAGTCTGGAAAATGATTTA	2400
Oy	4972	GGAC 4975	
Dd	2401	GGAC 2404	

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RESULT 28
US-09-816-494-3
; Sequence 3, Application US/09816494
; Patent No. US20020034807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-816-494-3.

Query Match          34.8%; Score 1896; DB 9; Length 1998;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1996; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      538  ATGGCCCATGAGATGATTTGAACTCAAAATTGTTACTGAGAGTGTGGCTCTGCTGGAA 597
DB      1    ATGGCCCATGAGATGATTTGAACTCAAAATTGTTACTGAGAGTGTGGCTCTGCTGGAA 60

QY      598  AGTGGAAACGGAANAAGTGCCTGTAATTGATAGCGCGCCATTGTGGATATCAATATCATCC 657
DB      61  AGTGAACGGAANAAGTGCCTGTAATTGATAGCGCGCCATTGTGGATATCAATATCATCC 120

QY      658  CACATTTTGAAGCCATTAATATCAACTGCTCCAAGCTTATGAACGGAAGTTGCAACAG 717
DB      121  CACATTTTGAAGCCATTAATATCAACTGCTCCAAGCTTATGAACGGAAGTTGCAACAG 180

QY      718  GACCAAGTGTAAATTACAGAGCTCATCCAGCATTCAGCGAATCATTAAGTTGACATTGAT 777
DB      181  GACCAAGTGTAAATTACAGAGCTCATCCAGCATTCAGCGAATCATTAAGTTGACATTGAT 240

QY      778  TGCAGTCAGAAAGTTGTAGTTTATGAGATCAAAAGCTCCCAAGATGTGCTCTCTCTTCA 837
DB      241  TGCAGTCAGAAAGTTGTAGTTTATGAGATCAAAAGCTCCCAAGATGTGCTCTCTCTTCA 300

QY      838  GACTGTTTTCATCACTGTACTTCTGGGTAACTGAGAAAGACTTCAACTCTGTTCACCTG 897
DB      301  GACTGTTTTCATCACTGTACTTCTGGGTAACTGAGAAAGACTTCAACTCTGTTCACCTG 360

QY      898  CTTGACAGGTGGCTTGTGAGATTCTCTCTGTTGTTCCCTGGCTCTGTGAAGAAATCC 957
DB      361  CTTGACAGGTGGCTTGTGAGATTCTCTCTGTTGTTCCCTGGCTCTGTGAAGAAATCC 420

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Db	361	CTTGCAGAGTGGGGTTGCTGAGTTCTCTGTTGTTTCCGTGGCCTGTGMAAGAAATTC	420
Qy	958	ACTCAAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCTGTTGCCAATGGGCAAC	1017
Db	421	ACTCAAGTCCCTACCTGCATTTCTCAGCCTTGCTTACCTGTTGCCAATGGGCAAC	480
Qy	1018	CGAATTCCTCCCAATCTTTATCTTGAGCTGCGCAGAGATGTCTCAACAAGAGCTGATA	1077
Db	481	CGAATTCCTCCCAATCTTTATCTTGAGCTGCGCAGAGATGTCTCAACAAGAGCTGATG	540
Qy	1078	CAGCAGAAATGGGATGGTTATGTGTTAATGCAAGCTTACTGTGCGAAAGCTGCATTT	1137
Db	541	CAGCAGAAATGGGATGGTTATGTGTTAATGCGCAAACTACTGTGCGAAAGCTGCATTT	600
Qy	1138	ATCCCGAGTCTCATTTCTCGCTGCTGCTGATGAATGACAGCTTTTGTAGAAATTTTG	1197
Db	601	ATCCCGAGTCTCATTTCTCGCTGCTGCTGATGAATGACAGCTTTTGTAGAAATTTTG	660
Qy	1198	CCGTGTTTGAACAATTCAGTGAATTTCAATTGAGAAAGCAAAAGCTCCATGTGATGTG	1257
Db	661	CCGTGTTTGAACAATTCAGTGAATTTCAATTGAGAAAGCAAAAGCTCCATGTGATGTG	720
Qy	1258	CTAGTGCATGTTTAACTGGGATCTCCGCGTCCGCACTATGCGATATGGCCCTACATG	1317
Db	721	CTAGTGCATGTTTAACTGGGATCTCCGCGTCCGCACTATGCGATATGGCCCTACATG	780
Qy	1318	AAGAGATGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAGAAAGCTACT	1377
Db	781	AAGAGATGACATGTCTTTAGATGAAGCTTACAGATTTGTGAAAGAAAGAAAGCTACT	840
Qy	1378	ATATCTCCAACTTCAATTTTCTGGGCCAATCTCTGACATATGAGAGAGATTAGAAC	1437
Db	841	ATATCTCCAACTTCAATTTTCTGGGCCAATCTCTGACATATGAGAGAGATTAGAAC	900
Qy	1438	CAGACTGGAGATCAGGGGCCAAAGCAACTCAAGCTGCGACCTGGAAGAGCAAT	1497
Db	901	CAGACTGGAGATCAGGGGCCAAAGCAACTCAAGCTGCGACCTGGAAGAGCAAT	960
Qy	1498	GAACCTGTCCTGCTGTCTCAGAGGGATGAGACAGAAAGCGAGAGCCCTCAGTCAACC	1557
Db	961	GAACCTGTCCTGCTGTCTCAGAGGGATGAGACAGAAAGCGAGAGCCCTCAGTCAACC	1022
Qy	1558	TGTGCGCATCTGTGCTACTCAGAGGCGACAGAGCAAAAGGCCGTGCAATCCGCGAGCTG	1617
Db	1021	TGTGCGCATCTGTGCTACTCAGAGGCGACAGAGCAAAAGGCCGTGCAATCCGCGAGCTG	1080
Qy	1618	CCGACGCTGCCAGCGCTGACAGCCGTCTGTTAAGGACAGCCCGCTGTGTACAGGCGCTC	1677
Db	1081	CCGACGCTGCCAGCGCTGACAGCCGTCTGTTAAGGACAGCCCGCTGTGTACAGGCGCTC	1140
Qy	1678	AGTGGGCTGCACCTGTCCGAGACAGAGCTGGAMGACAGCAATTAAGCTCAAGCTTCTTC	1737
Db	1141	AGTGGGCTGCACCTGTCCGAGACAGAGCTGGAMGACAGCAATTAAGCTCAAGCTTCTTC	1200
Qy	1738	TCTCTGATTAACAATCAGTTTCATATTTACGCCAGCATGAGCAGATCTTACATGCTTC	1797
Db	1201	TCTCTGATTAACAATCAGTTTCATATTTACGCCAGCATGAGCAGATCTTACATGCTTC	1260
Qy	1798	TCTCTCATAGAAAGTCTTTGGAATATCTACAAACCTTCACTACTGTGAGTGGAGCAAC	1857
Db	1261	TCTCTCATAGAAAGTCTTTGGAATATCTACAAACCTTCACTACTGTGAGTGGAGCAAC	1320
Qy	1858	AAGCTATCCAGTTCTCCCTGTTCAGGAACTATCGAGAGAGACTCCGGAATCAGTGTCT	1917
Db	1321	AAGCTATCCAGTTCTCCCTGTTCAGGAACTATCGAGAGAGACTCCGGAATCAGTGTCT	1380
Qy	1918	GATAAGAGGAAGCAGCATCCCAAGAAAGCTGCAACCGCCAGGCTTTCAGACGCGAG	1977
Db	1381	GATAAGAGGAAGCAGCATCCCAAGAAAGCTGCAACCGCCAGGCTTTCAGACGCGAG	1440
Qy	1978	AGCAAGCATTTGCATTTGGTGTAGAAACCAAGCAGCTGTGCACCGCCAGAGGTCCCTTTTA	2037
Db	1441	AGCAAGCATTTGCATTTGGTGTAGAAACCAAGCAGCTGTGCACCGCCAGAGGTCCCTTTTA	1500

QY	2038	TCGCCATGATGCAATGAGTGGAGGCGTGGAGGACAATTACACACCAAGCTCTCTTTGGGC	2097
Db	1501	TCGCCATGATGCAATGAGTGGAGGCGTGGAGGACAATTACACACCAAGCTCTCTTTGGGC	1560
QY	2098	CTTTCACACAGCCAGCAGCACTCAGCAAGTCTGCTGGCCCTTAAGGCGTGGAC	2157
Db	1561	CTTTCACACAGCCAGCAGCACTCAGCAAGTCTGCTGGCCCTTAAGGCGTGGAC	1620
QY	2158	TCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACACAGCTGTATTTGGC	2217
Db	1621	TCGGATATCTTGGCCCCCAGACCTCTACCCCTTCCCTGACACAGCTGTATTTGGC	1680
QY	2218	ACAGAGTCCTCAACTTCTACTCTGCTCAGCCATCTACGAGGCACTGCCATGTTACTCT	2277
Db	1681	ACAGAGTCCTCAACTTCTACTCTGCTCAGCCATCTACGAGGCACTGCCATGTTACTCT	1740
QY	2278	GCCTAAGCTGACGACGAGCTGCCACTTGGCGAGACAAGTCTATTCTGTGGCAGGCGG	2337
Db	1741	GCCTAAGCTGACGACGAGCTGCCACTTGGCGAGACAAGTCTATTCTGTGGCAGGCGG	1800
QY	2338	CAGAGCCAAAGTACACAGCTGACTCGCGCGGAGCTGGCATGAAGAGACCCCTTTGAA	2397
Db	1801	CAGAGCCAAAGTACACAGCTGACTCGCGCGGAGCTGGCATGAAGAGACCCCTTTGAA	1860
QY	2398	AAGCAGTTTAAACGAGAGCTGCGCAATGGAATTTGGAGAGCATCATGTCAAGAAC	2457
Db	1861	AAGCAGTTTAAACGAGAGCTGCGCAATGGAATTTGGAGAGCATCATGTCAAGAAC	1920
QY	2458	AGGTACCGGAAAGCTGGGAAAGTGGGCACTCAGTCTGCTTTTCGGCAGCATGAA	2517
Db	1921	AGGTACCGGAAAGCTGGGAAAGTGGGCACTCAGTCTGCTTTTCGGCAGCATGAA	1980
QY	2518	ATCATTGAGGTCTCTCGA	2535
Db	1981	ATCATTGAGGTCTCTCGA	1998
RESULT 29			
US-10-377-072-27			
; Sequence 27, Application US/10377072			
; Publication No. US2004009501A1			
GENERAL INFORMATION:			
; APPLICANT: Millennium Pharmaceuticals Inc.			
; APPLICANT: Curtis, Rory A.J.			
; APPLICANT: Logan, Thomas Joseph			
; APPLICANT: Glucksmann, Maria A.			
; APPLICANT: Meyers, Rachel E.			
; APPLICANT: Williamson, Mark J.			
; APPLICANT: Rudolph-Owen, Laura A.			
; APPLICANT: Chun, Miyoung			
; APPLICANT: Tsai, Fong-Ying			
TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,			
TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES			
FILE REFERENCE: MP103-0180MIM			
CURRENT APPLICATION NUMBER: US/10/377,072			
CURRENT FILING DATE: 2003-02-27			
PRIOR APPLICATION NUMBER: US 09/895,860			
PRIOR FILING DATE: 2001-06-29			
PRIOR APPLICATION NUMBER: US 60/215,370			
PRIOR FILING DATE: 2000-06-29			
PRIOR APPLICATION NUMBER: US 09/723,806			
PRIOR FILING DATE: 2000-11-28			
PRIOR APPLICATION NUMBER: US 60/187,455			
PRIOR FILING DATE: 2000-03-07			
PRIOR APPLICATION NUMBER: US 09/843,297			
PRIOR FILING DATE: 2001-04-25			
PRIOR APPLICATION NUMBER: US 60/199,801			
PRIOR FILING DATE: 2000-04-26			
PRIOR APPLICATION NUMBER: US 09/861,801			
PRIOR FILING DATE: 2001-05-21			
PRIOR APPLICATION NUMBER: US 60/205,508			

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? PRIOR FILING DATE: 2000-05-19
? PRIOR APPLICATION NUMBER: US 09/816,494
? PRIOR FILING DATE: 2001-03-23
? PRIOR APPLICATION NUMBER: US 09/815,419
? PRIOR FILING DATE: 2001-03-22
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 114
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 27
? LENGTH: 1998
? TYPE: DNA
? ORGANISM: Homo Sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)...(1998)
? US-10-377-072-27

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Query Match	34.8%	Score 1896;	DB 17;	Length 1998;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 1996; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	538	ATGGCCCATGAGATGATATGGAACTCAAAATTGTTACTGAGAGGTTGGTGCCTCGCTGGAA	597
Db	1	ATGGCCCATGAGATGATATGGAACTCAAAATTGTTACTGAGAGGTTGGTGCCTCGCTGGAA	60
QY	598	ACTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTGTGGAAATACATATCATCC	657
Db	61	ACTGGAACGGAAAAAGTGCTGCTAATTGATAGCCGGCCATTGTGGAAATACATATCATCC	120
QY	658	CACATTTTGGAAAGCATTATATCACTGCCTCCAAAGCTTATGAAAGCGAAGGTGGATAG	717
Db	121	CACATTTTGGAAAGCATTATATCACTGCCTCCAAAGCTTATGAAAGCGAAGGTGGATAG	180
QY	718	GACAAAGTGTTAATTATCAGAGCTCATCAGCAATTCAGGAAACATAAGGTTGACATGAT	777
Db	181	GACAAAGTGTTAATTATCAGAGCTCATCAGCAATTCAGGAAACATAAGGTTGACATGAT	240
QY	778	TGCAGTCAGAAAGTGTGATTTAGATCGATCAAAAGCTCCAAAGATGTGGCTCTCTCTTCA	837
Db	241	TGCAGTCAGAAAGTGTGATTTAGATCGATCAAAAGCTCCAAAGATGTGGCTCTCTCTTCA	300
QY	838	GACTGTTTTCCTCACTGTACTTCTGGGTAAACTGAGAAAGAGCTTCAACTCTGTTCACTG	897
Db	301	GACTGTTTTCCTCACTGTACTTCTGGGTAAACTGAGAAAGAGCTTCAACTCTGTTCACTG	360
QY	898	CTTGCAAGGTGGGTTTGCTGAGTGTCTCTGTTTCTCCCTGGCCCTGTGAAAGGAAAAATCC	957
Db	361	CTTGCAAGGTGGGTTTGCTGAGTGTCTCTGTTTCTCCCTGGCCCTGTGAAAGGAAAAATCC	420
QY	958	ACTCTAGTCCCTACCTGCAATTCACAGCCTGTCTTACCTGTGGCAACTTGGGCCCAAC	1017
Db	421	ACTCTAGTCCCTACCTGCAATTCACAGCCTGTCTTACCTGTGGCAACTTGGGCCCAAC	480
QY	1018	CGAATTCCTCCCAATCTTTATCTTGGGTGCAAGGAAATGTCTCTCAACAAGAGCTGATA	1077
Db	481	CGAATTCCTCCCAATCTTTATCTTGGGTGCAAGGAAATGTCTCTCAACAAGAGCTGATG	540
QY	1078	CAGCAGATGGATGTGTTATGTGTAAATGCCAGCTATACCTGTCCAAAGCCTGACTTT	1137
Db	541	CAGCAGATGGATGTGTTATGTGTAAATGCCAGCTATACCTGTCCAAAGCCTGACTTT	600
QY	1138	ATCCCCGAGTCTCAATTTCTGCGTGTGCTGTGTGATGACAGCTTTTGTGAAAAATTTTG	1197
Db	601	ATCCCCGAGTCTCAATTTCTGCGGCTGTGCTGTGTGATGACAGCTTTTGTGAAAAATTTTG	660
QY	1198	CCGGGTGTGGACAAATCAGTAGATTTCAATTGAGAAAGCAAAAGCCTCAATGATGTT	1257
Db	661	CCGGGTGTGGACAAATCAGTAGATTTCAATTGAGAAAGCAAAAGCCTCAATGATGTT	720
QY	1258	CTAGTGCACTGTTTAgCTGGGAATCTCCCGCTCCGCCAACAATGCTATAGCTTACATCATG	1317
Db	721	CTAGTGCACTGTTTAgCTGGGAATCTCCCGCTCCGCCAACAATGCTATAGCTTACATCATG	780

QY 1318 AAGAGATGACATGCTTTTATGATGAGCTTACAGATTGTGAAAGAAAAAGACTACT 1377
 DB 781 AAGAGATGACATGCTTTTATGATGAGCTTACAGATTGTGAAAGAAAAAGACTACT 840
 QY 1378 ATATCTCCAACTTCAATTTTCTGGGCCAATCTCTGACCTATGAGAAAGATTAGAAC 1437
 DB 841 ATATCTCCAACTTCAATTTTCTGGGCCAATCTCTGACCTATGAGAAAGATTAGAAC 900
 QY 1438 CAGACTGAGAGATCAGGGCCAAAGAGCAAACTCAAGCTGTGACCTGAGAGGCAAT 1497
 DB 901 CAGACTGAGAGATCAGGGCCAAAGAGCAAACTCAAGCTGTGACCTGAGAGGCAAT 960
 QY 1498 GAACCTGTCCCTGTCTGTCTAGAGGGTGAAGAGAAAGAGAGAGCCCTCAGTCCACC 1557
 DB 961 GAACCTGTCCCTGTCTGTCTAGAGGGTGAAGAGAAAGAGAGAGCCCTCAGTCCACC 1020
 QY 1558 TGTGCTCACTCTGTCTAATCTAGAGGACAGAGCAAAAGCCCTGTGACCTCCGACGCTG 1617
 DB 1021 TGTGCTCACTCTGTCTAATCTAGAGGACAGAGCAAAAGCCCTGTGACCTCCGACGCTG 1080
 QY 1618 CCCAGCGTCCAGGCTGACAGCCGCTGTGAGAGAGAGCCGCTGTACAGGCGCTC 1677
 DB 1081 CCCAGCGTCCAGGCTGACAGCCGCTGTGAGAGAGAGCCGCTGTACAGGCGCTC 1140
 QY 1678 AGTGGCTGACCTGTCCGACAGAGGCTGGAAGAGAGCAATTAAGCTCAAGCTTCCCTTC 1737
 DB 1141 AGTGGCTGACCTGTCCGACAGAGGCTGGAAGAGAGCAATTAAGCTCAAGCTTCCCTTC 1200
 QY 1738 TCTCTGATATCAATCATGTTTCAATTTACAGCCAGATGAGAGCATCTTACATGCTTC 1797
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 QY 1798 TCCCTCATAGAGAGATGCTTTGGAATATCAAACTTCCATCTCTGAGAGGAGAGCAAC 1857
 DB 1261 TCCCTCATAGAGAGATGCTTTGGAATATCAAACTTCCATCTCTGAGAGGAGAGCAAC 1320
 QY 1858 AAGCTATGCGAGTTCTCCCTGTCTAGAGAGCTATCGAGAGACTCCCGAAACAGAGTCT 1917
 DB 1321 AAGCTATGCGAGTTCTCCCTGTCTAGAGAGCTATCGAGAGACTCCCGAAACAGAGTCT 1380
 QY 1918 GATTAAGAGAGAGCGAGATCTCCCAAGAGCTGACAGCCGACAGGCTTACAGAGCCAG 1977
 DB 1381 GATTAAGAGAGAGCGAGATCTCCCAAGAGCTGACAGCCGACAGGCTTACAGAGCCAG 1440
 QY 1978 AGCAAGGATGATGCTTGGGTGAGAAACAGAGAGAGTGGCAACCCGCAAGGTCCCTTTTA 2037
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 QY 2038 TCTCCATGATGATGAGAGGAGGAGGAGCAATTAACAGAGAGTCTCTTTTGGGC 2097
 DB 1501 TCTCCATGATGATGAGAGGAGGAGGAGGAGCAATTAACAGAGAGTCTCTTTTGGGC 1560
 QY 2098 CTTTTCACAGCCAGAGAGAGCTTACAGAGAGTCTGTGCTGTGGCTTTAAGGGCTGGCAC 2157
 DB 1561 CTTTTCACAGCCAGAGAGAGCTTACAGAGAGTCTGTGCTGTGGCTTTAAGGGCTGGCAC 1620
 QY 2158 TCGGATATCTTGGGCCCCCAAGACCTTACACCTTCCCTGACAGAGAGTGTATTTTGGC 2217
 DB 1621 TCGGATATCTTGGGCCCCCAAGACCTTACACCTTCCCTGACAGAGAGTGTATTTTGGC 1680
 QY 2218 ACAGAGTCTTCACTTCTAATCTGTGCTCAGAGCTTACAGAGAGGAGGAGGAGTAACTCT 2277
 DB 1681 ACAGAGTCTTCACTTCTAATCTGTGCTCAGAGCTTACAGAGAGGAGGAGGAGTAACTCT 1740
 QY 2278 GCCTACAGCTGACAGCTGCTCCCACTTGCAGAGACCAAGTCTATTCTGTGCGAGGCGG 2337
 DB 1741 GCCTACAGCTGACAGCTGCTCCCACTTGCAGAGACCAAGTCTATTCTGTGCGAGGCGG 1800
 QY 2338 CAGAGAGCAAGTGAAGAGCTGATCTCGGAGGAGAGCTGAGTGAAGAGAGCCCTTTGAA 2397
 DB 1801 CAGAGAGCAAGTGAAGAGCTGATCTCGGAGGAGAGCTGAGTGAAGAGAGCCCTTTGAA 1860
 QY 2398 AAGAGTTTAAACGAGAGCTGCCAATGGAATTTGAGAGAGATCATGTCAAGAAC 2457

DB 1861 AAGAGTTTAAACGAGAGCTGCCAATGGAATTTGAGAGAGATCATGTCAAGAAC 1920
 QY 2458 AGTTCACGGAGAGCTGGGGAAGTGGGCACTGACGTCTACTTTTGGGAGAGATGGA 2517
 DB 1921 AGTTCACGGAGAGCTGGGGAAGTGGGCACTGACGTCTACTTTTGGGAGAGATGGA 1980
 QY 2518 ATCATGAGGTCTCTGA 2535
 DB 1981 ATCATGAGGTCTCTGA 1998
 RESULT 30
 US-10-377-072-27
 ; Sequence 27, Application US/10377072
 ; Publication No. US20040157221A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals Inc.
 ; APPLICANT: Curtis, Rory A. J.
 ; APPLICANT: Logan, Thomas Joseph
 ; APPLICANT: Glucksmann, Maria A.
 ; APPLICANT: Meyers, Rachel E. J.
 ; APPLICANT: Williamson, Mark J.
 ; APPLICANT: Rudolph-Owen, Laura A.
 ; APPLICANT: Chun, Miyoung
 ; APPLICANT: Tsai, Fong-Ying
 ; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
 ; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
 ; FILE REFERENCE: MP103-0180NMIM
 ; CURRENT APPLICATION NUMBER: US/10/377, 072
 ; CURRENT FILING DATE: 2003-02-27
 ; PRIOR APPLICATION NUMBER: US 09/895, 860
 ; PRIOR FILING DATE: 2001-06-29
 ; PRIOR APPLICATION NUMBER: US 60/215, 370
 ; PRIOR FILING DATE: 2000-06-29
 ; PRIOR APPLICATION NUMBER: US 09/723, 806
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: US 60/187, 455
 ; PRIOR FILING DATE: 2000-03-07
 ; PRIOR APPLICATION NUMBER: US 09/843, 297
 ; PRIOR FILING DATE: 2001-04-25
 ; PRIOR APPLICATION NUMBER: US 60/199, 801
 ; PRIOR FILING DATE: 2000-04-26
 ; PRIOR APPLICATION NUMBER: US 09/861, 801
 ; PRIOR FILING DATE: 2001-05-21
 ; PRIOR APPLICATION NUMBER: US 60/205, 508
 ; PRIOR FILING DATE: 2000-05-19
 ; PRIOR APPLICATION NUMBER: US 09/816, 494
 ; PRIOR FILING DATE: 2001-03-23
 ; PRIOR APPLICATION NUMBER: US 09/815, 419
 ; PRIOR FILING DATE: 2001-03-22
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 114
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 27
 ; LENGTH: 1998
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1998)
 ; US-10-377-072-27
 Query Match 34.8%; Score 1896; DB 18; Length 1998;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1996; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 538 ATGGCCCATGAGATGATTTGGAATCTCAATTTTACTAGAGAGTGTGGCTCTCTGGA 597
 DB 1 ATGGCCCATGAGATGATTTGGAATCTCAATTTTACTAGAGAGTGTGGCTCTCTGGA 60
 QY 598 AGTGAACGGAAGAGCTGCTAATGATAGCCGACATTTGTGAAATCAATATATCC 657

Db 61 AGTGAACGGAAAAAGTGTCTAATTGATAGCCGGCAATTTGTGAATACATATC 120
QY 658 CACATTTTGGAAACCATTAATATCACTGCTCCAGCTTAATGAAGGAAAGTTGCAACG 717
Db 121 CACATTTTGGAAACCATTAATATCACTGCTCCAGCTTAATGAAGGAAAGTTGCAACG 180
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Db 181 GACAAAGTGAATTAATACAGAGCTCATCCAGCATTCAGCGCAATATGAAGTTGACATGAT 240
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Db 241 TGCAGTCAAGAGTTGATTAACGATCAAAAGCTCCCAAGATGTTGCTCTCTCTTCA 300
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QY 1738 TCTCTGATATCAAAATCAGTTTCATATTCAGCCAGCATGAGCATCTTACATGCTTC 1797
Db 1201 TCTCTGATATCAAAATCAGTTTCATATTCAGCCAGCATGAGCATCTTACATGCTTC 1260
QY 1798 TCTCTGATAGAAAGTCTTTGGAATPACTACAAACCTTCCTACTCTGAGATGGAACCAAC 1857
Db 1261 TCTCTGATAGAAAGTCTTTGGAATPACTACAAACCTTCCTACTCTGAGATGGAACCAAC 1320
QY 1858 AAGCTATGCAAGTCTCCCTGTGTGAGAACTATCGAGAGCATGCTCCGAAACAGTCTC 1917
Db 1321 AAGCTATGCAAGTCTCCCTGTGTGAGAACTATCGAGAGCATGCTCCGAAACAGTCTC 1380
QY 1918 GATTAAGAGGAAGCCAGCATTCCTCAAGAGCTGCAAGCCGACAGCTTTCAGACGCAAG 1977
Db 1381 GATTAAGAGGAAGCCAGCATTCCTCAAGAGCTGCAAGCCGACAGCTTTCAGACGCAAG 1440
QY 1978 AGCAAGGCAATGCAATGCGGTGAGAACAGACAGAGTGGCAACCGCCAGAGGTCCCTTTA 2037
Db 1441 AGCAAGGCAATGCAATGCGGTGAGAACAGACAGAGTGGCAACCGCCAGAGGTCCCTTTA 1500
QY 2038 TCTCCACTGATCGAAGTGGAGGCGTGGAGACATTAACCAACAGCTTCTTTTGGC 2097
Db 1501 TCTCCACTGATCGAAGTGGAGGCGTGGAGACATTAACCAACAGCTTCTTTTGGC 1560
QY 2098 CTTTCCACAGCCAGCGACACTTCAGCAAGTCTGCTGGGCTTGAAGGCTGGCAC 2157
Db 1561 CTTTCCACAGCCAGCGACACTTCAGCAAGTCTGCTGGGCTTGAAGGCTGGCAC 1620
QY 2158 TCGGATATCTTTGGCCCCCAGCACTCTAACCCCTTCCCTGACAGAGCTGTAATTTTGGC 2217
Db 1621 TCGGATATCTTTGGCCCCCAGCACTCTAACCCCTTCCCTGACAGAGCTGTAATTTTGGC 1680
QY 2218 ACAGAGTCTCAACATTTCTACTGTGCTCAGCCATCTACGAGAGCAAGTCACTCT 2277
Db 1681 ACAGAGTCTCAACATTTCTACTGTGCTCAGCCATCTACGAGAGCAAGTCACTCT 1740
QY 2278 GCTTACAGCTGACAGCCAGCGTCCCACTTGGGAGAACCAAGTCTAATCTGTGGCAGAGCG 2337
Db 1741 GCTTACAGCTGACAGCCAGCGTCCCACTTGGGAGAACCAAGTCTAATCTGTGGCAGAGCG 1800
QY 2338 CAGAGCCAAAGTACAGAGCTGACTCGCGCGAGCTGAGATGAAGAGAGCCCTTTGAA 2397
Db 1801 CAGAGCCAAAGTACAGAGCTGACTCGCGCGAGCTGAGATGAAGAGAGCCCTTTGAA 1860
QY 2398 AAGCAGTTTAAACGACAGAGCTGCCAATGGAATTTGAGAGAGCATGTTCAGAAAC 2457
Db 1861 AAGCAGTTTAAACGACAGAGCTGCCAATGGAATTTGAGAGAGCATGTTCAGAAAC 1920
QY 2458 AGGTCAAGGGAAGAGCTGGGGAAGAGGCGCAGTCACTTTCGGGCGAGCATGGA 2517
Db 1921 AGGTCAAGGGAAGAGCTGGGGAAGAGGCGCAGTCACTTTCGGGCGAGCATGGA 1980
QY 2518 ATCATTGAAGTCTCTGA 2535
Db 1981 ATCATTGAAGTCTCTGA 1998

RESULT 31
US-10-094-749-673
; Sequence 673, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAT, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI

```

1  APPLICANT: OTSUKA, KAORU
2  APPLICANT: NAGAI, KEIICHI
3  APPLICANT: IRIE, RYOTARO
4  APPLICANT: TAMECHIKA, ICHIRO
5  APPLICANT: SEKI, NAOHICO
6  APPLICANT: YOSHIKAWA, TSUTOMU
7  APPLICANT: OTSUKA, MOTOKYUKI
8  APPLICANT: NAGAHARI, KENJII
9  APPLICANT: MASUHO, YASUHIKO
10 TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
11 FILE REFERENCE: 084335/0160
12 CURRENT APPLICATION NUMBER: US/10/094,749
13 CURRENT FILING DATE: 2002-03-12
14 PRIOR APPLICATION NUMBER: 60/350,435
15 PRIOR FILING DATE: 2002-01-24
16 PRIOR APPLICATION NUMBER: JP 2001-328361
17 PRIOR FILING DATE: 2001-09-14
18 NUMBER OF SEQ ID NOS: 3381
19 SOFTWARE: PatentIn Ver. 2.1
20 SEQ ID NO 673
21 LENGTH: 2102
22 TYPE: DNA
23 ORGANISM: Homo sapiens
24 US-10-094-749-673

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Query Match	34.78	Score 1889	DB 17	Length 2102
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QY	483	TACATCATCGTGGCAAAATTAAAGAGAGAGTGGGAAAAGAGACCTTATGTGTGTCATGGC	542
Db	1	TACATCATCGTGGCAAAATTAAAGAGAGTGGGAAAAGAGACCTTATGTGTGTCATGGC	60
QY	543	CCATGAGATGATTTGGAACTCAAAATTGTTACTGAGAGTTGTGTGCTCTGTGGAAAGTGG	602
Db	61	CCATGAGATGATTTGGAACTCAAAATTGTTACTGAGAGTTGTGTGCTCTGTGGAAAGTGG	120
QY	603	AAACGAAAAAAGTCGCTGCTTAATTGATTAAGCCGGCACTTTGTGGAAATCAATACATCCCAAT	662
Db	121	AAACGAAAAAAGTCGCTGCTTAATTGATTAAGCCGGCACTTTGTGGAAATCAATACATCCCAAT	180
QY	663	TTTGGAAACCATTTAATATCAACTGCTCCAGACTTATGGAAGCAAGTGTGCAACAGACAA	722
Db	181	TTTGGAAACCATTTAATATCAACTGCTCCAGACTTATGGAAGCAAGTGTGCAACAGACAA	240
QY	723	AGCTTAATTAACAAGCTCATTCAGACATTCAGCGAAACATAAGTTGACATTTGATTTGACG	782
Db	241	AGCTTAATTAACAAGCTCATTCAGACATTCAGCGAAACATAAGTTGACATTTGATTTGACG	300
QY	783	TCACAAGGTTGTAGTTAAGTTAAGATCAAAAGCTCCCAAAATGTGTGCTCTCTCTTCACAGCTG	842
Db	301	TCACAAGGTTGTAGTTAAGTTAAGATCAAAAGCTCCCAAAATGTGTGCTCTCTCTTCACAGCTG	360
QY	843	TTTTCTCACTGTACTTCGGGTAAACTGGAAGAGAGCTTCAACTGTGTCACTGCTGTGC	902
Db	361	TTTTCTCACTGTACTTCGGGTAAACTGGAAGAGAGCTTCAACTGTGTCACTGCTGTGC	420
QY	903	AGGTGGGTTTGTGTGATCTCTCGTTGTTTCCGTGGCTCTGTGAAGAAAATCCACTCT	962
Db	421	AGGTGGGTTTGTGTGATCTCTCGTTGTTTCCGTGGCTCTGTGAAGAAAATCCACTCT	480
QY	963	AGTCCCTATCCGCAATTTCTCAAGCCTGTGCTAACCTGTGCGCAACATTTGGGCCAACCCGAT	1022
Db	481	AGTCCCTATCCGCAATTTCTCAAGCCTGTGCTAACCTGTGCGCAACATTTGGGCCAACCCGAT	540
QY	1023	TCTTCCCAATCTTATCTTGGCTGCGACGAGATGCTCTCAACAAAGAGCTGATACACA	1082
Db	541	TCTTCCCAATCTTATCTTGGCTGCGACGAGATGCTCTCAACAAAGAGCTGATACACA	600
QY	1083	GAATGGGATTTGGTTATGTGTTAAAGCAGAGTATCTGTCCAAAGCCTGACTTATATCC	1144
Db	601	GAATGGGATTTGGTTATGTGTTAAAGCAGAGTATCTGTCCAAAGCCTGACTTATATCC	660

[illegible]

Db 1741 GTCTCACTCTACTCTCTCTCAGCCATCTAAGAGGCGAGGTCAGTTACTCTCTCTA 1800
Qy 2283 CAGGTGAGCGACGTGCGCCACTTGGCGAGACCAAGCTATTTCTGTGCGAGGCGGAGAA 2342
Db 1801 CAGGTGAGCGACGTGCGCCACTTGGCGAGACCAAGCTATTTCTGTGCGAGGCGGAGAA 1860
Qy 2343 GCCAAGTGAAGAGCTGACTCGCGGCGAGCTGCGATGAAAGAGGCCCTTTGAAAAGCA 2402
Db 1861 GCCAAGTGAAGAGCTGACTCGCGGCGAGCTGCGATGAAAGAGGCCCTTTGAAAAGCA 1920
Qy 2403 GTTTAAACGAGAACTGCTCCAAATGGAATTTGAGAGAGCATATGTCAAGAAACAGTTC 2462
Db 1921 GTTTAAACGAGAACTGCTCCAAATGGAATTTGAGAGAGCATATGTCAAGAAACAGTTC 1980
Qy 2463 ACCGGAAGAGCTGGGGAAGAGTGGGAGTCACTAGTCTTTGGGCGAGATGGAATCAT 2522
Db 1981 ACCGGAAGAGCTGGGGAAGAGTGGGAGTCACTAGTCTTTGGGCGAGATGGAATCAT 2040
Qy 2523 TGAAGTCTCTGAGAAAGAACACTTGTGACTTCTATAGACAATTTTTTTT 2575
Db 2041 TGAAGTCTCTGAGAAAGAACACTTGTGACTTCTATAGACAATTTTTTTT 2093

RESULT 32
US-10-108-260A-2429
; Sequence 2429, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2429
; LENGTH: 1916
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-2429

Query Match 27.3%; Score 1486; DB 17; Length 1916;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1776; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Qy 1694 CCGCAGACAGGCTGGAGAGACAGCATTAAGCTCAAGCTTCTCTCTGGAATTCAAAT 1753
Db 140 CCGCAGACAGGCTGGAGAGACAGCATTAAGCTCAAGCTTCTCTCTGGAATTCAAAT 199
Qy 1754 CAGTTTCATTTACGCCGACATGCGAGCATCTTATCATGCTTCTCTCATCAGAAAGT 1813
Db 200 CAGTTTCATTTACGCCGACATGCGAGCATCTTATCATGCTTCTCTCATCAGAAAGT 259
Qy 1814 CTTTGAATATCTAACAACCTTCACTACTCTGANTGGAGCAACAAGTATGCCAGTTCT 1873
Db 260 CTTTGAATATCTAACAACCTTCACTACTCTGANTGGAGCAACAAGTATGCCAGTTCT 319
Qy 1874 CCCCCTTTACAGAACTATCGAGAGACACTCCGAAACAGTCTCTGATTAAGAGAGCA 1933
Db 320 CCCCCTTTACAGAACTATCGAGAGACACTCCGAAACAGTCTCTGATTAAGAGAGCA 379
Qy 1934 GCATCCCCCAAGAACTGACACCGCCAGGCTTCAAGACGCGAGAGCAAGGATTCATT 1993
Db 380 GCATCCCCCAAGAACTGACACCGCCAGGCTTCAAGACGCGAGAGCAAGGATTCATT 439
Qy 1994 CGATCAGAACCGAGAGAGTGGACCGCGCCAGAGTCCCTTTATCTCCACTGATGAA 2053
Db 440 CGATCAGAACCGAGAGAGTGGACCGCGCCAGAGTCCCTTTATCTCCACTGATGAA 499
Qy 2054 GTGGAGCGTGGAGAGCAATTAACCAACAGCTTCTTTTCGCGCTTCCACAGCCAGC 2113
Db 500 GTGGAGCGTGGAGAGCAATTAACCAACAGCTTCTTTTCGCGCTTCCATCAGCCAGC 559

Qy 2114 AGCACTTCAAGAAAGTCTGCTGAGCTGGGCTTTAAAGGCTGGCACTCGGATATCTTGGCCC 2173
Db 560 AGCACTTCAAGAAAGTCTGCTGAGCTGGGCTTTAAAGGCTGGCACTCGGATATCTTGGCCC 619
Qy 2174 CCCAAGCTCTAACCCCTTCCCTGACCAAGCAGCTGTATTTTGGCAAGAGTCCACACT 2233
Db 620 CCCAAGCTCTAACCCCTTCCCTGACCAAGCAGCTGTATTTTGGCAAGAGTCCACACT 679
Qy 2234 TCTACTGCTCTCAGCCATCTACGAGAGCAGTGCAGTTACTCTGCTTACAGTGCAGCC 2293
Db 680 TCTACTGCTCTCAGCCATCTACGAGAGCAGTGCAGTTACTCTGCTTACAGTGCAGCC 739
Qy 2294 AGCTGCCCACTTGGGAGACCAAGTATTTCTGTGCGCAGGCGGACAGACCAAGTACA 2353
Db 740 AGCTGCCCACTTGGGAGACCAAGTATTTCTGTGCGCAGGCGGACAGACCAAGTACA 799
Qy 2354 GAGCTGACTCGCGCGAGAGTGCATGAGAGAGCCCTTTGAAAAGCAAGTTAAACGA 2413
Db 800 GAGCTGACTCGCGCGAGAGTGCATGAGAGAGCCCTTTGAAAAGCAAGTTAAACGA 859
Qy 2414 GAAGCTGCAAAATGGAATTTGAGAGAGCATCATGTCAAGAAACAGGTCACGGAAAGC 2473
Db 860 GAAGCTGCAAAATGGAATTTGAGAGAGCATCATGTCAAGAAACAGGTCACGGAAAGC 919
Qy 2474 TGGGGAAGTGGGCGAGTCACTAGCTTTTGGGCGAGCAAGGAATCATAGAGTCTCT 2533
Db 920 TGGGGAAGTGGGCGAGTCACTAGCTTTTGGGCGAGCAAGGAATCATAGAGTCTCT 979
Qy 2534 GAGAAAGAAACACTTGTGACTTCTATAGACAATTTTTTTTCTTGTTCACAAAAAAT 2593
Db 980 GAGAAAGAAACACTTGTGACTTCTATAGACA - TTTTTTTTCTTGTTCACAAAAAAT 1038
Qy 2594 TCCCTGTAATCTGAAAT 2653
Db 1039 TCCCTGTAATCTGAAAT 1098
Qy 2654 TGGTGTAAAGCAACAGTGGATCAACCCAGTGTACTCTCTTAAACATGTGATTTGAG 2713
Db 1099 TGGTGTAAAGCAACAGTGGATCAACCCAGTGTACTCTCTTAAACATGTGATTTGAG 1158
Qy 2714 AGATCAGCTAATATCTTCTCAACAAAAATGGAAGGCGAGATGTAGAAATCCCCCTAGA 2773
Db 1159 AGATCAGCTAATATCTTCTCAACAAAAATGGAAGGCGAGATGTAGAAATCCCCCTAGA 1218
Qy 2774 CGAGAGAAACCAATTTATAGTGAATTAACATCTCTTGTCTTAAAAAAGCAAGT 2833
Db 1219 CGAGAGAAACCAATTTATAGTGAATTAACATCTCTTGTCTTAAAAAAGCAAGT 1278
Qy 2834 TCTTGGTGTGGAGGACAAAATCCCTTACCAATTTTCAAGTGTGCTAAGAGATCTC 2893
Db 1279 TCTTGGTGTGGAGGACAAAATCCCTTACCAATTTTCAAGTGTGCTAAGAGATCTC 1338
Qy 2894 AAATATATAGTCTTGTCCGAGCCCTTCAATAGTACCTTACGCTGAGATGAGCCAGC 2953
Db 1339 AAATATATAGTCTTGTCCGAGCCCTTCAATAGTACCTTACGCTGAGATGAGCCAGC 1398
Qy 2954 TTGGGGGTGAGGTAGTAGACCTGTGTAGGAGCAGAGCTTATGTGTAATCCAAAGAA 3013
Db 1399 TTGGGGGTGAGGTAGTAGACCTGTGTAGGAGCAGAGCTTATGTGTAATCCAAAGAA 1458
Qy 3014 TGAATCTATCAAAAGGTATTCACAAACCAAGCTTACCTGACACCGAGGAGCAGAGC 3073
Db 1459 TGAATCTATCAAAAGGTATTCACAAACCAAGCTTACCTGACACCGAGGAGCAGAGC 1518
Qy 3074 ATCACTCTGCTGAGAGGACCAATTAAGGGGCTTTGCCAAGGTCTAAGAGCAACCAAG 3133
Db 1519 ATCACTCTGCTGAGAGGACCAATTAAGGGGCTTTGCCAAGGTCTAAGAGCAACCAAG 1578
Qy 3134 TACCTCAGACAGGAAGTGGGGGCTTTGACCACTACATCTGTGTAGCCCATTTTCTAG 3193
Db 1579 TACCTCAGACAGGAAGTGGGGGCTTTGACCACTACATCTGTGTAGCCCATTTTCTAG 1638

Qy 3194 GCATTGCAATAGTAGTAGTACTACTACATTTTTCAGACCAATTCATGCTATGCA 3253
Db 1639 GCATTGCAATAGTAGTAGTACTACTACATTTTTCAGACCAATTCATGCTATGCA 1698
Qy 3254 CAAATTCCTGCGGCTAGATGAGATATTTTTCCTTCAGCTTTATGAGAGA 3313
Db 1699 CAAATTCCTGCGGCTAGATGAGATATTTTTCCTTCAGCTTTATGAGAGA 1757
Qy 3314 AGGAAATGCTCTGAGTTCAGCTGACCAACCAAGACCTGCAACATCAGATTAGC 3373
Db 1758 AGGAAATGCTCTGAGTTCAGCTGACCAACCAAGACCTGCAACATCAGATTAGC 1817
Qy 3374 TAAGTTGGAGGCTTAACGAGTCTACCTCCTTTGTAATCAAGATTGTTAAAT 3433
Db 1818 TAAGTTGGAGGCTTAACGAGTCTACCTCCTTTGTAATCAAGATTGTTAAAT 1877
Qy 3434 GGGATTGCAATCCTTTAAATTAAGATGAACCTGTTTC 3472
Db 1878 GGGATTGCAATCCTTTAAATTAAGATGAACCTGTTTC 1916

RESULT 33
US-10-072-012-257
; Sequence 257, Application US/10072012
; Publication No. US2004003493A1
GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zehrhusen, Bryan
APPLICANT: Paturajan, Meera
APPLICANT: Shinkens, Richard
APPLICANT: Li, Li
APPLICANT: Gangolli, Beha
APPLICANT: Padigaru, Muralidhara
APPLICANT: Anderson, David W.
APPLICANT: Raestelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Coleman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grose, William M.
APPLICANT: Alsbrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OR INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072, 012
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 257
; LENGTH: 2071
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-012-257

Query Match 24.2%; Score 1318; DB 17; Length 2071;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2068; Conservative 0; Mismatches 3; Indels 9; Gaps 1;

Qy 478 ACCATTACATCATGCTGGCAATTAAGAAAGAGGTGGAAAGAGCAATTATGTTGC 537
Db 1 ACCATTACATCATGCTGGCAATTAAGAAAGAGGTGGAAAGAGCAATTATGTTGC 60
Qy 538 ATGGCCCATGAGATGATGGAATCAATTTGTAATGTAAGAGTTGGTGGCTCTGTGAA 597
Db 61 ATGGCCCATGAGATGATGGAATCAATTTGTAATGTAAGAGTTGGTGGCTCTGTGAA 120
Qy 598 AGTGAACGAAAAAGTCTCTAATGATAGCCGGCCATTGGGAATACATATATCC 657
Db 121 AGTGAACGAAAAAGTCTCTAATGATAGCCGGCCATTGGGAATACATATATCC 180
Qy 658 CACATTTGGAAGCATTAATATCACTGCTCAAGCTTATGAAGCGAAGGTGCAACG 717
Db 181 CACATTTGGAAGCATTAATATCACTGCTCAAGCTTATGAAGCGAAGGTGCAACG 240
Qy 718 GACAAAGTGAATTAACAGAGCTCATCAGCATTCAGGAAACATTAAGTTGACATTGAT 777
Db 241 GACAAAGTGAATTAACAGAGCTCATCAGCATTCAGGAAACATTAAGTTGACATTGAT 300
Qy 778 TGCACTCAAGAGTTGTAAGTTAAGATGAAGCTCCCAAGATGTTGCTCTCTCTCA 837
Db 301 TGCACTCAAGAGTTGTAAGTTAAGATGAAGCTCCCAAGATGTTGCTCTCTCTCA 360
Qy 838 GACTGTTTTCACGTACTCTGGGTAACTGGGAAAGAGCTTCACTCTGTCACCTG 897
Db 361 GACTGTTTTCACGTACTCTGGGTAACTGGGAAAGAGCTTCACTCTGTCACCTG 420
Qy 898 CTTCAGAGTGGTTGCTGAGTCTCTGTTGTTCCCTGAGCTCTGTGAAGAAATCC 957
Db 421 CTTCAGAGTGGTTGCTGAGTCTCTGTTGTTCCCTGAGCTCTGTGTGAAGAAATCC 480
Qy 958 ACTCTAGTCCCTACCTGATTTCTCAGCTTGTCTTACCTGTTGCCACATTTGGCCAAAC 1017
Db 481 ACTCTAGTCCCTACCTGATTTCTCAGCTTGTCTTACCTGTTGCCACATTTGGCCAAAC 540
Qy 1018 CGAATTTCTCCCATCTTATCTTGGCTGCGCAAGAGATGTCMAACAAGAGCTGATA 1077
Db 541 CGAATTTCTCCCATCTTATCTTGGCTGCGCAAGAGATGTCMAACAAGAGCTGATA 600
Qy 1078 CAGCAGATGGAGTTGTTATGTTAAATSCAGACTTACCTGTCCAAAGCCTGACTTT 1137
Db 601 CAGCAGATGGAGTTGTTATGTTAAATSCAGACTTACCTGTCCAAAGCCTGACTTT 660
Qy 1138 ATCCCCGAGTCAATTTCTGCGTGTGCTGTGAATGACAGCTTTTGTGAAGAAATTTTG 1197
Db 661 ATCCCCGAGTCAATTTCTGCGTGTGCTGTGAATGACAGCTTTTGTGAAGAAATTTTG 720
Qy 1198 CCGTGTGGAACAATCAGTATGATTTCAATGAAGAAAGAAAGCTCCAAAGAGATGCTT 1257
Db 721 CCGTGTGGAACAATCAGTATGATTTCAATGAAGAAAGAAAGCTCCAAAGAGATGCTT 780
Qy 1258 CTATGCACTGTTAGCTGGGATCTCCGCTCCGCAACATGCTATGCTATCATCATG 1317
Db 781 CTATGCACTGTTAGCTGGGATCTCCGCTCCGCAACATGCTATGCTATCATCATG 840
Qy 1318 AAGAGATGACATGCTTTTATGATGAAGCTTACAGATTTGTGAAGAAAGAAAGCTTACT 1377
Db 841 AAGAGATGACATGCTTTTATGATGAAGCTTACAGATTTGTGAAGAAAGAAAGCTTACT 900

QY 1378 ATATCTCAAACTTCAATTTTCTGGGCCAACTCTGAGCTATGAGAAGATTAAAGAC 1437
DB 901 ATATCTCAAACTTCAATTTTCTGGGCCAACTCTGAGCTATGAGAAGATTAAAGAC 960
QY 1438 CAGATCGAGCATCAGGGGCCAAGAGCAACTCAGCTGTGTGCACTTGAGAAAGCCAAAT 1497
DB 961 CAGATCGAGCATCAGGGGCCAAGAGCAACTCAGCTGTGTGCACTTGAGAAAGCCAAAT 1020
QY 1498 GAACTGTCTCTGTCTCTGAGAGGTGAGCAGAAAAGGAGAGCCCTCGAGTCCACCC 1557
DB 1021 GAACCTGTCTCTGTCTCTGAGAGGTGAGCAGAAAAGGAGAGCCCTCGAGTCCACCC 1080
QY 1558 TGTGCGCATCTCTCTCTCTCAGAGCAGAGCAAAAGCCCGTGCATCCCGCAGCCGTG 1617
DB 1081 TGTGCGCATCTCTCTCTCTCAGAGCAGAGCAAAAGCCCGTGCATCCCGCAGCCGTG 1132
QY 1618 CCCAGGCTGCGCAGCGGTGAGCCGTGTGTGAGAGCAGAGCCCGTGTGAGAGCGCTC 1677
DB 1133 -CCAGGCTGCGCAGCGGTGAGCCGTGTGTGAGAGCAGAGCCCGTGTGAGAGCGCTC 1191
QY 1678 AGTGGGCTGCACTCTCTGCGCAGAGAGCTGGAAGCAGCAATTAAGCTCAAGGCTTCC 1737
DB 1192 AGTGGGCTGCACTCTCTGCGCAGAGAGCTGGAAGCAGCAATTAAGCTCAAGGCTTCC 1251
QY 1738 TCTCTGAGATCAAAATCAATTTTCAATTTTCAAGCAGAGCTGCAAGTCTTACATG 1797
DB 1252 TCTCTGAGATCAAAATCAATTTTCAATTTTCAAGCAGAGCTGCAAGTCTTACATG 1311
QY 1798 TCTCTCACTGAGAGATCTTGTGAAATCTCAAACTTCCACTCTGAGAGTGGAGCAAC 1857
DB 1312 TCTCTCACTGAGAGATCTTGTGAAATCTCAAACTTCCACTCTGAGAGTGGAGCAAC 1371
QY 1858 AAGCTATGCAAGTCTTCTCTGTGTTGAGAACTATCGAGCAGACTCCGAAACCACTGCT 1917
DB 1372 AAGCTATGCAAGTCTTCTCTGTGTTGAGAACTATCGAGCAGACTCCGAAACCACTGCT 1431
QY 1918 GATTAAGGAGGAGCAGAGCATCTCCCAAGAGCTGAGACCCGAGGCTTTCAGACCCAG 1977
DB 1432 GATTAAGGAGGAGCAGAGCATCTCCCAAGAGCTGAGACCCGAGGCTTTCAGACCCAG 1491
QY 1978 AAGCAAGCATGTCATCTGCTGAGAACTGAGCAGAGCAGTGGCAGCCGAGAGGCTCTTTA 2037
DB 1492 AAGCAAGCATGTCATCTGCTGAGAACTGAGCAGAGCAGTGGCAGCCGAGAGGCTCTTTA 1551
QY 2038 TCTCACTGTCATCGAAGTGGAGCGGTGAGAGCAATTAACAACAGGCTTCTTTTGGCC 2097
DB 1552 TCTCACTGTCATCGAAGTGGAGCGGTGAGAGCAATTAACAACAGGCTTCTTTTGGCC 1611
QY 2098 CTTTCACAGCAGCAGCAGACCTCAAGAGTCTGCTGGCCCTTAAAGGCTGGCAG 2157
DB 1612 CTTTCACAGCAGCAGCAGACCTCAAGAGTCTGCTGGCCCTTAAAGGCTGGCAG 1671
QY 2158 TCGGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACACAGAGCTGTATTTTGGC 2217
DB 1672 TCGGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACACAGAGTGTATTTTGGC 1731
QY 2218 ACAAGTCTCTCACTTCTTACTCTGCTCAAGCCTTACGAGAGCAGTGGCAGTACTCT 2277
DB 1732 ACAAGTCTCTCACTTCTTACTCTGCTCAAGCCTTACGAGAGCAGTGGCAGTACTCT 1791
QY 2278 GCTTACAGCTGACAGCAGCTGCCCACTTGGGAGAGCAAGCTTCTGTTGCGGAGGCGG 2337
DB 1792 GCTTACAGCTGACAGCAGCTGCCCACTTGGGAGAGCAAGCTTCTGTTGCGGAGGCGG 1851
QY 2338 CAGAGCCAAAGTGAACAAGCTGACTGCGCGGAGAGCTGAGCAAGAGAGAGAGCCCTTTGAA 2397
DB 1852 CAGAGCCAAAGTGAACAAGCTGACTGCGCGGAGAGCTGAGCAAGAGAGAGAGCCCTTTGAA 1911
QY 2398 AAGCAGTTTAAACGACAGAGTGGCAATGGAATTTTGAAGAGCATCATGTGAGAGAC 2457
DB 1912 AAGCAGTTTAAACGACAGAGTGGCAATGGAATTTTGAAGAGCATCATGTGAGAGAC 1971
QY 2458 AAGTCAAGGAGAGAGCTGGGAGAAAGTGGGAGTCAAGTCTTTCGGGAGAGATGGA 2517

DB 1972 AGTCAAGGAGAGAGCTGGGAGAGTGGGAGTCAAGTCTTCTGCGGAGAGTGA 2031
QY 2518 ATCATTTAGGTCTCTCTGAGAGAGAGACATTTGTGACTTC 2557
DB 2032 ATCATTTAGGTCTCTCTGAGAGAGAGACATTTGTGACTTC 2071

RESULT 34
US-10-072-012-255
Sequence 255, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
APPLICANT: Tcherev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zernusen, Bryan
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard
APPLICANT: Li, Li
APPLICANT: Gangolli, Esha
APPLICANT: Padigaru, Muralidhara
APPLICANT: Anderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Coiman, Steven D.
APPLICANT: Wolenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072, 012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265, 102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265, 514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265, 517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265, 412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265, 395
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266, 406
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266, 767
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267, 057
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266, 975
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267, 459
PRIOR FILING DATE: 2001-02-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 255
LENGTH: 2200
TYPE: DNA
ORGANISM: Homo sapiens
US-10-072-012-255

Query Match 22.5%; Score 1225; DB 17; Length 2200;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1351	AGATTGGAGAGAAAAAGACCTCACTATATCTCCAAACTTCAATTTTCTGGGCGCAATC	1411
Db	919	AGATTGGAGAGAAAAAGACCTCACTATATCTCCAAACTTCAATTTTCTGGGCGCAATC	978
QY	1411	CTGCACTATGAGAGAGATTAAAGACGAGCTGGAGCATCAGGGCCAAAGCAATCTC	1470
Db	979	CTGCACTATGAGAGAGATTAAAGACGAGCTGGAGCATCAGGGCCAAAGCAATCTC	1038
QY	1471	AACTGCTGACCTGGAGAGCCAAATGAACTGTTCCTGCTGTCTCAGAGGGTGGACAG	1530
Db	1039	AACTGCTGACCTGGAGAGCCAAATGAACTGTTCCTGCTGTCTCAGAGGGTGGACAG	1098
QY	1531	AAAAAGGAGAGGGCCCTCAGTCCACCCTGTGCGCATCTGTCACCTCGAAGGACGACGGA	1590
Db	1099	AAAAAGGAGAGGGCCCTCAGTCCACCCTGTGCGCATCTGTCACCTCGAAGGACGACGGA	1158
QY	1591	CAAAAGCCCGCTGATCCCGCCAGCGTGGCCACAGCGTCCACAGCGTCCAGCCGTGTTA	1650
Db	1159	CAAAAGCCCGCTGATCCCGCCAGCGTGGCCACAGCGTCCACAGCGTCCAGCCGTGTTA	1218
QY	1651	GAGGACAGCCCGCTGATCAGGCGCTCAGTGGGCTGCACCTGTCCGACGACGAGCTGGA	1710
Db	1219	GAGGACAGCCCGCTGATCAGGCGCTCAGTGGGCTGCACCTGTCCGACGACGAGCTGGA	1278
QY	1711	GACGCAATTAAGCTCAACCGTTCTCTCTCTGATATCAATCAGTTCTATTTACACC	1770
Db	1279	GACGCAATTAAGCTCAACCGTTCTCTCTCTGATATCAATCAGTTCTATTTACACC	1338
QY	1771	AGCATGGCAGCATCTTCAATGACTTCTCTCATCAGAAAGATGCTTGGATATCAAA	1830
Db	1339	AGCATGGCAGCATCTTCAATGACTTCTCTCATCAGAAAGATGCTTGGATATCAAA	1398
QY	1831	CTTTCGACTACTTGGATGGAGCAACCAAGCTATGCAATTCCTCCCTGTTCAGAACTA	1890
Db	1399	CTTTCGACTACTTGGATGGAGCAACCAAGCTATGCAATTCCTCCCTGTTCAGAACTA	1458
QY	1891	TCGGAGCAGATCTCCCGAAACCAAGTCTCTATTAAGAGGAAAGCCAGATTCCTCAAGAGCTG	1950
Db	1459	TCGGAGCAGATCTCCCGAAACCAAGTCTCTATTAAGAGGAAAGCCAGATTCCTCAAGAGCTG	1518
QY	1951	CAGACCGCGCAGGCTTTCAGACAGCCAGAGCAATGCAATTCGGCTCAGAAACGACAGC	2010
Db	1519	CAGACCGCGCAGGCTTTCAGACAGCCAGAGCAATGCAATTCGGCTCAGAAACGACAGC	1578
QY	2011	AGTGGCACCGCCACAGAGTCCCTTTTATCTCCATGCTCATCGAAGTGGAGCGTGGAGGAC	2070
Db	1579	AGTGGCACCGCCACAGAGTCCCTTTTATCTCCATGCTCATCGAAGTGGAGCGTGGAGGAC	1638
QY	2071	AATTACACACACAGCTTCTTTTGGGCTTTTCACACAGCCAGACGACCTTACGAAAGTCT	2130
Db	1639	AATTACACACACAGCTTCTTTTGGGCTTTTCACACAGCCAGACGACCTTACGAAAGTCT	1698
QY	2131	GCTGGCCCTGGGCTTTAAGGGCTGGGACCTCGGATATCTTGGGCCCCCACAACCTTAAACCCCT	2190
Db	1699	GCTGGCCCTGGGCTTTAAGGGCTGGGACCTCGGATATCTTGGGCCCCCACAACCTTAAACCCCT	1758
QY	2191	TCCCTGACCAAGAGCTGTATTTTGGCCAGAGTCTTCAACTTCTTACTCTGTGCTCAGCC	2250
Db	1759	TCCCTGACCAAGAGCTGTATTTTGGCCAGAGTCTTCAACTTCTTACTCTGTGCTCAGCC	1818
QY	2251	ATCTACGAGGACAGTGCAGTTTACTCTGCTTACAGCTGCAGCCAGCTGCCACCTTTCGGA	2310
Db	1819	ATCTACGAGGACAGTGCAGTTTACTCTGCTTACAGCTGCAGCCAGCTGCCACCTTTCGGA	1878
QY	2311	GACCAAGCTATTTCTGTGCGCAGGCGGCGAAGCCAAATGACAGAGCTGACTCTCGCGGCG	2370
Db	1879	GACCAAGCTATTTCTGTGCGCAGGCGGCGAAGCCAAATGACAGAGCTGACTCTCGCGGCG	1938
QY	2371	AGCTGGCATGAAGAGAGCCCTTTTGAAGAAGATTAAACCAAGAGCTGCGCAATGGAA	2430
Db	1939	AGCTGGCATGAAGAGAGCCCTTTTGAAGAAGATTAAACCAAGAGCTGCGCAATGGAA	1998
QY	2431	TTTGAGAGAGCATCATGTCAAGAGAACGTTCACGGAGAGAGCTGGGAAAGTGGGCGAT	2490

Accession	Sequence	Position
Db	TTTGGAGAGGCAATCATGTCAAGAAACGGTCAACGGGAAGCTGGGGAAAAGTGGCAGT	2058
Qy	2491 CAGCTTCAGCTTTTGGGCGACATGGAATCATTTAGGTCCTCTGAGAAAGACACTTG	2550
Db	2059 CAGCTTCAGCTTTTGGGCGACATGGAATCATTTAGGTCCTCTGAGAAAGACACTTG	2118
Qy	2551 TGAATCTATGACAAATTTTTTTT	2575
Db	2119 TGAATCTATGACAAATTTTTTTT	2143

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RESULT 35
US-10-172-118-2599/c
Sequence 2599, Application US/10172118
Publication No. US2003022437A1
GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter
APPLICANT: Mao, Mao
APPLICANT: Roberts, Chris
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 2599
LENGTH: 940
TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Conf556574
DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-2599

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Query Match	17.2%	Score 940;	DB 17;	Length 940;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 940;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy	4206	GTATTTCTCTGTTTTGAGAAATGGACAGTTTTTTGACCAAGATGTGACTTCATGTTTCC	4265
Db	940	GTATTTCTCTGTTTTGAGAAATGGACAGTTTTTTGACCAAGATGTGACTTCATGTTTCC	881
Oy	4266	TATGTGACTTCTTAAACCAAGCAGAAATATATGACTCAACAGACCGACTTGGTTAT	4325
Db	880	TATGTGACTTCTTAAACCAAGCAGAAATATATGACTCAACAGACCGACTTGGTTAT	821
Oy	4326	GGGGATGATGAGCCGACAGACCTCACTAGTTGTGCACAAATAATGTCTATGATGGGGT	4385
Db	820	GGGGATGATGAGCCGACAGACCTCACTAGTTGTGCACAAATAATGTCTATGATGGGGT	761
Oy	4386	GTTAAAGTAAAGCAGAAAGGGGTCAGCCGATTTGTAATGTAATCTGGAAAGTGCTGCTCA	4445
Db	760	GTTAAAGTAAAGCAGAAAGGGGTCAGCCGATTTGTAATGTAATCTGGAAAGTGCTGCTCA	701
Oy	4446	ACGATTTGAGTTAGTTTTTATGATATATACATTGGAATCTTTAATCAGACATTTCTCAAGTTTC	4505
Db	700	ACGATTTGAGTTAGTTTTTATGATATATACATTGGAATCTTTAATCAGACATTTCTCAAGTTTC	641
Oy	4506	ACACAGTAGTTTTTGATGTTATGTACACACACCAAAATGTGTACAGTTCAACACACTTCC	4565
Db	640	ACACAGTAGTTTTTGATGTTATGTACACACACCAAAATGTGTACAGTTCAACACACTTCC	581
Oy	4566	AGAGTGTGTCATGCCCCAAACATGTTTAAGAAAGAAACAGTAGTCTCTTGCTTAACGA	4625
Db	580	AGAGTGTGTCATGCCCCAAACATGTTTAAGAAAGAAACAGTAGTCTCTCTGCTTAACGA	521

Qy	4626	TGTTTACAGAGGCTTTCGGGCACTTGGTTTAAATGAGCTTCGTCACTTTAAGGACTTCTCTT	4685
Db	520	TGTTTACAGAGGCTTTCGGGCACTTGGTTTAAATGAGCTTCGTCACTTTAAGGACTTCTCTT	461
Qy	4686	GGCACATGCTCCCTTCTCTGGAACGTGATGATGACACATCCACAGCCTTAAGGCT	4745
Db	460	GGCACATGCTCCCTTCTCTGGAACGTGATGATGACACATCCACAGCCTTAAGGCT	401
Qy	4746	GGTTCACTTGTGTGATATATCAATTCTTGGATCGAAGCTCCGTCGGAAGGGTGGC	4805
Db	400	GGTTCACTTGTGTGATATATCAATTCTTGGATCGAAGCTCCGTCGGAAGGGTGGC	341
Qy	4806	CTCGAGGAGAGGCTCTGAGAGCTGCTTGGATGCTTAAAGTGGGGGTGGGCTGGCTCTCT	4865
Db	340	CTCGAGGAGAGGCTCTGAGAGCTGCTTGGATGCTTAAAGTGGGGGTGGGCTGGCTCTCT	281
Qy	4866	TCAGCATGTAAATTTGGGAAAACCTCGCGTCTACTAGGGGTATACAGATGGTGATTTTAA	4925
Db	280	TCAGCATGTAAATTTGGGAAAACCTCGCGTCTACTAGGGGTATACAGATGGTGATTTTAA	221
Qy	4926	AAGCAAAACTAGACTTCTTATGTGAAAGTCTGGAATAATATTTAGACATGTGTAAAG	4985
Db	220	AAGCAAAACTAGACTTCTTATGTGAAAGTCTGGAATAATATTTAGACATGTGTAAAG	161
Qy	4986	TTAGATGGAAGACCTGTAAATGTTTAAATATATATAGTGTCTTTTGAATGAAGCGAG	5045
Db	160	TTAGATGGAAGACCTGTAAATGTTTAAATATATATAGTGTCTTTTGAATGAAGCGAG	101
Qy	5046	CTGTTGAACGGTTAAACTGTGCATTTCTCATTTTGAATGTGTATGTTAAATGTATGA	5105
Db	100	CTGTTGAACGGTTAAACTGTGCATTTCTCATTTTGAATGTGTATGTTAAATGTATGA	41
Qy	5106	AATGATTAATTAATTAATCAAAACTGGTACCTGTTATATCAT	5145
Db	40	AATGATTAATTAATTAATCAAAACTGGTACCTGTTATATCAT	1
RESULT 36			
/ US-10-342-887-2599/c			
/ Sequence 2599, Application US/10342887			
/ Publication No. US20040058340A1			
/ GENERAL INFORMATION:			
/ APPLICANT: Dai, Hongyue			
/ APPLICANT: He, Yudong			
/ APPLICANT: Linsley, Peter S.			
/ APPLICANT: Mao, Mao			
/ APPLICANT: Roberts, Christopher J.			
/ APPLICANT: Van 't Veer, Laura Johanna			
/ APPLICANT: Van de Vijver, Marc J.			
/ APPLICANT: Bernards, Rene			
/ TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients			
/ FILE REFERENCE: 9301-188-999			
/ CURRENT APPLICATION NUMBER: US/10/342,887			
/ CURRENT FILING DATE: 2003-01-15			
/ PRIOR APPLICATION NUMBER: 60/238,918			
/ PRIOR FILING DATE: 2001-06-18			
/ PRIOR APPLICATION NUMBER: 60/380,710			
/ PRIOR FILING DATE: 2002-05-14			
/ PRIOR APPLICATION NUMBER: 10/172,118			
/ PRIOR FILING DATE: 2002-06-14			
/ NUMBER OF SEQ ID NOS: 2699			
/ SEQ ID NO 2599			
/ LENGTH: 940			
/ TYPE: DNA			
/ ORGANISM: Homo sapiens			
/ US-10-342-887-2599			

Query Match	17.2%	Score 940	DB 17	Length 940
Best Local Similarity	100.0%	Pred. No. 0		
Matches 940	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Oy 4206 GTTTTCTCTTTTGGAAATGACAGTTTTTGACACAGATGTACTTCATGTTTCC 4265
|||||

Db	940	GTITTTCTCGTTTTGGAAAATGACAGTTTTTTGACAGATGTGACCTTACGTGTTCC	881
QY	4266	TATGTGACTCTTAAACCAGCACAGAAATGATATGACTCAACACAGACCGACTTGGTAT	4322
Db	880	TATGTGACTCTTAAACCAGCACAGAAATGATATGACTCAACACAGACCGACTTGGTAT	821
QY	4326	GGGAGATGAGGCGGACAGACCTCACTAGTGTGACAAATATATGCTATGATGAGGAT	438
Db	820	GGGAGATGAGGCGGACAGACCTCACTAGTGTGACAAATATATGCTATGATGAGGAT	761
QY	4386	GTAAGTGAAGCAGAAAGGGTCAGCCGACTTGTATGATACTGGGAAAGTCTGTCA	4441
Db	760	GTAAGTGAAGCAGAAAGGGTCAGCCGACTTGTATGATACTGGGAAAGTCTGTCA	701
QY	4446	ACGATTTGAGTTAGTTTTAGATATATCATTTGAATCTTCAAGATTTC	4501
Db	700	ACGATTTGAGTTAGTTTTAGATATATCATTTGAATCTTCAAGATTTC	641
QY	4506	ACACAGTACTTTTGTATGTATGTATACACACACACCAATATGTGTACAGTTCCACTTCC	4566
Db	640	ACACAGTACTTTTGTATGTATGTATACACACACCAATATGTGTACAGTTCCACTTCC	581
QY	4566	AAGATGTGTCATGCCCAAAACATGTTTAAAGAGAAAGCAGTACTCTTGTCTAACGA	4622
Db	580	AAGATGTGTCATGCCCAAAACATGTTTAAAGAGAAAGCAGTACTCTTGTCTAACGA	521
QY	4626	TGTTTCAGAGGTTTTGGGCACTTGATTTTATAGACTTCGTCAATTAAGGGCTCTCTT	4688
Db	520	TGTTTCAGAGGTTTTGGGCACTTGATTTTATAGACTTCGTCAATTAAGGGCTCTCTT	461
QY	4686	GGCCATGTCCTCCCTCTTCTTCTGGAACGTGATGATGACATCTCTAACGCTTTAGTCT	4745
Db	460	GGCCATGTCCTCCCTCTTCTTCTGGAACGTGATGATGACATCTCTAACGCTTTAGTCT	401
QY	4746	GGTTCACATAGTGTGATATACGATCTTGGAAATGGAACCTGCGGTGCGAAAGGGGTGC	4800
Db	400	GGTTCACATAGTGTGATATACGATCTTGGAAATGGAACCTGCGGTGCGAAAGGGGTGC	341
QY	4806	CTCGAGGCGAGGCTCTGAGCTGCTGTGATGTCTTTAGTGGGGTGATGTGCGCTCTCT	4865
Db	340	CTCGAGGCGAGGCTCTGAGCTGCTGTGATGTCTTTAGTGGGGTGATGTGCGCTCTCT	281
QY	4866	TCAGATGTAAATTTGGGGAAACCTTCGCGCTCTACAGAGGCTATACATATGCTGATTTAA	4923
Db	280	TCAGATGTAAATTTGGGGAAACCTTCGCGCTCTACAGAGGCTATACATATGCTGATTTAA	221
QY	4926	AGAGCAAACTAGACTTCTATGTGAGAGTCTCGGAAATGATTTAGACATGTGTAAAG	4985
Db	220	AGAGCAAACTAGACTTCTATGTGAGAGTCTCGGAAATGATTTAGACATGTGTAAAG	161
QY	4986	TTAAGTGAAGACTGTAAATGTTTAATATGAATATATGTGTTCTTTGAAAGTAAAGCCAG	5045
Db	160	TTAAGTGAAGACTGTAAATGTTTAATATGAATATATGTGTTCTTTGAAAGTAAAGCCAG	101
QY	5046	CTGTGGAACGTTAACTGTGCAATTTCTCATTTTGAATGTGCATGTAAAGTATGA	5105
Db	100	CTGTGGAACGTTAACTGTGCAATTTCTCATTTTGAATGTGCATGTAAAGTATGA	41
QY	5106	AATGATTTAATAAATCAAACTGTGATCTGTTTATACAT	5145
Db	40	AATGATTTAATAAATCAAACTGTGATCTGTTTATACAT	1

```

RESULT 37
US-10-027-632-144266/c
: Sequence 144266, Application US/10027632
: Publication No. US20020198371A1
: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotides
: TITLE OF INVENTION: Polymorphisms in the Human Genome
: FILE REFERENCE: 108827.129
: CURRENT APPLICATION NUMBER: US/10/027.632

```


;; CURRENT FILING DATE: 2002-04-30
;; PRIOR APPLICATION NUMBER: US 60/218, 006
;; PRIOR FILING DATE: 2000-07-12
;; PRIOR APPLICATION NUMBER: US 60/198, 676
;; PRIOR FILING DATE: 2000-04-20
;; PRIOR APPLICATION NUMBER: US 60/193, 483
;; PRIOR FILING DATE: 2000-03-29
;; PRIOR APPLICATION NUMBER: US 60/185, 218
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: US 60/167, 363
;; PRIOR FILING DATE: 1999-11-23
;; PRIOR APPLICATION NUMBER: US 60/156, 358
;; PRIOR FILING DATE: 1999-09-28
;; PRIOR APPLICATION NUMBER: US 60/146, 002
;; PRIOR FILING DATE: 1999-08-09
;; NUMBER OF SEQ ID NOS: 325720
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 144266
;; LENGTH: 860
;; TYPE: DNA
;; ORGANISM: Human
US-10-027-632-144266

Query Match 11.6%; Score 631; DB 13; Length 860;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 681; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4364 AATAATGCTGATATGAGGCTGTAAAGTGAAGGAGGAGGCTACCGCATTTGTTAT 4423
DB 638 AATAATGCTGATATGAGGCTGTAAAGTGAAGGAGGAGGCTACCGCATTTGTTAT 639
QY 4424 GATACCTGGAAAAGTCTGCTCAACGATTGATTGATTGATTGATTGATTGATTGATT 4483
DB 638 GATACCTGGAAAAGTCTGCTCAACGATTGATTGATTGATTGATTGATTGATTGATT 579
QY 4484 TAATCAGACATTCTCAAGTTTACACAGTAGTTTGTATGTTATGTTATGTTATGTTAT 4543
DB 578 TAATCAGACATTCTCAAGTTTACACAGTAGTTTGTATGTTATGTTATGTTATGTTAT 519
QY 4544 TGTGTAAAGTTCACACATTCCTCAGAGTGTGTCAAGTCCCAAAACATGTTTAAAGAA 4603
DB 518 TGTGTAAAGTTCACACATTCCTCAGAGTGTGTCAAGTCCCAAAACATGTTTAAAGAA 459
QY 4604 AGCAGTAGCTCTCTCTCAACGATGTTTCAAGAGTGTGTGAGGAGCTTGTGTTTAAATGAGT 4663
DB 458 AGCAGTAGCTCTCTCTCAACGATGTTTCAAGAGTGTGTGAGGAGCTTGTGTTTAAATGAGT 399
QY 4664 TCTGTCAATTAGGGCTTCTCTTGCCATGTGTCCTCTCTCTCTCTCTCTCTCTCTCTCT 4723
DB 398 TCTGTCAATTAGGGCTTCTCTTGCCATGTGTCCTCTCTCTCTCTCTCTCTCTCTCTCT 339
QY 4724 ACATCTCAACGCTTTAGTGTGTGTCTCAAGTGTGTCAAGTATCAAGTGTGTGTGTGTGT 4783
DB 338 ACATCTCAACGCTTTAGTGTGTGTCTCAAGTGTGTCAAGTATCAAGTGTGTGTGTGTGT 279
QY 4784 ACTGCCGAGGCGAAGAGGAGGCTGCGAGGAGGCTGAGAGCTGTGAGTGTGTGTGTGTGT 4843
DB 278 ACTGCCGAGGCGAAGAGGAGGCTGCGAGGAGGCTGAGAGCTGTGAGTGTGTGTGTGTGT 219
QY 4844 GTGGGGT 4903
DB 218 GTGGGGT 159
QY 4904 GTGATACAGATGTGTATTTTAAAGCAAACTAAGCTTTATGTGTGAAGTGTGTGA 4963
DB 158 GTGATACAGATGTGTATTTTAAAGCAAACTAAGCTTTATGTGTGAAGTGTGTGA 99
QY 4964 ATGATTTAGGACATGTGTAAAGTGTGTGAAGGAGGCTGTTAAATGTTTAAATGATATAG 5023
DB 98 ATGATTTAGGACATGTGTAAAGTGTGTGAAGGAGGCTGTTAAATGTTTAAATGATATAG 39
QY 5024 TGTCTTTTGAAGTGAAGCCAG 5045
|||||

DB 38 TGTCTTTTGAAGTGAAGCCAG 17

RESULT 38

US-10-027-632-144266/C
; Sequence 144266, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218, 006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198, 676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193, 483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185, 218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167, 363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156, 358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146, 002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 144266

LENGTH: 860

TYPE: DNA

ORGANISM: Human

US-10-027-632-144266

Query Match 11.6%; Score 631; DB 17; Length 860;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 681; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4364 AATAATGCTGATATGAGGCTGTAAAGTGAAGGAGGAGGCTACCGCATTTGTTAT 4423
DB 638 AATAATGCTGATATGAGGCTGTAAAGTGAAGGAGGAGGCTACCGCATTTGTTAT 639
QY 4424 GATACCTGGAAAAGTCTGCTCAACGATTGATTGATTGATTGATTGATTGATTGATT 4483
DB 638 GATACCTGGAAAAGTCTGCTCAACGATTGATTGATTGATTGATTGATTGATTGATT 579
QY 4484 TAATCAGACATTCTCAAGTTTACACAGTAGTTTGTATGTTATGTTATGTTATGTTAT 4543
DB 578 TAATCAGACATTCTCAAGTTTACACAGTAGTTTGTATGTTATGTTATGTTATGTTAT 519
QY 4544 TGTGTAAAGTTCACACATTCCTCAGAGTGTGTCAAGTCCCAAAACATGTTTAAAGAA 4603
DB 518 TGTGTAAAGTTCACACATTCCTCAGAGTGTGTCAAGTCCCAAAACATGTTTAAAGAA 459
QY 4604 AGCAGTAGCTCTCTCTCAACGATGTTTCAAGAGTGTGTGAGGAGCTTGTGTTTAAATGAGT 4663
DB 458 AGCAGTAGCTCTCTCTCAACGATGTTTCAAGAGTGTGTGAGGAGCTTGTGTTTAAATGAGT 399
QY 4664 TCTGTCAATTAGGGCTTCTCTTGCCATGTGTCCTCTCTCTCTCTCTCTCTCTCTCTCT 4723
DB 398 TCTGTCAATTAGGGCTTCTCTTGCCATGTGTCCTCTCTCTCTCTCTCTCTCTCTCTCT 339
QY 4724 ACATCTCAACGCTTTAGTGTGTGTCTCAAGTGTGTCAAGTATCAAGTGTGTGTGTGTGT 4783
DB 338 ACATCTCAACGCTTTAGTGTGTGTCTCAAGTGTGTCAAGTATCAAGTGTGTGTGTGTGT 279
QY 4784 ACTGCCGAGGCGAAGAGGAGGCTGCGAGGAGGCTGAGAGCTGTGAGTGTGTGTGTGTGT 4843
DB 278 ACTGCCGAGGCGAAGAGGAGGCTGCGAGGAGGCTGAGAGCTGTGAGTGTGTGTGTGTGT 219
QY 4844 GTGGGGT 4903

Accession	Sequence	Position
Db	GTGGGGTGTGGCTGTCTCTTCACGACATGTAAATTGGGAAACCTCGCGTCTACTAGGG	159
Qy	GTGATATCAGATGGTGATTTTAAAGACAAACTAGACTTCTATGTGAGAAAGTGTGAAA	4963
Db	GTGATACAGATGGTGATTTTAAAGGCAAACTGACTTCTATGTGAGAAAGTGTGAAA	99
Qy	ATGATTTAGACATGTGTAAAGTTAGATGAGAAAGCTGTAATGTGTTAATGTGAATATAG	5023
Db	ATGATTTAGACATGTGTAAAGTTAGATGAGAAAGCTGTAATGTGTTAATGTGAATATAG	39
Qy	TGTTCTTTTGAAGTAAGGCCAG	5045
Db	TGTTCTTTTGAAGTAAGGCCAG	17

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RESULT 39
US-10-027-632-147620
; Sequence 147620, Application US/10027632
; Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
PRIORITY FILING DATE: 2002-04-30
PRIORITY APPLICATION NUMBER: US 60/218,006
PRIORITY FILING DATE: 2000-07-12
PRIORITY APPLICATION NUMBER: US 60/198,676
PRIORITY FILING DATE: 2000-04-20
PRIORITY APPLICATION NUMBER: US 60/193,483
PRIORITY FILING DATE: 2000-03-29
PRIORITY APPLICATION NUMBER: US 60/185,218
PRIORITY FILING DATE: 2000-02-24
PRIORITY APPLICATION NUMBER: US 60/167,363
PRIORITY FILING DATE: 1999-11-23
PRIORITY APPLICATION NUMBER: US 60/156,358
PRIORITY FILING DATE: 1999-09-28
PRIORITY APPLICATION NUMBER: US 60/146,002
PRIORITY FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 147620
LENGTH: 841
TYPE: DNA
ORGANISM: Human
US-10-027-632-147620

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QY	4305	AACAAGACCCAGCTGGTTATGGGGATGATGAGCCGACAAACCTCACTAATTGGACA	4364
Db	301	AACAAGACCCAGCTGGTTATGGGGATGATGAGCCGACAAACCTCACTAATTGGACA	360
QY	4365	AATAATGTGCTATGATGGGGGTGTAAAGTGAAGGAGAAAGAGGTCAAGCCGATTGGTATG	4424
Db	361	AATAATGTGCTATGATGGGGGTGTAAAGTGAAGGAGGAGAAAGAGGTCAAGCCGATTGGTATG	420
QY	4425	ATACGGGAAAGTGGTGTGCAACGATTGAGTGGTTTTGATGATATCAATTGAAATCTTT	4484
Db	421	ATACTGGGAAAGTGGTGTGCAACGATTGAGTGGTTTTGATGATATCAATTGAAATCTTT	480
QY	4485	AATCAGACATTCTCAAGTTTACAACAGTAGTTTTGATGTTATGTATGACACACACCAAT	4544
Db	481	AATCAGACATTCTCAAGTTTACAACAGTAGTTTTGATGTTATGTATGACACACACCAAT	540
QY	4545	GTGTAACAGTTCACACCTCCAGAGTGTGTGTCATGCCCAAAACATGTTTAAAGAAAGAA	4604
Db	541	GTGTAACAGTTCACACCTCCAGAGTGTGTGTCATGCCCAAAACATGTTTAAAGAAAGAA	600
QY	4605	GCAGTAGCTCTTGTCTACAGATGTTTACAGAGAGTTTGAGGCACATCTGGTTTTAATGACCT	4664
Db	601	GCAGTAGCTCTTGTCTACAGATGTTTACAGAGAGTTTGAGGCACATCTGGTTTTAATGACCT	660
QY	4665	CTGTCAATTAGAGGCTTCTTTGGCCATGATGCCCTTCTCTGGAATCTGTAGTATGTC	4724
Db	661	CTGTCAATTAGAGGCTTCTTTGGCCATGATGCCCTTCTCTGGAACCTGTAGTATGTC	720
QY	4725	CATCCTACAGCCTTTAGTGTGTTCACTAGTGCAGATATACGTTCTTGGAAATGAGA	4784
Db	721	CATCCTACAGCCTTTAGTGTGTTCACTAGTGCAGATATACGTTCTTGGAAATGAGA	780
QY	4785	CTGCCGTGGCGAAGGGGTGGCTTC	4808
Db	781	CTGCCGTGGCGAAGGGGTGGCTTC	804

```

RESULT 40
US-10-027-632-147620
; Sequence 147620, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Mang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147620
; LENGTH: 841
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-147620

Query Match          11.0%; Score 600; DB 17; Length 841;
Best Local Similarity 99.5%; Pred. No. 6,5e-310;
Matches 800; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 4005 AACATAGAGGTCACTGGAACAAGTATAGTCAGATTGGCTTTCAAAATCTCTCTGGC 4064
DB 1 AACATAGAGGTCACTGGAACAAGTATAGTCAGATTGGCTTTCAAAATCTCTCTGGC 60
QY 4065 TTGAGTTTATCAGCTTCAATATGAGGCTCTTTTGAAGCTTAAATTCACACAGAGCT 4124
DB 61 TTGAGTTTATCAGCTTCAATATGAGGCTCTTTTGAAGCTTAAATTCACACAGAGCT 120
QY 4125 TTTTGGGGGTGGGGCTGGGGGGGTGTGTGATTTTCTTCCCTCTGTAGTGTCT 4184
DB 121 TTTTGGGGGTGGGGCTGGGGGGGTGTGTGATTTTCTTCCCTCTGTAGTGTCT 180
QY 4185 AGTTCGCTGCTGTATCTCAGGTTTCTCTGTTTGAAGAAATGACAGTTTGTGACC 4244
DB 181 AGTTCGCTGCTGTATCTCAGGTTTCTCTGTTTGAAGAAATGACAGTTTGTGACC 240
QY 4245 AGGATGTGACTTCAATGTTTCTTCTATGATGATCTTAAACACAGACAGATGATGACTC 4304
DB 241 AGGATGTGACTTCAATGTTTCTTCTATGATGATCTTAAACACAGACAGATGATGACTC 300
QY 4305 AACACAGACCACTTGTGTTATGAGGATGATAGCCGACACAGCTTCACTAGTTGTGACA 4364
DB 301 AACACAGACCACTTGTGTTATGAGGATGATAGCCGACACAGCTTCACTAGTTGTGACA 360
QY 4365 AATAATGCTATGATGAGGGGTGTAAGTGAAGCAGAAAGAGGCTCAGCCGATGTTATG 4424
DB 361 AATAATGCTATGATGAGGGGTGTAAGTGAAGCAGAAAGAGGCTCAGCCGATGTTATG 420
QY 4425 ATACTGGGAAAGTGTGCTGATCAAGATTTGATTTTATGATTTATGATGAAATCTTT 4484
DB 421 ATACTGGGAAAGTGTGCTGATCAAGATTTGATTTTATGATTTATGATGAAATCTTT 480
QY 4485 AATCAGACATTTCTCAAGTTTTCACACAGTATTTTGAATTTATGACACACACCAAT 4544
DB 481 AATCAGACATTTCTCAAGTTTTCACACAGTATTTTGAATTTATGACACACACCAAT 540
QY 4545 GTGTACAGTTCACACACTTCCAGAGTGTGATGATGATGATGATGATGATGATGATG 4604
DB 541 GTGTACAGTTCACACACTTCCAGAGTGTGATGATGATGATGATGATGATGATGATG 600
QY 4605 GCAGTAGTCTCTTGTCTAAGATTTTCAGAGAGTTTGGGGCACTTGTATGATGACTT 4664
DB 601 GCAGTAGTCTCTTGTCTAAGATTTTCAGAGAGTTTGGGGCACTTGTATGATGACTT 660
QY 4665 CTGTCAATTTAAGGGCTTCTTGTGCGATGATGATGATGATGATGATGATGATGATG 4724
DB 661 CTGTCAATTTAAGGGCTTCTTGTGCGATGATGATGATGATGATGATGATGATGATG 720
QY 4725 CATCTTACAGCTTATAGTCTGTGTTCACTAGTGTCAATATCACTTCTTGAATTCGAGA 4784
DB 721 CATCTTACAGCTTATAGTCTGTGTTCACTAGTGTCAATATCACTTCTTGAATTCGAGA 780
QY 4785 CTGCCGTGGCGAAGGGGTGGCCTC 4808
DB 781 CTGCCGTGGCGAAGGGGTGGCCTC 804

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RESULT 41
US-10-027-632-24920/c
; Sequence 24920, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20

```

```

; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 24920
; LENGTH: 803
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-24920

```

Query Match 9.9%; Score 541; DB 13; Length 803;

Best Local Similarity 99.7%; Pred. No. 2,8e-278;

Matches 641; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 4389 AAGTGAAGCAGAAAGAGGCTACGCCGATTTGATGATGATGATGATGATGATGATG 4448
DB 643 AAGTGAAGCAGAAAGAGGCTACGCCGATTTGATGATGATGATGATGATGATGATG 584
QY 4449 ATTTGAGTTTATTTTATATATATATATATATATATATATATATATATATATATATAT 4508
DB 583 ATTTGAGTTTATTTTATATATATATATATATATATATATATATATATATATATATAT 524
QY 4509 CAGTATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4568
DB 523 CAGTATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 464
QY 4569 GTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4628
DB 463 GTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 404
QY 4629 TTTGAGAGTTTGGGGCACTTGTGTTTATGAGCTTCTGTATTTAAGGGCTTCTTGGC 4688
DB 403 TTTGAGAGTTTGGGGCACTTGTGTTTATGAGCTTCTGTATTTAAGGGCTTCTTGGC 344
QY 4689 CATGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4748
DB 343 CATGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 284
QY 4749 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4808
DB 283 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 224
QY 4809 GAGGCGAGGCTCTGAGCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATG 4868
DB 223 GAGGCGAGGCTCTGAGCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATG 164
QY 4869 GCATGTAATTTGGGGAAACCTCGGCTACTAGAGGGGTATACAGATGATGATTTAAAGA 4928
DB 163 GCATGTAATTTGGGGAAACCTCGGCTACTAGAGGGGTATACAGATGATGATTTAAAGA 104
QY 4929 GCAAAACTAGACTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4988
DB 103 GCAAAACTAGACTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 44
QY 4989 GATGAAAGACTGTATATGTTTATATGATGATGATGATGATGATGATGATGATGATG 5031
DB 43 GATGAAAGACTGTATATGTTTATATGATGATGATGATGATGATGATGATGATGATG 1

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RESULT 42
US-10-027-632-24921/c
; Sequence 24921, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

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Db 163 GCATGTAAATTTGGGGAAACCTTCGYKTCYACTAGAGGGTATACAGATGTGATTTTAAAGA 104
Qy 4929 GCAAAACCTAGACTTCTATGTGAGAGTCTGGAAATGATTTAGACATGTGTAAAGTTA 4988
Db 103 GCAAAACCTAGACTTCTATGTGAGAGTCTGGAAATGATTTAGACATGTGTAAAGTTA 44
Qy 4989 GATGGAAGACTGTAAATGTTTAAATATGATATAGTCTTT 5031
Db 43 GATGGAAGACTGTAAATGTTTAAATATGATATAGTCTTT 1

RESULT 44
US-10-027-632-24921/c
; Sequence 24921, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24921
; LENGTH: 803
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-24921

Query Match 9.9%; Score 541; DB 17; Length 803;
Best Local Similarity 99.7%; Pred. No. 2.8e-278;
Matches 641; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4389 AAGTGAAGCAGAGAGGCTGACCGCATTTGATGATACGGAAGTGTGCTCAACG 4448
Db 643 AAGTGAAGCAGAGAGGCTGACCGCATTTGATGATACGGAAGTGTGCTCAACG 584
Qy 4449 ATTTGAGTTAGTTTATGATATACATTTAAATCTTTAATCAGACATTTCAAGTTTCA 4508
Db 583 ATTTGAGTTAGTTTATGATATACATTTAAATCTTTAATCAGACATTTCAAGTTTCA 524
Qy 4509 CAGTATGTTTGTATGATATGATACACACACACCAAAATGTGTAACTTCAACATTTCCA 4568
Db 523 CAGTATGTTTGTATGATATGATACACACACCAAAATGTGTAACTTCAACATTTCCA 464
Qy 4569 GTGTGTGATGATCCCAAAACATGTTTAAAGAAAGAAAGAGTACGCTTGTCAACGAT 4628
Db 463 GTGTGTGATGATCCCAAAACATGTTTAAAGAAAGAAAGAGTACGCTTGTCAACGAT 404
Qy 4629 TTCAGAGATTTGGGGCACTTGTTTATGAGCTTGTCTATTTAGAGGCTTCTTGGC 4688
Db 403 TTCAGAGATTTGGGGCACTTGTTTATGAGCTTGTCTATTTAGAGGCTTCTTGGC 344
Qy 4689 CATGTCCCTTCTTCTTGTGAACTGTGATGTATGATCCTACAGCTTTAGTGTGT 4748
Db 343 CATGTCCCTTCTTCTTGTGAACTGTGATGTATGATCCTACAGCTTTAGTGTGT 284

Qy 4749 TCACAGTGTGATATACATTTCACTTGTGATATGAGACTCCGTGCGAAGGGGTGCTC 4808
Db 283 TCACAGTGTGATATACATTTCACTTGTGATATGAGACTCCGTGCGAAGGGGTGCTC 224
Qy 4809 GGAGCAGGCTCTGAGAGTGTGATGTCTTTAGATGGGGTGTGCTGTCTCTTCA 4868
Db 223 GGAGCAGGCTCTGAGAGTGTGATGTCTTTAGATGGGGTGTGCTGTCTCTTCA 164
Qy 4869 GCATGTAAATTTGGGGAAACCTTCGCTCTACTAGAGGGTATACAGATGTGATTTAAAGA 4928
Db 163 GCATGTAAATTTGGGGAAACCTTCGCTCTACTAGAGGGTATACAGATGTGATTTAAAGA 104
Qy 4929 GCAAAACCTAGACTTCTATGTGAGAGTCTGGAAATGATTTAGACATGTGTAAAGTTA 4988
Db 103 GCAAAACCTAGACTTCTATGTGAGAGTCTGGAAATGATTTAGACATGTGTAAAGTTA 44
Qy 4989 GATGGAAGACTGTAAATGTTTAAATATGATATAGTCTTT 5031
Db 43 GATGGAAGACTGTAAATGTTTAAATATGATATAGTCTTT 1

RESULT 45
US-10-357-930-43560
; Sequence 43560, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43560
; LENGTH: 518
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-43560

Query Match 7.9%; Score 431; DB 18; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.6e-219;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4175 AAGTGTGCTAGTGTGCTGCTGCTGATCTCAGATTTTCTCGTTTGTGAGAAATGACAG 4234
Db 13 AAGTGTGCTAGTGTGCTGCTGCTGATCTCAGATTTTCTCGTTTGTGAGAAATGACAG 72
Qy 4235 TTTTGTGACAGATGTGACTTCAATGTTTCTATGTGACTTTAAACAGCAGAT 4294
Db 73 TTTTGTGACAGATGTGACTTCAATGTTTCTATGTGACTTTAAACAGCAGAT 132
Qy 4295 GATATGACTCAACACAGACGACTTGTGTTATGGAGATGATAGCGCAGACACTCACTA 4354
Db 133 GATATGACTCAACACAGACGACTTGTGTTATGGAGATGATAGCGCAGACACTCACTA 192

QY 4355 GTTGTGACAAATATATGCTATGATGGGGTGTAAATGAGGACAGAGAGGCTCAGCCG 4414
DB 193 GTTGTGACAAATATATGCTATGATGGGGTGTAAATGAGGACAGAGAGGCTCAGCCG 252
QY 4415 CATTTTATGATCTCTGGGAAAGTCTGCTCAACGATTTGAGTTAGTTTATATATACAT 4474
DB 253 CATTTTATGATCTCTGGGAAAGTCTGCTCAACGATTTGAGTTTATATATACAT 312
QY 4475 TGAATCTTTAATCAGACATCTTCAAGTTTACACAGATGTTTATGATTTATGACACA 4534
DB 313 TGAATCTTTAATCAGACATCTTCAAGTTTACACAGATGTTTATGATTTATGACACA 372
QY 4535 CACACCAATATGTTAAACAGTTCAACCTTCCAGAGTGTGTCATGCCCCAAATCTTTTA 4594
DB 373 CACACCAATATGTTAAACAGTTCAACCTTCCAGAGTGTGTCATGCCCCAAATCTTTTA 432
QY 4595 AGAAGAGAAAG 4605
DB 433 AGAAGAGAAAG 443

RESULT 46
US-10-357-930-10717/c
; Sequence 10717, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10717
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-10717

Query Match 7.6%; Score 416; DB 18; Length 425;
Best Local Similarity 100.0%; Pred. No. 2.8e-211;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1254 TGTTCATGACATGTTTATGCTGGGATTCCTCGCTCGGCCACATTCGCTATGCTTACAT 1313
DB 424 TGTTCATGACATGTTTATGCTGGGATTCCTCGCTCGGCCACATTCGCTATGCTTACAT 365
QY 1314 CATGAAGAGATGACATGCTTTAGATGAAGCTTAAAGATTTGTAAGAAAGAAAAGAACCC 1373
DB 364 CATGAAGAGATGACATGCTTTAGATGAAGCTTAAAGATTTGTAAGAAAGAAAAGAACCC 305
QY 1374 TACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCTCGGACCTATGAGAAGATTTAA 1433
DB 304 TACTATATCTCCAAACTTCAATTTTCTGGGCCAACTCTCGGACCTATGAGAAGATTTAA 245

QY 1434 GAACCAAGCTGAGCATGAGGAGCCAAAGAGAACTCAAGCTGCTGACCTGGAAGAGCC 1493
DB 244 GAACCAAGCTGAGCATGAGGAGCCAAAGAGAACTCAAGCTGCTGACCTGGAAGAGCC 185
QY 1494 AAATGAACCTGTCCCTGCTGTCTCAAGAGGTGACAGAAAAAGCAGACGCCCTCAGTCC 1553
DB 184 AAATGAACCTGTCCCTGCTGTCTCAAGAGGTGACAGAAAAAGCAGACGCCCTCAGTCC 125
QY 1554 ACCCTGAGCAGCTCTGTACTTCAAGAGGACAGACAAAGGCCCTGTCATCCCCGACG 1613
DB 124 ACCCTGAGCAGCTCTGTACTTCAAGAGGACAGACAAAGGCCCTGTCATCCCCGACG 65
QY 1614 CGTGCCAGCGTGCAGCGTGCAGCGCTGCTTAAAGAGACAGCCCGCTGTATC 1669
DB 64 CGTGCCAGCGTGCAGCGTGCAGCGCTGCTTAAAGAGACAGCCCGCTGTATC 9

RESULT 47
US-10-357-930-31909/c
; Sequence 31909, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31909
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-31909

Query Match 7.6%; Score 414; DB 18; Length 467;
Best Local Similarity 100.0%; Pred. No. 3.4e-210;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1256 TTCTAGGACATGTTTATGCTGGGATTCCTCGCTCGGCCACATTCGCTATGCTTACATCA 1315
DB 467 TTCTAGGACATGTTTATGCTGGGATTCCTCGCTCGGCCACATTCGCTATGCTTACATCA 408
QY 1316 TGAAGAGATGACATGCTTTAGATGAAGCTTAAAGATTTGTAAGAAAGAAAAGACCTA 1375
DB 407 TGAAGAGATGACATGCTTTAGATGAAGCTTAAAGATTTGTAAGAAAGAAAAGACCTA 348
QY 1376 CTATATCTCCAAACTTCAATTTTCTGGGCCAACTCTCGGACCTATGAGAAGATTTAAG 1435
DB 347 CTATATCTCCAAACTTCAATTTTCTGGGCCAACTCTCGGACCTATGAGAAGATTTAAG 288
QY 1436 ACCAGCTGAGATCAGGAGCCAAAGAGCAACTCAAGCTGTGACCTGGAAGAGCCAA 1495
DB 287 ACCAGCTGAGATCAGGAGCCAAAGAGCAACTCAAGCTGTGACCTGGAAGAGCCAA 228

QY 1496 ATGAACCTGCTCTGCTCTCTCAAGAGGGTGAACAGAAAAAGCGAGCGCCCTCACTGATCCAC 1555
DB 227 ATGAACCTGCTCTGCTCTCTCAAGAGGGTGAACAGAAAAAGCGAGCGCCCTCACTGATCCAC 168
QY 1556 CCTGTGCCGACTCTGTCTACTCTCAAGAGGAGCGAGCAAAAGGCCCTGTGATCCCGGCAAGC 1615
DB 167 CCTGTGCCGACTCTGTCTACTCTCAAGAGGAGCGAGCAAAAGGCCCTGTGATCCCGGCAAGC 108
QY 1616 TGCCGAGGTCGCCAGCGCTGACAGCGCTGTAGAGAGACAGCCCGCTGTATC 1669
DB 107 TGCCGAGGTCGCCAGCGCTGACAGCGCTGTAGAGAGACAGCCCGCTGTATC 54

RESULT 48

US-10-357-930-40868/c
; Sequence 40868, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40868
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-40868

Query Match 7.6%; Score 414; DB 18; Length 467;

Best Local Similarity 100.0%; Pred. No. 3.4e-210; Indels 0; Gaps 0;

Matches 414; Conservative 0; Mismatches 0;

QY 1256 TTCTAGTCACTGTTTATGCTGGATCTCCCGCTCCGACCATCTGCTTATCGCTTACATCA 1315
DB 467 TTCTAGTCACTGTTTATGCTGGATCTCCCGCTCCGACCATCTGCTTATCGCTTACATCA 408
QY 1316 TGAAGAGATGACATGCTCTTATGATGAAGCTTACAGATTGTGAAAAAGAAAGACCTA 1375
DB 407 TGAAGAGATGACATGCTCTTATGATGAAGCTTACAGATTGTGAAAAAGAAAGACCTA 348
QY 1376 CTATATCTCCAACTTCAATTTTCTGGGCCAACTCTGAGCATATGAGAAAGATTAGA 1435
DB 347 CTATATCTCCAACTTCAATTTTCTGGGCCAACTCTGAGCATATGAGAAAGATTAGA 288
QY 1436 ACCGAGCTGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGTCGACCTTGAGAGACCAA 1495
DB 287 ACCGAGCTGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGTCGACCTTGAGAGACCAA 228
QY 1496 ATGAACCTGCTCTGCTCTCTCAAGAGGGTGAACAGAAAAAGCGAGCGCCCTCACTGATCCAC 1555
DB 227 ATGAACCTGCTCTGCTCTCTCAAGAGGGTGAACAGAAAAAGCGAGCGCCCTCACTGATCCAC 168

QY 1556 CCTGTGCCGACTCTGTCTACTCTCAAGAGGAGCGAGCAAAAGGCCCTGTGATCCCGGCAAGC 1615
DB 167 CCTGTGCCGACTCTGTCTACTCTCAAGAGGAGCGAGCAAAAGGCCCTGTGATCCCGGCAAGC 108
QY 1616 TGCCGAGGTCGCCAGCGCTGACAGCGCTGTAGAGAGACAGCCCGCTGTATC 1669
DB 107 TGCCGAGGTCGCCAGCGCTGACAGCGCTGTAGAGAGACAGCCCGCTGTATC 54

RESULT 49

US-10-357-930-41017/c
; Sequence 41017, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41017
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-41017

Query Match 7.6%; Score 414; DB 18; Length 467;

Best Local Similarity 100.0%; Pred. No. 3.4e-210; Indels 0; Gaps 0;

Matches 414; Conservative 0; Mismatches 0;

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QY 1316 TGAAGAGATGACATGCTCTTATGATGAAGCTTACAGATTGTGAAAAAGAAAGACCTA 1375
DB 407 TGAAGAGATGACATGCTCTTATGATGAAGCTTACAGATTGTGAAAAAGAAAGACCTA 348
QY 1376 CTATATCTCCAACTTCAATTTTCTGGGCCAACTCTGAGCATATGAGAAAGATTAGA 1435
DB 347 CTATATCTCCAACTTCAATTTTCTGGGCCAACTCTGAGCATATGAGAAAGATTAGA 288
QY 1436 ACCGAGCTGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGTCGACCTTGAGAGACCAA 1495
DB 287 ACCGAGCTGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGTCGACCTTGAGAGACCAA 228
QY 1496 ATGAACCTGCTCTGCTCTCTCAAGAGGGTGAACAGAAAAAGCGAGCGCCCTCACTGATCCAC 1555
DB 227 ATGAACCTGCTCTGCTCTCTCAAGAGGGTGAACAGAAAAAGCGAGCGCCCTCACTGATCCAC 168
QY 1556 CCTGTGCCGACTCTGTCTACTCTCAAGAGGAGCGAGCAAAAGGCCCTGTGATCCCGGCAAGC 1615
DB 167 CCTGTGCCGACTCTGTCTACTCTCAAGAGGAGCGAGCAAAAGGCCCTGTGATCCCGGCAAGC 108


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1616 TGCCGAGCGTGCAGCGTCGACGCGTCGCTGTAGAGCAGCCCGCTGGTAC 1669
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RESULT 50
US-10-220-891-86/c
Sequence 86, Application US/10220891
Publication No. US20030207286A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, AKIRA
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES HAVING CHARACTERISTICS OF ENHANCED
TITLE OF INVENTION: EXPRESSION IN HUMAN NEUROBLASTOMA WITH FAVORABLE PROGNOSIS
TITLE OF INVENTION: BASED ON COMPARISON BETWEEN HUMAN NEUROBLASTOMA WITH FAVORABLE
TITLE OF INVENTION: PROGNOSIS AND HUMAN NEUROBLASTOMA WITH UNFAVORABLE PROGNOSIS
FILE REFERENCE: 7388-73435
CURRENT APPLICATION NUMBER: US/10/220,891
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: JP 2000/140387
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: JP 2000/159195
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn version 3.2
SEQ ID NO 86
LENGTH: 789
TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: modified_base
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5  NAME/KEY: modified_base
6  LOCATION: (693)..(693)
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10 LOCATION: (695)..(695)
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18 LOCATION: (710)..(710)
19 OTHER INFORMATION: a, t, c, g, unknown or other
20 FEATURE:
21 NAME/KEY: modified_base
22 LOCATION: (766)..(766)
23 OTHER INFORMATION: a, t, c, g, unknown or other
24 FEATURE:
25 NAME/KEY: modified_base
26 LOCATION: (783)..(783)
27 OTHER INFORMATION: a, t, c, g, unknown or other
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29 US-10-220-891-86

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Search completed: February 15, 2005, 22:17:30
Job time : 2782 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2005, 12:09:54 ; Search time 125.848 Seconds
(without alignments)
1721.062 Million cell updates/sec

Title: US-10-029-345A-109

Perfect score: 3418

Sequence: 1 MAHEMIGQIVTERLVALL.....LGKVGSGSFGSGMEIIEVS 665

Scoring table:

BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3406	99.6	665	US-09-816-494-2	Sequence 2, Appl1
2	3406	99.6	665	US-09-964-277-2	Sequence 26, Appl1
3	3406	99.6	665	US-10-377-072-26	Sequence 680, App
4	3406	99.6	665	US-10-072-012-680	Sequence 14, Appl1
5	3406	99.6	665	US-10-168-506-14	Sequence 7, Appl1
6	3406	99.6	665	US-10-343-357-7	Sequence 240, App
7	3406	99.6	665	US-10-257-026-2	Sequence 247, App
8	3406	99.6	665	US-10-648-593-240	Sequence 26, Appl1
9	3406	99.6	665	US-10-648-593-247	Sequence 679, App
10	3406	99.6	665	US-10-377-072-26	Sequence 703, App
11	3406	99.6	690	US-10-072-012-679	Sequence 54204, A
12	3406	99.6	690	US-10-072-012-703	
13	3406	99.6	690	US-10-425-114-54204	

14	3399	99.4	665	US-10-094-749-2312	Sequence 2312, App
15	3399	99.4	665	US-10-072-012-681	Sequence 681, App
16	3379.5	98.9	662	US-10-072-012-258	Sequence 258, App
17	3358.5	98.3	680	US-10-072-012-256	Sequence 256, App
18	3079.5	90.1	660	US-10-072-012-682	Sequence 682, App
19	2930	85.7	672	US-10-296-115-1259	Sequence 1259, App
20	2721.5	79.6	677	US-10-072-012-683	Sequence 683, App
21	2500	73.1	517	US-09-964-277-21	Sequence 21, Appl1
22	1326	38.8	665	US-10-072-012-659	Sequence 659, App
23	1302	38.1	663	US-10-072-012-700	Sequence 700, App
24	1297	37.9	253	US-10-108-260A-4872	Sequence 4872, App
25	1075.5	31.5	616	US-10-072-012-266	Sequence 266, App
26	917	26.8	501	US-10-072-012-702	Sequence 702, App
27	807	23.6	155	US-09-964-277-7	Sequence 7, Appl1
28	732.5	21.4	461	US-10-072-012-701	Sequence 701, App
29	654.5	19.1	169	US-10-346-356-15	Sequence 15, Appl1
30	654.5	19.1	170	US-09-775-925-26	Sequence 26, Appl1
31	654.5	19.1	170	US-09-847-519A-11	Sequence 11, Appl1
32	654.5	19.1	170	US-10-314-058-14	Sequence 14, Appl1
33	654.5	19.1	170	US-10-405-808-16	Sequence 16, Appl1
34	654.5	19.1	170	US-10-655-073-16	Sequence 16, Appl1
35	619	18.1	155	US-09-964-277-6	Sequence 6, Appl1
36	619	18.1	155	US-09-955-732-6	Sequence 12, Appl1
37	566	13.7	140	US-10-803-728-12	Sequence 47, Appl1
38	469	13.7	444	US-09-964-899-47	Sequence 130, App
39	469	13.7	482	US-10-346-356-2	Sequence 164, App
40	469	13.7	482	US-10-058-270A-130	Sequence 2, Appl1
41	469	13.7	482	US-10-648-593-164	Sequence 805, App
42	466.5	13.6	381	US-10-184-832-2	Sequence 805, App
43	453	13.3	394	US-09-736-457-805	Sequence 805, App
44	453	13.3	394	US-09-902-941-805	Sequence 805, App
45	453	13.3	394	US-09-849-628-805	Sequence 805, App

ALIGNMENTS

RESULT 1
US-09-816-494-2
Sequence 2, Application US/09816494
Patent No. US20020034807A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
FILE REFERENCE: 10448-030002
CURRENT APPLICATION NUMBER: US/09/816,494
PRIORITY FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,858
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 665
TYPE: PRT
ORGANISM: Homo sapiens
US-09-816-494-2

Query Match	99.6%	Score 3406	DB 9	Length 665
Best Local Similarity	99.7%	Pred. No. 9e-238		
Matches 663	Conservative	1	Mismatches 1	Indels 0
			Gaps	0
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QY	61	DKVLTTELIOHSAHKVDIDCSOKVWVYDOSQDVASISDCFLTVLLGKLEKSFNSVHL		120
Db	61	DKVLTTELIOHSAHKVDIDCSOKVWVYDOSQDVASISDCFLTVLLGKLEKSFNSVHL		120
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Db	121	LAGGAFAFSRCPGGLCEGKSTLVPTCISQPCLPVANIPTRIPLNVLGCGQDVANKELI		180

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DB 181 QONGIGYVLANASNTCPKDPFIPESHFLRVPVNDSPCEKILPWLKSVDFIEKAKASNGCV 240
QY 241 LVHCLAGISRSATTAIAIYIMKMDMSLDEAVRFVEKERPTTSPNPNFLGQLLDYEKKIKN 300
DB 241 LVHCLAGISRSATTAIAIYIMKMDMSLDEAVRFVEKERPTTSPNPNFLGQLLDYEKKIKN 300
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DB 301 QTGASGPKSKLKLHLKEKNEPVPAVSGGQKSETPPLSPCADSATSBAAQRPVHPASV 360
QY 361 PSVPVQBPBLEDSPVLQALSGHLISADRLSDSKLKRFSLDIKSVSYASMAASLHGF 420
DB 361 PSVPVQBPBLEDSPVLQALSGHLISADRLSDSKLKRFSLDIKSVSYASMAASLHGF 420
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DB 421 SSSBDALFYKRPSTTLDTGNKLCOPSPVOELSEQTPETSPDKEBASIPKKLQIARPSDSQ 480
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DB 541 SDIILAPOTSTPLTSSWYFATESHFFYSASAIYGGASYSYSCSOLPTCGDQVYVRRR 600
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DB 601 QKPSDRADSRSRWSHBESPFKQFRKRSQOMEFGESIMSENRSRRELKVGOSQSSFFSGSME 660
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DB 661 IIEVS 665

Query Match 99.6%; Score 3406; DB 9; Length 665;
Beet Local Similarity 99.7%; Pred. No. 9e-238;
Matches 663; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 361 PSVPVQBPBLEDSPVLQALSGHLISADRLSDSKLKRFSLDIKSVSYASMAASLHGF 420
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DB 481 SKRLHSVNTSSSGTAQRSLSPLRSGSVEDNHTSFLFGLSTSQOHLTKSAGLKGWH 540
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DB 601 QKPSDRADSRSRWSHBESPFKQFRKRSQOMEFGESIMSENRSRRELKVGOSQSSFFSGSME 660
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DB 661 IIEVS 665

RESULT 3
US-10-377-072-26
; Sequence 26, Application US/10377072
; Publication No. US2004009501A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Miyoung
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; FILE REFERENCE: AND USES THEREFOR
; FILE REFERENCE: MEI03-0180NMIM
; CURRENT APPLICATION NUMBER: US/10/377, 072
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895, 860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215, 370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723, 806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187, 455
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/843, 297
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199, 801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861, 801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205, 508
; PRIOR FILING DATE: 2000-05-19

; PRIOR APPLICATION NUMBER: US 09/816,494
 ; PRIOR FILING DATE: 2001-03-23
 ; PRIOR APPLICATION NUMBER: US 09/815,419
 ; PRIOR FILING DATE: 2001-03-22
 ; Remaining prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 114
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 26
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 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-377-072-26

Query Match 99.6%; Score 3406; DB 15; Length 665;
 Best Local Similarity 99.7%; Pred. No. 9e-238; Indels 0; Gaps 0;
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DB 121 LAGFAERSPCPGCEGKSTLVPTCISOPCLPVANIGPTRILPVLNYGCGORDVANKELI 180
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DB 181 QONGIGYVLNASTYTCPKDFIPESHFLRPVNDSPCEKILPWLKDSVDFIEKAKSNGCV 240
QY 241 LVHCLAGISRSATIAIAYIMKMDMSLDAYRFVKEKPTISPNNFLGQLLDYEKKIKN 300
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QY 421 SSSSEDALEYYKSTLIDGTNKLCOFSPVOELSEQTPETSPDKEASIPKCLQTARPSDQ 480
DB 421 SSSSEDALEYYKSTLIDGTNKLCOFSPVOELSEQTPETSPDKEASIPKCLQTARPSDQ 480
QY 481 SKRLHSVTSSTSGTQORSLISPLHRSAGVEDNYHTSFLGLSTSOQHLTKSAGLKGWH 540
DB 481 SKRLHSVTSSTSGTQORSLISPLHRSAGVEDNYHTSFLGLSTSOQHLTKSAGLKGWH 540
QY 541 SDILAPOTSPLTSSWYFATESHFPYASAIYGGASASAYSQSLPTCGDQVYSVRR 600
DB 541 SDILAPOTSPLTSSWYFATESHFPYASAIYGGASASAYSQSLPTCGDQVYSVRR 600
QY 601 QKPSRADSRSRHESPEKQFKRRSCMEFGEISIMSENRSREELGKVGSSFSGSME 660
DB 601 QKPSRADSRSRHESPEKQFKRRSCMEFGEISIMSENRSREELGKVGSSFSGSME 660
QY 661 IIEVS 665
DB 661 IIEVS 665
  
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RESULT 4
 US-10-072-012-680
 ; Sequence 680, Application US/10072012
 ; Publication No. US2004003493A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tchernev, Velizar
 ; APPLICANT: Spytek, Kimberly

```

; APPLICANT: Zehrusen, Bryan
; APPLICANT: Patumajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangoli, Esba
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Penac, Adam R.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 680
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-680

Query Match 99.6%; Score 3406; DB 15; Length 665;
Best Local Similarity 99.7%; Pred. No. 9e-238; Indels 0; Gaps 0;
Matches 663; Conservative 1; Mismatches 1;

QY 1 MAHEMIGTQVTERLVALLSGTEKVLIDSRPFVEYNTSHLEAININCSKLMKRLQ 60
DB 1 MAHEMIGTQVTERLVALLSGTEKVLIDSRPFVEYNTSHLEAININCSKLMKRLQ 60
QY 61 DKVLTTELIOHSAKHKVDIDCSQKVVYVDQSQDVASLSSDCFLTVLLGKLEKSNVHL 120
DB 61 DKVLTTELIOHSAKHKVDIDCSQKVVYVDQSQDVASLSSDCFLTVLLGKLEKSNVHL 120
QY 121 LAGFAERSPCPGCEGKSTLVPTCISOPCLPVANIGPTRILPVLNYGCGORDVANKELI 180
DB 121 LAGFAERSPCPGCEGKSTLVPTCISOPCLPVANIGPTRILPVLNYGCGORDVANKELI 180
QY 181 QONGIGYVLNASTYTCPKDFIPESHFLRPVNDSPCEKILPWLKDSVDFIEKAKSNGCV 240
DB 181 QONGIGYVLNASTYTCPKDFIPESHFLRPVNDSPCEKILPWLKDSVDFIEKAKSNGCV 240
  
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Qy	241	LHCHLAGISBSATIAIAYIMKRMDSIDEAYRFVKEKRPISIPNFNFGQLLDYEKKIKN	300
Db	241	LHCHLAGISRSATIAIAYIMKRMDSIDEAYRFVKEKRPISIPNFNFGQLLDYEKKIKN	300
Qy	301	QTGASGPKSKLKLHLKEKNEPVAVSSEGQKETPLSPCCASATSSEAGQPHVPAST	360
Db	301	QTGASGPKSKLKLHLKEKNEPVAVSSEGQKETPLSPCCASATSSEAGQPHVPAST	360
Qy	361	PSVPSVQPSLLEDSPLVQALSGIHLGADRLLEDNKLKRSFLDIKSVSYASMAASLHGF	420
Db	361	PSVPSVQPSLLEDSPLVQALSGIHLGADRLLEDNKLKRSFLDIKSVSYASMAASLHGF	420
Qy	421	SSSEBDLXYKXSTLLDGTNKKQSPVOELSTQTEPSPDKKEASIPKTLQTARPSDSQ	480
Db	421	SSSEBDLXYKXSTLLDGTNKKQSPVOELSTQTEPSPDKKEASIPKTLQTARPSDSQ	480
Qy	481	SKRLHSVRTSSSGTQORSLSLPLHRSGVEDNVHTSFLGLSTSQOHLTKSAGLGLKGMH	540
Db	481	SKRLHSVRTSSSGTQORSLSLPLHRSGVEDNVHTSFLGLSTSQOHLTKSAGLGLKGMH	540
Qy	541	SDIILAPQSTPEBLTSSWYFATSSHFYASASAIYGSASATSAVSCSQLPTCGDQVYSVRR	600
Db	541	SDIILAPQSTPEBLTSSWYFATSSHFYASASAIYGSASATSAVSCSQLPTCGDQVYSVRR	600
Qy	601	QKSPDRADSRNRMHESPPKQFKKRS COMERGESIMSNRRREBELGKXGSSSFSGSME	660
Db	601	QKSPDRADSRNRMHESPPKQFKKRS COMERGESIMSNRRREBELGKXGSSSFSGSME	660
Qy	661	IIIEVS 665	
Db	661	IIIEVS 665	

```

RESULT 5
US-10-168-506-14
/ Sequence 14, Application US/10168506
/ Publication No. US200400053229A1
/ GENERAL INFORMATION:
/ APPLICANT: PLOWMAN, GREGORY D.
/ APPLICANT: MARTINEZ, RICARDO
/ APPLICANT: WHITE, DAVID
/ APPLICANT: MANNING, GERRARD
/ APPLICANT: SUDARSANAM, SUCHA
/ APPLICANT: HILL, RON
/ APPLICANT: FLANAGAN, PETER
/ TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
/ FILE REFERENCE: 038602/1351
/ CURRENT APPLICATION NUMBER: US/10/168, 506
/ CURRENT FILING DATE: 2002-06-21
/ PRIOR APPLICATION NUMBER: PCT/US00/34736
/ PRIOR FILING DATE: 2000-12-21
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 14
/ LENGTH: 665
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-168-506-14

```

	Query Match	99.6%;	Score 3406;	DB 15;	Length 665;
	Best Local Similarity	99.7%;	Pred. No. 9e-238;		
	Matches 663;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	MAHEMIGQIYTERLVALLSEGTKEVLLIDBRPFVENVYTHILEAININCSKLMKRRIQQ	60		
Db	1	MAHEMIGQIYTERLVALLSEGTKEVLLIDBRPFVENVYTHILEAININCSKLMKRRIQQ	60		
QY	61	DKVLITELIQHSAAHKVDIDCSQKVVYDQSSQVAAISLSPCCFLTVLLIGKLEKSFNSVHL	120		
Db	61	DKVLITELIQHSAAHKVDIDCSQKVVYDQSSQVAAISLSPCCFLTVLLIGKLEKSFNSVHL	120		
QY	121	LAGGFAPFBSRCFPLCEBCKSTLVPTCTISQPLCPVANIPTIRLEPNLYIGCORDVINKELI	180		

Db	121	LHGFAHRSRCFBGLCGKSTLVPCTISQCPCLPVANI	IGFTRLLPMLVYGQCRDVLNKLMM	180
Qy	181	QONGIGVYLANASYCPCPDPFI	PESHFLRPVYVDSFCEKILPMLDKSVFIEKAXASNGCV	240
Db	181	QONGIGVYLANASNTCPKDPFI	PESHFLRPVYVDSFCEKILPMLDKSVFIEKAXASNGCV	240
Qy	241	LVHCLAGISRSATTAIAYIMKRDMSLDEA	RYFVKEKPTTISPNFNLGOLLIDYEKKIKN	300
Db	241	LVHCLAGISRSATTAIAYIMKRDMSLDEA	RYFVKEKPTTISPNFNLGOLLIDYEKKIKN	300
Qy	301	QTGASGPKSKLKLHLEKPNRPVPA	SEGGQSETPPLSPCCADSAITSEAAQORVHPASV	360
Db	301	QTGASGPKSKLKLHLEKPNRPVPA	SEGGQSETPPLSPCCADSAITSEAAQORVHPASV	360
Qy	361	PSVPSVOPSLIEDSPVLVQALSGHLH	SADRLBDSNKLKKSFSLIDIKSVSYASMAASLHGF	420
Db	361	PSVPSVOPSLIEDSPVLVQALSGHLH	SADRLBDSNKLKKSFSLIDIKSVSYASMAASLHGF	420
Qy	421	SSSDALEYKPKSTLIDGNKLCQSP	VPQELSEOPETSPDKERASIPKLCQTPARPSDQ	480
Db	421	SSSDALEYKPKSTLIDGNKLCQSP	VPQELSEOPETSPDKERASIPKLCQTPARPSDQ	480
Qy	481	SKRLHVSRTSSSGTAORSLSLPLHRS	GSVEDNYHTSFLPGJSTSQOHLTSAGLGLKGMH	540
Db	481	SKRLHVSRTSSSGTAORSLSLPLHRS	GSVEDNYHTSFLPGJSTSQOHLTSAGLGLKGMH	540
Qy	541	SDILAPOTSTPPLTSSWYPATSSHF	YFASAIYGGASAYSACSOULPTCGDOVYSVRRR	600
Db	541	SDILAPOTSTPPLTSSWYPATSSHF	YFASAIYGGASAYSACSOULPTCGDOVYSVRRR	600
Qy	601	QKPEDRADSRSHHESPEKQFKKRS	COMERGESIMSENNRREILDKVYSQSSPFGSME	660
Db	601	QKPEDRADSRSHHESPEKQFKKRS	COMERGESIMSENNRREILDKVYSQSSPFGSME	660
Qy	661	IIIVS	665	
Db	661	IIIVS	665	

RESULT 6
US-10-343-357-7
Sequence 7, Application US/10343357
Publication No. US20040058341A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.; TANG, Y
APPLICANT: ELLIOTT, VICKI S.; RAKHMUR
APPLICANT: YAO, Monique G.; BURPOD, Ne
APPLICANT: WANG, Yumei E.; STEWART, Eli
APPLICANT: GANDHI, Ameena R.; ARATZU, Ch
APPLICANT: LEE, Ernestine A.; HAFALIA, A
APPLICANT: LU, Dying Aina M.; TRIBOULEY
APPLICANT: GRIFFIN, Jennifer A.; BAUGHN
APPLICANT: YUE, Henry; WARREN, Bridget
APPLICANT: NGUYEN, Daniel B.; CHAWLA, N
APPLICANT: KEARNEY, Liam
TITLE OF INVENTION: PROTEIN PHOSPHATASES
FILE REFERENCE: PI-0173 PCT
CURRENT APPLICATION NUMBER: US/10/343,357
CURRENT FILING DATE: 2003-01-28
PRIORITY APPLICATION NUMBER: PCT/US01/23716
PRIORITY FILING DATE: 2001-07-26
PRIORITY APPLICATION NUMBER: US 60/221,679
PRIORITY FILING DATE: 2000-07-28
PRIORITY APPLICATION NUMBER: US 60/223,272
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: US 60/224,309
PRIORITY FILING DATE: 2000-08-10
PRIORITY APPLICATION NUMBER: US 60/226,728
PRIORITY FILING DATE: 2000-08-18
PRIORITY APPLICATION NUMBER: US 60/229,254
PRIORITY FILING DATE: 2000-08-30
PRIORITY APPLICATION NUMBER: US 60/231,366

;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 20
;; SOFTWARE: PERL Program
;; SEQ ID NO 7
;; LENGTH: 665
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: m1agc feature
;; OTHER INFORMATION: Incyte ID No. US20040058341A1 7480570CD1
US-10-343-357-7

Query Match 99.6%; Score 3406; DB 15; Length 665;
Best Local Similarity 99.7%; Pred. No. 9e-238;
Matches 663; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAHEMIGTQIVTERLVALLSEGTETKLLIDSRPFVEYNTSHLEAININCSKLMKRRLOQ 60
DB 1 MAHEMIGTQIVTERLVALLSEGTETKLLIDSRPFVEYNTSHLEAININCSKLMKRRLOQ 60
QY 61 DKVLTTELIQHSAKHKVDIDCSQKVVVYDQSSODVASLSDCFETVLLGKLEKSFNSVHL 120
DB 61 DKVLTTELIQHSAKHKVDIDCSQKVVVYDQSSODVASLSDCFETVLLGKLEKSFNSVHL 120
QY 121 LAGFAEFRCFPGICEGKSTLVPTCISQPCLPVANIGPTRIIPNLVLCQORDVANKELI 180
DB 121 LAGFAEFRCFPGICEGKSTLVPTCISQPCLPVANIGPTRIIPNLVLCQORDVANKELI 180
QY 121 LAGFAEFRCFPGICEGKSTLVPTCISQPCLPVANIGPTRIIPNLVLCQORDVANKELI 180
DB 121 LAGFAEFRCFPGICEGKSTLVPTCISQPCLPVANIGPTRIIPNLVLCQORDVANKELI 180
QY 181 QONGIGYVLANASYTCRPPFIPESHFLRPVNDSPCEKILPMLDKSVDFIERAKASNGCV 240
DB 181 QONGIGYVLANASYTCRPPFIPESHFLRPVNDSPCEKILPMLDKSVDFIERAKASNGCV 240
QY 241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRTISPENFELGQLLDYEKKIKN 300
DB 241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRTISPENFELGQLLDYEKKIKN 300
QY 301 QTGASGPKSKLKLHLKEKNEPVPAVSEGGQKSETPLSPPCADSATSEAAQORPVHPASV 360
DB 301 QTGASGPKSKLKLHLKEKNEPVPAVSEGGQKSETPLSPPCADSATSEAAQORPVHPASV 360
QY 361 PSVPSVQPSLLEDSPLVQALSGHLISADRLSDNSKLRKSFSLDIKSVSASAMAASLHGF 420
DB 361 PSVPSVQPSLLEDSPLVQALSGHLISADRLSDNSKLRKSFSLDIKSVSASAMAASLHGF 420
QY 421 SSSSEDALEYKSTTLDGNTKLCQPSVQELSEQPTETSPDKBEASIPKKLQTARPSDQ 480
DB 421 SSSSEDALEYKSTTLDGNTKLCQPSVQELSEQPTETSPDKBEASIPKKLQTARPSDQ 480
QY 481 SKRLHSVRTSSSGTAQRSLISPLHRSGSVEDNYHTSFLGSLSTSOQHLTKSAGLGKGMH 540
DB 481 SKRLHSVRTSSSGTAQRSLISPLHRSGSVEDNYHTSFLGSLSTSOQHLTKSAGLGKGMH 540
QY 541 SDILAPQSTPSTPLTSSWYFATESSHFYASAIYGGASAYSAYSCGLPTCGQOVYSVRRR 600
DB 541 SDILAPQSTPSTPLTSSWYFATESSHFYASAIYGGASAYSAYSCGLPTCGQOVYSVRRR 600
QY 601 QKPSRADSRMRHESPEPEKQFKRRSCOMERGESIMSNRREELGKVGSSQSSFGSME 660
DB 601 QKPSRADSRMRHESPEPEKQFKRRSCOMERGESIMSNRREELGKVGSSQSSFGSME 660
QY 661 IIEVS 665
DB 661 IIEVS 665

RESULT 7
US-10-257-026-2
;; Sequence 2, Application US/10257026
;; Publication No. US20040086659A1
;; GENERAL INFORMATION:
;; APPLICANT: Merck Patent GmbH
;; TITLE OF INVENTION: New dual specificity phosphatase
;; FILE REFERENCE: DUSP10KOWS

;; CURRENT APPLICATION NUMBER: US/10/257,026
;; CURRENT FILING DATE: 2003-11-07
;; NUMBER OF SEQ ID NOS: 3
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 665
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-257-026-2

Query Match 99.6%; Score 3406; DB 15; Length 665;
Best Local Similarity 99.7%; Pred. No. 9e-238;
Matches 663; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAHEMIGTQIVTERLVALLSEGTETKLLIDSRPFVEYNTSHLEAININCSKLMKRRLOQ 60
DB 1 MAHEMIGTQIVTERLVALLSEGTETKLLIDSRPFVEYNTSHLEAININCSKLMKRRLOQ 60
QY 61 DKVLTTELIQHSAKHKVDIDCSQKVVVYDQSSODVASLSDCFETVLLGKLEKSFNSVHL 120
DB 61 DKVLTTELIQHSAKHKVDIDCSQKVVVYDQSSODVASLSDCFETVLLGKLEKSFNSVHL 120
QY 121 LAGFAEFRCFPGICEGKSTLVPTCISQPCLPVANIGPTRIIPNLVLCQORDVANKELI 180
DB 121 LAGFAEFRCFPGICEGKSTLVPTCISQPCLPVANIGPTRIIPNLVLCQORDVANKELI 180
QY 121 LAGFAEFRCFPGICEGKSTLVPTCISQPCLPVANIGPTRIIPNLVLCQORDVANKELI 180
DB 121 LAGFAEFRCFPGICEGKSTLVPTCISQPCLPVANIGPTRIIPNLVLCQORDVANKELI 180
QY 181 QONGIGYVLANASYTCRPPFIPESHFLRPVNDSPCEKILPMLDKSVDFIERAKASNGCV 240
DB 181 QONGIGYVLANASYTCRPPFIPESHFLRPVNDSPCEKILPMLDKSVDFIERAKASNGCV 240
QY 241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRTISPENFELGQLLDYEKKIKN 300
DB 241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRTISPENFELGQLLDYEKKIKN 300
QY 301 QTGASGPKSKLKLHLKEKNEPVPAVSEGGQKSETPLSPPCADSATSEAAQORPVHPASV 360
DB 301 QTGASGPKSKLKLHLKEKNEPVPAVSEGGQKSETPLSPPCADSATSEAAQORPVHPASV 360
QY 361 PSVPSVQPSLLEDSPLVQALSGHLISADRLSDNSKLRKSFSLDIKSVSASAMAASLHGF 420
DB 361 PSVPSVQPSLLEDSPLVQALSGHLISADRLSDNSKLRKSFSLDIKSVSASAMAASLHGF 420
QY 421 SSSSEDALEYKSTTLDGNTKLCQPSVQELSEQPTETSPDKBEASIPKKLQTARPSDQ 480
DB 421 SSSSEDALEYKSTTLDGNTKLCQPSVQELSEQPTETSPDKBEASIPKKLQTARPSDQ 480
QY 481 SKRLHSVRTSSSGTAQRSLISPLHRSGSVEDNYHTSFLGSLSTSOQHLTKSAGLGKGMH 540
DB 481 SKRLHSVRTSSSGTAQRSLISPLHRSGSVEDNYHTSFLGSLSTSOQHLTKSAGLGKGMH 540
QY 541 SDILAPQSTPSTPLTSSWYFATESSHFYASAIYGGASAYSAYSCGLPTCGQOVYSVRRR 600
DB 541 SDILAPQSTPSTPLTSSWYFATESSHFYASAIYGGASAYSAYSCGLPTCGQOVYSVRRR 600
QY 601 QKPSRADSRMRHESPEPEKQFKRRSCOMERGESIMSNRREELGKVGSSQSSFGSME 660
DB 601 QKPSRADSRMRHESPEPEKQFKRRSCOMERGESIMSNRREELGKVGSSQSSFGSME 660
QY 661 IIEVS 665
DB 661 IIEVS 665

RESULT 8
US-10-648-593-240
;; Sequence 240, Application US/10648593
;; Publication No. US20040106132A1
;; GENERAL INFORMATION:
;; APPLICANT: Bristol-Myers Squibb Company
;; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
;; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
;; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
;; FILE REFERENCE: D0273 NP

```

; CURRENT APPLICATION NUMBER: US/10/648,593
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 240
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-593-240

```

```

Query Match      99.6%; Score 3406; DB 16; Length 665;
Best Local Similarity 99.7%; Pred. No. 9e-238;
Matches 663; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MAHEMIGTQIVTERLVALLESSTGEKVLIDSRPFVEYNTSHILEAININCSKLMKRRLQ 60
    |||||||
DB 1 MAHEMIGTQIVTERLVALLESSTGEKVLIDSRPFVEYNTSHILEAININCSKLMKRRLQ 60
    |||||||
QY 61 DKVLITELIOWSAKHKVDIDCSQKVVYVDQSSQDVASLSDCFVLTVLGLKLEKSPNSVHL 120
    |||||||
DB 61 DKVLITELIOWSAKHKVDIDCSQKVVYVDQSSQDVASLSDCFVLTVLGLKLEKSPNSVHL 120
    |||||||
QY 121 LAGGFAEFSRCFPGICGKSTLVPTCISQPCLPVANIGPTRILPNLYLGGQRDVYNKEML 180
    |||||||
DB 121 LAGGFAEFSRCFPGICGKSTLVPTCISQPCLPVANIGPTRILPNLYLGGQRDVYNKEML 180
    |||||||
QY 181 QONGIGVYLNASTCPKDPFIPESHFLRPVNDSPCEKILPWLKSVDFIEKAKASNGCV 240
    |||||||
DB 181 QONGIGVYLNASTCPKDPFIPESHFLRPVNDSPCEKILPWLKSVDFIEKAKASNGCV 240
    |||||||
QY 241 LVHCLAGISRSATIAIAYIMKRDMSLDEAYRFYKEKRPITSPNPNFLGQLLDYEKKIKN 300
    |||||||
DB 241 LVHCLAGISRSATIAIAYIMKRDMSLDEAYRFYKEKRPITSPNPNFLGQLLDYEKKIKN 300
    |||||||
QY 301 QTGASGPKSKLKLHLEKPNRPVAVSEGGQKSTPLSPCADSATSEAAQRPVHPASV 360
    |||||||
DB 301 QTGASGPKSKLKLHLEKPNRPVAVSEGGQKSTPLSPCADSATSEAAQRPVHPASV 360
    |||||||
QY 361 PSVSVQPSLLEDSPLVQALSGHLASDRLEDSNKLKRSFSLDIKVSYSASMAASLHGF 420
    |||||||
DB 361 PSVSVQPSLLEDSPLVQALSGHLASDRLEDSNKLKRSFSLDIKVSYSASMAASLHGF 420
    |||||||
QY 421 SSSSDALEYKPSFTLLDGTNKLCOFSPVOELSEQTPEPSPDKEASIPKKLQTPARPSDQ 480
    |||||||
DB 421 SSSSDALEYKPSFTLLDGTNKLCOFSPVOELSEQTPEPSPDKEASIPKKLQTPARPSDQ 480
    |||||||
QY 481 SKRLHSVRTSSSGTAQRSLSLPLHRSGSVEDNYHTSFLGLSTSQOHLTKSAGLGKGMH 540
    |||||||
DB 481 SKRLHSVRTSSSGTAQRSLSLPLHRSGSVEDNYHTSFLGLSTSQOHLTKSAGLGKGMH 540
    |||||||
QY 541 SDILAPQTSPTSLTSSWYFATESHFPYSASAIYGSASAYSAYSCSLPTCGQVYSVRRR 600
    |||||||
DB 541 SDILAPQTSPTSLTSSWYFATESHFPYSASAIYGSASAYSAYSCSLPTCGQVYSVRRR 600
    |||||||
QY 601 QKPSDRADSRSRWHEESPFEKQFKRRSCQMEFGESIMSENRREBELGKVGSSFSGSM 660
    |||||||
DB 601 QKPSDRADSRSRWHEESPFEKQFKRRSCQMEFGESIMSENRREBELGKVGSSFSGSM 660
    |||||||
QY 661 IIEVS 665
    |||||
DB 661 IIEVS 665
    |||||

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```

RESULT 9
US-10-648-593-247
; Sequence 247, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR

```

```

; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 247
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-593-247

```

```

Query Match      99.6%; Score 3406; DB 16; Length 665;
Best Local Similarity 99.7%; Pred. No. 9e-238;
Matches 663; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 MAHEMIGTQIVTERLVALLESSTGEKVLIDSRPFVEYNTSHILEAININCSKLMKRRLQ 60
    |||||||
DB 1 MAHEMIGTQIVTERLVALLESSTGEKVLIDSRPFVEYNTSHILEAININCSKLMKRRLQ 60
    |||||||
QY 61 DKVLITELIOWSAKHKVDIDCSQKVVYVDQSSQDVASLSDCFVLTVLGLKLEKSPNSVHL 120
    |||||||
DB 61 DKVLITELIOWSAKHKVDIDCSQKVVYVDQSSQDVASLSDCFVLTVLGLKLEKSPNSVHL 120
    |||||||
QY 121 LAGGFAEFSRCFPGICGKSTLVPTCISQPCLPVANIGPTRILPNLYLGGQRDVYNKEML 180
    |||||||
DB 121 LAGGFAEFSRCFPGICGKSTLVPTCISQPCLPVANIGPTRILPNLYLGGQRDVYNKEML 180
    |||||||
QY 181 QONGIGVYLNASTCPKDPFIPESHFLRPVNDSPCEKILPWLKSVDFIEKAKASNGCV 240
    |||||||
DB 181 QONGIGVYLNASTCPKDPFIPESHFLRPVNDSPCEKILPWLKSVDFIEKAKASNGCV 240
    |||||||
QY 241 LVHCLAGISRSATIAIAYIMKRDMSLDEAYRFYKEKRPITSPNPNFLGQLLDYEKKIKN 300
    |||||||
DB 241 LVHCLAGISRSATIAIAYIMKRDMSLDEAYRFYKEKRPITSPNPNFLGQLLDYEKKIKN 300
    |||||||
QY 301 QTGASGPKSKLKLHLEKPNRPVAVSEGGQKSTPLSPCADSATSEAAQRPVHPASV 360
    |||||||
DB 301 QTGASGPKSKLKLHLEKPNRPVAVSEGGQKSTPLSPCADSATSEAAQRPVHPASV 360
    |||||||
QY 361 PSVSVQPSLLEDSPLVQALSGHLASDRLEDSNKLKRSFSLDIKVSYSASMAASLHGF 420
    |||||||
DB 361 PSVSVQPSLLEDSPLVQALSGHLASDRLEDSNKLKRSFSLDIKVSYSASMAASLHGF 420
    |||||||
QY 421 SSSSDALEYKPSFTLLDGTNKLCOFSPVOELSEQTPEPSPDKEASIPKKLQTPARPSDQ 480
    |||||||
DB 421 SSSSDALEYKPSFTLLDGTNKLCOFSPVOELSEQTPEPSPDKEASIPKKLQTPARPSDQ 480
    |||||||
QY 481 SKRLHSVRTSSSGTAQRSLSLPLHRSGSVEDNYHTSFLGLSTSQOHLTKSAGLGKGMH 540
    |||||||
DB 481 SKRLHSVRTSSSGTAQRSLSLPLHRSGSVEDNYHTSFLGLSTSQOHLTKSAGLGKGMH 540
    |||||||
QY 541 SDILAPQTSPTSLTSSWYFATESHFPYSASAIYGSASAYSAYSCSLPTCGQVYSVRRR 600
    |||||||
DB 541 SDILAPQTSPTSLTSSWYFATESHFPYSASAIYGSASAYSAYSCSLPTCGQVYSVRRR 600
    |||||||
QY 601 QKPSDRADSRSRWHEESPFEKQFKRRSCQMEFGESIMSENRREBELGKVGSSFSGSM 660
    |||||||
DB 601 QKPSDRADSRSRWHEESPFEKQFKRRSCQMEFGESIMSENRREBELGKVGSSFSGSM 660
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QY 661 IIEVS 665
    |||||
DB 661 IIEVS 665
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RESULT 10
US-10-377-072-26
; Sequence 26, Application US/10377072
; Publication No. US20040157221A9
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.

```



```
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Myoung
; APPLICANT: Teal, Peng-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; FILE REFERENCE: MP103-0180NMIM
; CURRENT APPLICATION NUMBER: US/10/377,072
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895,860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/843,297
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; PRIOR FILING DATE: 2001-03-22
; Remaining Prior Application data removed - See file wrapper or PAM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-377-072-26

Query Match      99.6%; Score 3406; DB 16; Length 665;
Best Local Similarity 99.7%; Pred. No. 9e-238;
Matches 663; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Db      361 PSVPSVQPSLLEDSPLVQALSGHLSDRLLEDNSNKLKRSFSLDIKVSYSASMAASLHGCF 420
Qy      421 SSSDALFYKRSSTLTDGNNKLCQSPVQELSSEQTPETSPPDEKASIPKKLQTPARPSDQ 480
Db      421 SSSDALFYKRSSTLTDGNNKLCQSPVQELSSEQTPETSPPDEKASIPKKLQTPARPSDQ 480
Qy      481 SKRLHSVTRSSSGTQORSLSLPLHRSQSVEDNYHTSFLGLSTSOQHLTKSAGLKGW 540
Db      481 SKRLHSVTRSSSGTQORSLSLPLHRSQSVEDNYHTSFLGLSTSOQHLTKSAGLKGW 540
Qy      541 SDILAPQSTPSTLSSWTFATESHPYSASAIYGSASYSAYSCSQLPTCGDQVYSVRR 600
Db      541 SDILAPQSTPSTLSSWTFATESHPYSASAIYGSASYSAYSCSQLPTCGDQVYSVRR 600
Qy      601 QKPSRPAOSRRRWHESSPEKQPKRRSCMGECSIMSNRRREPLGKYGSSSFSGSM 660
Db      601 QKPSRPAOSRRRWHESSPEKQPKRRSCMGECSIMSNRRREPLGKYGSSSFSGSM 660
Qy      661 IIEVS 665
Db      661 IIEVS 665

RESULT 11
US-10-072-012-679
; Sequence 679, Application US/10072012
; Publication No. US2004003493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zernusen, Bryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Shinkete, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Bsha
; APPLICANT: Padigaru, Muraidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Coleman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Groese, William M.
; APPLICANT: Alsbrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
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; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 679
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-679

Query Match      99.6%; Score 3406; DB 15; Length 690;
Best Local Similarity 99.7%; Pred. No. 9.5e-238;
Matches 663; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAHEMIGTOIVTEBLVALLSGTEKVLIDSRPVEVNTSHIIIEAININSKIMKRLQ 60
DB 26 MAHEMIGTOIVTEBLVALLSGTEKVLIDSRPVEVNTSHIIIEAININSKIMKRLQ 85
QY 61 DKVLITELIHSANHKVDIDCSQKVVVYDQSDVASSDCEFLTVLLGLKLEKSFNSVHL 120
DB 86 DKVLITELIHSANHKVDIDCSQKVVVYDQSDVASSDCEFLTVLLGLKLEKSFNSVHL 145
QY 121 LAGGFAEFRCFPGLCGKSTLVPTCISQCLPVANIGPTRLIPNLYLGGQRDVLNKEIL 180
DB 146 LAGGFAEFRCFPGLCGKSTLVPTCISQCLPVANIGPTRLIPNLYLGGQRDVLNKEIL 205
QY 181 QONGIGVYLNASTCPEPDIPIESHFLRPVNDSPCEKILPMTDKSVDFIEKAKANGCV 240
DB 206 QONGIGVYLNASTCPEPDIPIESHFLRPVNDSPCEKILPMTDKSVDFIEKAKANGCV 265
QY 241 LVHCLAGISRSATIALAYIMKMDMSLDEAYRFVKEKRPITISPNFNLGQLDYEKKIKN 300
DB 266 LVHCLAGISRSATIALAYIMKMDMSLDEAYRFVKEKRPITISPNFNLGQLDYEKKIKN 325
QY 301 QTCASGPKSKLKLHLEKPEPVPAVSEGGKSETLSPPCADSATSEAAQRPVHPASV 360
DB 326 QTCASGPKSKLKLHLEKPEPVPAVSEGGKSETLSPPCADSATSEAAQRPVHPASV 385
QY 361 PSVPSVQPSLIEDSPVQALSGHLTADRLSDNKLKRSPLDIKSVSASMAASLHGF 420
DB 386 PSVPSVQPSLIEDSPVQALSGHLTADRLSDNKLKRSPLDIKSVSASMAASLHGF 445
QY 421 SSSSEDLAEYKKBSTLLDGTNKLQCFSPVQELSEQTPETSPPDKEASIPKCLQTARPSDQ 480
DB 446 SSSSEDLAEYKKBSTLLDGTNKLQCFSPVQELSEQTPETSPPDKEASIPKCLQTARPSDQ 505
QY 481 SKRIHSVRTSSSGTAQRSLSPLRSGSVEDNYHTSFLGLSTSOQHLTKSAGLKGWH 540
DB 506 SKRIHSVRTSSSGTAQRSLSPLRSGSVEDNYHTSFLGLSTSOQHLTKSAGLKGWH 565
QY 541 SDILAPQISTPSTLTSWYFATESHFPYSASAIYGSASAYSAYSCSOLPTCGDQVYSVRR 600
DB 566 SDILAPQISTPSTLTSWYFATESHFPYSASAIYGSASAYSAYSCSOLPTCGDQVYSVRR 625
QY 601 QKPSRADSRRRWHEESPPEKQPKRRSCOMEFGEISMSENRSREELGKVGSGSFGSWE 660
DB 626 QKPSRADSRRRWHEESPPEKQPKRRSCOMEFGEISMSENRSREELGKVGSGSFGSWE 685
QY 661 IIEVS 665
DB 686 IIEVS 690

```

```

; APPLICANT: Shinketsu, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie E.
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Coleman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol B. A
; APPLICANT: Furtak, Karazyna
; APPLICANT: Grose, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 703
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-703

Query Match      99.6%; Score 3406; DB 15; Length 690;
Best Local Similarity 99.7%; Pred. No. 9.5e-238;
Matches 663; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAHEMIGTOIVTEBLVALLSGTEKVLIDSRPVEVNTSHIIIEAININSKIMKRLQ 60
DB 26 MAHEMIGTOIVTEBLVALLSGTEKVLIDSRPVEVNTSHIIIEAININSKIMKRLQ 85
QY 61 DKVLITELIHSANHKVDIDCSQKVVVYDQSDVASSDCEFLTVLLGLKLEKSFNSVHL 120
DB 86 DKVLITELIHSANHKVDIDCSQKVVVYDQSDVASSDCEFLTVLLGLKLEKSFNSVHL 145
QY 121 LAGGFAEFRCFPGLCGKSTLVPTCISQCLPVANIGPTRLIPNLYLGGQRDVLNKEIL 180
DB 146 LAGGFAEFRCFPGLCGKSTLVPTCISQCLPVANIGPTRLIPNLYLGGQRDVLNKEIL 205
QY 181 QONGIGVYLNASTCPEPDIPIESHFLRPVNDSPCEKILPMTDKSVDFIEKAKANGCV 240
DB 206 QONGIGVYLNASTCPEPDIPIESHFLRPVNDSPCEKILPMTDKSVDFIEKAKANGCV 265
QY 241 LVHCLAGISRSATIALAYIMKMDMSLDEAYRFVKEKRPITISPNFNLGQLDYEKKIKN 300

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Db      266 LVHCLAGISRSATIAIAYIMKRMDSLDEAYRFVKEKRPITISPNFNLQQLDYEEKIKX 325
Qy      301 QTGASGPBKSKLKLHLHEKNEPVPVASEGQKSETPLSPPCADSAITSEAAQRPVHPASV 360
Db      326 QTGASGPBKSKLKLHLHEKNEPVPVASEGQKSETPLSPPCADSAITSEAAQRPVHPASV 385
Qy      361 PSVPSVQPSLLEDSPLVQALSGHLHSAADLEDSNKLKRSFSLDIKVSYSASMAASLHGF 420
Db      386 PSVPSVQPSLLEDSPLVQALSGHLHSAADLEDSNKLKRSFSLDIKVSYSASMAASLHGF 445
Qy      421 SSSSEDALEYKRPSTLLDGTNKLCOFSVQVQLSEQTPETSPDXKEASIPKKLQTPARPSDQ 480
Db      446 SSSSEDALEYKRPSTLLDGTNKLCOFSVQVQLSEQTPETSPDXKEASIPKKLQTPARPSDQ 505
Qy      481 SKRLHSVRTSSSGTQARSLSLPLHRSQVEDNYHTSFLGLSTSOQHLTKSAGLGKGMH 540
Db      506 SKRLHSVRTSSSGTQARSLSLPLHRSQVEDNYHTSFLGLSTSOQHLTKSAGLGKGMH 565
Qy      541 SDILAPQSTPLTSSWYFATESSHFYASAIYGASASAYSCSOLPTCGDQVSVRRR 600
Db      566 SDILAPQSTPLTSSWYFATESSHFYASAIYGASASAYSCSOLPTCGDQVSVRRR 625
Qy      601 QKPSDRADSRSMHESPEPEKQFKRRSCOMEFGESIMSENRRREELGKVGSSPFGSME 660
Db      626 QKPSDRADSRSMHESPEPEKQFKRRSCOMEFGESIMSENRRREELGKVGSSPFGSME 685
Qy      661 IIEVS 665
Db      686 IIEVS 690

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RESULT 13

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US-10-425-114-54204
; Sequence 54204, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54204
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4119-028-He_Fli pep
US-10-425-114-54204

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Query Match      99.6%; Score 3406; DB 15; Length 690;
Best Local Similarity 99.7%; Pred. No. 9,5e-238;
Matches 663; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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```

Qy      1 MAHEMGTQIVTERVALLESGETEKLALDSRPVYVNSHILEANINCSKLMKRLQO 60
Db      26 MAHEMGTQIVTERVALLESGETEKLALDSRPVYVNSHILEANINCSKLMKRLQO 85
Qy      61 DYVLITELIQHSAXHKVDIDCSQKVVVYDQSSQDVASLSDFLTVLLGKLEKSFNSVHL 120
Db      86 DYVLITELIQHSAXHKVDIDCSQKVVVYDQSSQDVASLSDFLTVLLGKLEKSFNSVHL 145
Qy      121 LAGGFABSRCPGLCEGSGSTLVPTCISQPCLPVANIGFTRILPNLYLGCQRDVINKELI 180
Db      146 LAGGFABSRCPGLCEGSGSTLVPTCISQPCLPVANIGFTRILPNLYLGCQRDVINKELI 205

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Qy      181 QONGIGVYLNASVTCPEKDFIPESHFLRPVNDSPCEKILPWLDKSVDFIERAKANGCV 240
Db      206 QONGIGVYLNASVTCPEKDFIPESHFLRPVNDSPCEKILPWLDKSVDFIERAKANGCV 265
Qy      241 LVHCLAGISRSATIAIAYIMKRMDSLDEAYRFVKEKRPITISPNFNLQQLDYEEKIKX 300
Db      266 LVHCLAGISRSATIAIAYIMKRMDSLDEAYRFVKEKRPITISPNFNLQQLDYEEKIKX 325
Qy      301 QTGASGPBKSKLKLHLHEKNEPVPVASEGQKSETPLSPPCADSAITSEAAQRPVHPASV 360
Db      326 QTGASGPBKSKLKLHLHEKNEPVPVASEGQKSETPLSPPCADSAITSEAAQRPVHPASV 385
Qy      361 PSVPSVQPSLLEDSPLVQALSGHLHSAADLEDSNKLKRSFSLDIKVSYSASMAASLHGF 420
Db      386 PSVPSVQPSLLEDSPLVQALSGHLHSAADLEDSNKLKRSFSLDIKVSYSASMAASLHGF 445
Qy      421 SSSSEDALEYKRPSTLLDGTNKLCOFSVQVQLSEQTPETSPDXKEASIPKKLQTPARPSDQ 480
Db      446 SSSSEDALEYKRPSTLLDGTNKLCOFSVQVQLSEQTPETSPDXKEASIPKKLQTPARPSDQ 505
Qy      481 SKRLHSVRTSSSGTQARSLSLPLHRSQVEDNYHTSFLGLSTSOQHLTKSAGLGKGMH 540
Db      506 SKRLHSVRTSSSGTQARSLSLPLHRSQVEDNYHTSFLGLSTSOQHLTKSAGLGKGMH 565
Qy      541 SDILAPQSTPLTSSWYFATESSHFYASAIYGASASAYSCSOLPTCGDQVSVRRR 600
Db      566 SDILAPQSTPLTSSWYFATESSHFYASAIYGASASAYSCSOLPTCGDQVSVRRR 625
Qy      601 QKPSDRADSRSMHESPEPEKQFKRRSCOMEFGESIMSENRRREELGKVGSSPFGSME 660
Db      626 QKPSDRADSRSMHESPEPEKQFKRRSCOMEFGESIMSENRRREELGKVGSSPFGSME 685
Qy      661 IIEVS 665
Db      686 IIEVS 690

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RESULT 14

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US-10-094-749-2312
; Sequence 2312, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHITO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYOKU
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 2312
; LENGTH: 665
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-094-749-2312
Query Match      99.4%; Score 3399; DB 15; Length 665;
Best Local Similarity 99.5%; Pred. No. 2.9e-237;
Matches 662; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 MAHEMIGQIYTERLVALLBSGTEKVLIDSRPVEYNTSHILEAININCSKLMKRRLQ 60
DB      1 MAHEMIGQIYTERLVALLBSGTEKVLIDSRPVEYNTSHILEAININCSKLMKRRLQ 60
QY      61 DKVLITELIOHSAGHKVYIDCSQKVYVYDSSQDVASLSSDCFLTVLLGKLEKSFNSVHL 120
DB      61 DKVLITELIOHSAGHKVYIDCSQKVYVYDSSQDVASLSSDCFLTVLLGKLEKSFNSVHL 120
QY      121 LAGGFAFRSFCFPLCGKSTLVPTCISQCLPVANIGPRLIPNLVLCQORDVNLKELI 180
DB      121 LAGGFAFRSFCFPLCGKSTLVPTCISQCLPVANIGPRLIPNLVLCQORDVNLKELI 180
QY      181 QONGIGVVLNASTYCPKPDFIPESHFLRVVNDSPCEKILPMIDKSVDFIEKAKANGCV 240
DB      181 QONGIGVVLNASTYCPKPDFIPESHFLRVVNDSPCEKILPMIDKSVDFIEKAKANGCV 240
QY      241 LVHCLAGISSRATIAIAYIMKMDMSIDEAYRFVKEKRPITSPNPNFLGQLLDYEKKIKN 300
DB      241 LVHCLAGISSRATIAIAYIMKMDMSIDEAYRFVKEKRPITSPNPNFLGQLLDYEKKIKN 300
QY      301 QGTASGPKSKLKLHLKEKPEVPVAVSEGQKSETPLSPCADSATSEAGORPVHPASV 360
DB      301 QGTASGPKSKLKLHLKEKPEVPVAVSEGQKSETPLSPCADSATSEAGORPVHPASV 360
QY      361 PSVPVQPSLLEDSPLVQALSGHLISADRLSDSNKLKRSPLDIKSVSYASMAASIHGF 420
DB      361 PSVPVQPSLLEDSPLVQALSGHLISADRLSDSNKLKRSPLDIKSVSYASMAASIHGF 420
QY      421 SSSSEDALEYKPSSTTLDGNTKLCQFSPVQELSEQTEPSPDKEASIPKKLQTAAPSDSQ 480
DB      421 SSSSEDALEYKPSSTTLDGNTKLCQFSPVQELSEQTEPSPDKEASIPKKLQTAAPSDSQ 480
QY      481 SKRLHSVRSSSGTQARSLISPLHRSQVYEDNHTFTFLGSLSQOHLTKSAGLGKGMH 540
DB      481 SKRLHSVRSSSGTQARSLISPLHRSQVYEDNHTFTFLGSLSQOHLTKSAGLGKGMH 540
QY      541 SDLIAPQTSPTSLTSSMYFATESSHFYASAIYGSASAYASCSQLPCTGPOVYSVRR 600
DB      541 SDLIAPQTSPTSLTSSMYFATESSHFYASAIYGSASAYASCSQLPCTGPOVYSVRR 600
QY      601 QKPSDPAISRHSWHEESPKEQPKRRSCQMEFGESIMSENRREBELGKVGQSFPQSGME 660
DB      601 QKPSDPAISRHSWHEESPKEQPKRRSCQMEFGESIMSENRREBELGKVGQSFPQSGME 660
QY      661 IIEVS 665
DB      661 IIEVS 665

RESULT 15
US-10-072-012-681
; Sequence 681, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zehnusen, Bryan
; APPLICANT: Patnurejan, Meera
; APPLICANT: Shimke, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangoli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rasfelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
```

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; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Wolman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Groose, William M.
; APPLICANT: Alsdorok II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 681
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-681
Query Match      99.4%; Score 3399; DB 15; Length 665;
Best Local Similarity 99.5%; Pred. No. 2.9e-237;
Matches 662; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 MAHEMIGQIYTERLVALLBSGTEKVLIDSRPVEYNTSHILEAININCSKLMKRRLQ 60
DB      1 MAHEMIGQIYTERLVALLBSGTEKVLIDSRPVEYNTSHILEAININCSKLMKRRLQ 60
QY      61 DKVLITELIOHSAGHKVYIDCSQKVYVYDSSQDVASLSSDCFLTVLLGKLEKSFNSVHL 120
DB      61 DKVLITELIOHSAGHKVYIDCSQKVYVYDSSQDVASLSSDCFLTVLLGKLEKSFNSVHL 120
QY      121 LAGGFAFRSFCFPLCGKSTLVPTCISQCLPVANIGPRLIPNLVLCQORDVNLKELI 180
DB      121 LAGGFAFRSFCFPLCGKSTLVPTCISQCLPVANIGPRLIPNLVLCQORDVNLKELI 180
QY      181 QONGIGVVLNASTYCPKPDFIPESHFLRVVNDSPCEKILPMIDKSVDFIEKAKANGCV 240
DB      181 QONGIGVVLNASTYCPKPDFIPESHFLRVVNDSPCEKILPMIDKSVDFIEKAKANGCV 240
QY      241 LVHCLAGISSRATIAIAYIMKMDMSIDEAYRFVKEKRPITSPNPNFLGQLLDYEKKIKN 300
DB      241 LVHCLAGISSRATIAIAYIMKMDMSIDEAYRFVKEKRPITSPNPNFLGQLLDYEKKIKN 300
QY      301 QGTASGPKSKLKLHLKEKPEVPVAVSEGQKSETPLSPCADSATSEAGORPVHPASV 360
DB      301 QGTASGPKSKLKLHLKEKPEVPVAVSEGQKSETPLSPCADSATSEAGORPVHPASV 360
QY      361 PSVPVQPSLLEDSPLVQALSGHLISADRLSDSNKLKRSPLDIKSVSYASMAASIHGF 420
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2005, 12:00:17 ; Search time 42.637 Seconds
(without alignments)
1164.285 Million cell updates/sec

Title: US-10-029-345A-109

Perfect score: 3418

Sequence: 1 MAHEMIGQIVTERLVALL...LKVGSGSSFGSGMEIIEVS 665

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: Issued Patents AA: *
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7: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3406	99.6	665	US-09-816-494-2	Sequence 2, Appli
2	1324	38.7	661	US-09-949-016-9121	Sequence 9121, Ap
3	654.5	19.1	170	US-09-544-716-14	Sequence 14, Appl
4	654.5	19.1	170	US-09-557-921-15	Sequence 15, Appl
5	654.5	19.1	170	US-09-564-357-17	Sequence 17, Appl
6	654.5	19.1	170	US-09-619-380-16	Sequence 16, Appl
7	619	18.1	155	US-09-955-732A-6	Sequence 6, Appl
8	470.5	13.8	491	US-09-949-016-8486	Sequence 8486, Ap
9	469	13.7	482	US-09-557-921-2	Sequence 2, Appli
10	453	13.3	394	US-09-702-705-805	Sequence 805, App
11	453	13.3	394	US-09-736-457-805	Sequence 805, App
12	453	13.3	394	US-09-614-124B-805	Sequence 805, App
13	453	13.3	394	US-09-671-325-805	Sequence 805, App
14	453	13.3	394	US-09-589-184-805	Sequence 805, App
15	453	13.3	394	US-09-658-824-805	Sequence 805, App
16	445	13.0	394	US-08-530-290-23	Sequence 23, Appl
17	445	13.0	394	US-09-702-705-827	Sequence 827, App
18	445	13.0	394	US-09-736-457-827	Sequence 827, App
19	445	13.0	394	US-09-614-124B-827	Sequence 827, App
20	445	13.0	394	US-09-671-325-827	Sequence 827, App
21	445	13.0	394	US-09-589-184-827	Sequence 827, App
22	445	13.0	394	US-09-658-824-827	Sequence 827, App
23	445	13.0	413	US-09-949-016-8081	Sequence 8081, App
24	439.5	12.9	395	US-08-990-379-5	Sequence 5, Appli
25	433	12.7	367	US-08-990-379-6	Sequence 6, Appli
26	425	12.4	314	US-09-371-671B-11	Sequence 11, Appl
27	420	12.3	367	US-08-530-290-24	Sequence 24, Appl

28	420	12.3	367	4	US-09-919-497-60	Sequence 60, Appl
29	420	12.3	449	4	US-09-949-016-10840	Sequence 10840, A
30	417	12.2	421	4	US-09-949-016-10488	Sequence 10488, A
31	409.5	12.0	313	2	US-08-990-379-7	Sequence 7, Appli
32	409	12.0	314	3	US-09-164-193-22	Sequence 22, Appl
33	409	12.0	314	3	US-09-221-448A-22	Sequence 22, Appl
34	393.5	11.5	393	2	US-08-990-379-4	Sequence 4, Appli
35	377	11.0	302	4	US-09-702-705-806	Sequence 806, App
36	377	11.0	302	4	US-09-736-457-806	Sequence 806, App
37	377	11.0	302	4	US-09-614-124B-806	Sequence 806, App
38	377	11.0	302	4	US-09-671-325-806	Sequence 806, App
39	377	11.0	302	4	US-09-589-184-806	Sequence 806, App
40	377	11.0	302	4	US-09-658-824-806	Sequence 806, App
41	366	10.7	397	2	US-08-990-379-8	Sequence 8, Appli
42	360.5	10.5	384	4	US-09-949-016-6494	Sequence 6494, Ap
43	346.5	10.1	168	4	US-09-544-716-13	Sequence 13, Appl
44	346.5	10.1	168	4	US-09-557-921-13	Sequence 13, Appl
45	346.5	10.1	168	4	US-09-564-357-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1						
US-09-816-494-2						
; Sequence 2, Application US/09816494						
; Patent No. 6664089						
; GENERAL INFORMATION:						
; APPLICANT: Meyers, Rachel A.						
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY						
; FILE REFERENCE: 10448-030002						
; CURRENT APPLICATION NUMBER: US/09/816,494						
; PRIOR FILING DATE: 2001-03-23						
; PRIOR APPLICATION NUMBER: 60/191,858						
; NUMBER OF SEQ ID NOS: 10						
; SOFTWARE: FastSeq for Windows Version 4.0						
; SEQ ID NO 2						
; LENGTH: 665						
; TYPE: PRT						
; ORGANISM: Homo sapiens						
US-09-816-494-2						
Query Match						
Best Local Similarity 99.6%; Score 3406; DB 4; Length 665;						
Matches 663; Conservative 1; Mismatches 1; Indels 0; Gaps 0;						
QY	1	MAHEMIGQIVTERLVALLSGSTGTEKVLIDSPFVYNTSHILEAININCSKLMKRRLLQ	60			
DB	1	MAHEMIGQIVTERLVALLSGSTGTEKVLIDSPFVYNTSHILEAININCSKLMKRRLLQ	60			
QY	61	DKVLITELIHSARKKVDIDCSQKVVVYDQSQDVASISDCEFLTVLLGKLEKSFNSVHL	120			
DB	61	DKVLITELIHSARKKVDIDCSQKVVVYDQSQDVASISDCEFLTVLLGKLEKSFNSVHL	120			
QY	121	LAGFAEASRCPGICCEKSTLVPTICISOPCLPVANIGTRILPMLYIGCCQDVANKELI	180			
DB	121	LAGFAEASRCPGICCEKSTLVPTICISOPCLPVANIGTRILPMLYIGCCQDVANKELI	180			
QY	181	QONGIGVYLVNNTCEKDFIPESHFLRVPNVDSCEKILPWLDSVPFIEAKASNGCV	240			
DB	181	QONGIGVYLVNNTCEKDFIPESHFLRVPNVDSCEKILPWLDSVPFIEAKASNGCV	240			
QY	241	LHCHLAGISRSATTAIAIYIMKMDMSLDEAVRFVKEKPTISPENFLGQLLDYERKIKN	300			
DB	241	LHCHLAGISRSATTAIAIYIMKMDMSLDEAVRFVKEKPTISPENFLGQLLDYERKIKN	300			
QY	301	QTGASGPKSKLKLHLKRPNEPVAVSGGQKSEFPLSPCADSATSEAGQRPVHPASV	360			
DB	301	QTGASGPKSKLKLHLKRPNEPVAVSGGQKSEFPLSPCADSATSEAGQRPVHPASV	360			
QY	361	PSVSVQGSLLSDPSLVLQSLHLSADRLSDSNKLKSFSLDIKSVSYASMAASLNGCF	420			

Dp	361	PSVPSVPSLLEBSPLVQALSGHLHSADLLEENSLKKSFSJLDIKSVSASMAASLHGF	4200
Qy	421	SSSEDALEYKPSSTLLDGTNKLQCFSPVOELSEOTPETSPPDKEEASLPKKLTQARPSDSQ	4800
Dp	421	SSSEDALEYKPSSTLLDGTNKLQCFSPVOELSEOTPETSPPDKEEASLPKKLTQARPSDSQ	4800
Qy	481	SKRLHSVRITSSGCTAORSLSLPLHRSGSVEDNYHTSFLPLGLSTSQOHLTKSAGLGLGMH	5400
Dp	481	SKRLHSVRITSSGCTAORSLSLPLHRSGSVEDNYHTSFLPLGLSTSQOHLTKSAGLGLGMH	5400
Qy	541	SDLIAPOTSPSLTSSWYFATSSSHYSASAIYGSASAYSASQQLPTCGDQVYSRRR	6000
Dp	541	SDLIAPOTSPSLTSSWYFATSSSHYSASAIYGSASAYSASQQLPTCGDQVYSRRR	6000
Qy	601	QKPSDRADSRHSWHBSPFKKRSCOMEFGESIMEENRSREHLKVGVSQSFSGSME	6600
Dp	601	QKPSDRADSRHSWHBSPFKKRSCOMEFGESIMEENRSREHLKVGVSQSFSGSME	6600
Qy	661	IIIVS 665	
Dp	661	IIIVS 665	

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RESULT 2
US-09-949-016-9121
? Sequence 9121, Application US/09949016
? Patent No. 6812319
? GENERAL INFORMATION:
? APPLICANT: VENTER, J. Craig et al.
? TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
? TITLE OR INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
? FILE REFERENCE: C1001307
? CURRENT APPLICATION NUMBER: US/09/949,016
? CURRENT FILING DATE: 2000-04-14
? PRIOR APPLICATION NUMBER: 60/241,755
? PRIOR FILING DATE: 2000-10-20
? PRIOR APPLICATION NUMBER: 60/237,768
? PRIOR FILING DATE: 2000-10-03
? PRIOR APPLICATION NUMBER: 60/231,498
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 207012
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 9121
? LENGTH: 661
? TYPE: PRT
? ORGANISM: Human
? US-09-949-016-9121

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Query Match	38.7%	Score 1324	DB 4	Length 661
Best Local Similarity	45.1%	Pred. No. 2.4e-106		
Matches 314	Conservative 93	Mismatches 186	Indels 104	Gaps 21
QY	1 MAHEMIGTQIV-TERLVALLSSTGEKVLIIIDSRPFVEYNTSHILEAININCSKLMKRRLO	59		
DB	37 MAGDRLPRKMDAKTASILIRGSPGFLVIDRSFVEYNMWHYLSINVCISKFLYKRRO	96		
QY	60 QDKVLITELIHSAGHKVDIDCSQKVVYVYDSSQDVASLSDFELVTYLGKLEKSNVSH	119		
DB	97 QGKVITIELIHPAANSQVEATEPDDVVYDSTIDSVLADNLFSLISLKKIDGCFDSVA	156		
QY	120 ILAGGFAEBSRCFPELCEGK-STLVPTCISQCLIPVANIPTNILENLYIGCORVDYLNKE	178		
DB	157 ILYGFAFATFSSCFPELCEGKPAALLPMSLSQPCLPVPSVGLITRILPHLYIGSQOVLYAND	216		
QY	179 LIIQONGIGVLYNASTYCEKPDPIFESHLRPVNVDSCEKILPMLKSDVFTEKKAASNG	238		
DB	217 LMTQNGISVLYNANSKCPDPIFESHRPMVPIINDNCETLLPMDKSLTEFIDKAKLASC	276		
QY	238 CVLYHCLAGISRSATIAIAYIMKMDMSLDEARFVKEKAPPTISNNPNLGGQLDYEKTI	298		
DB	277 QVIYHCLAGISRSATIAIAYIMKMGMSDDAAYFVDRDPSISPNFNTLGGQLLEKESLI	336		

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OY      299  KNQNGASGPKSKUKLHLEKVN---EPVPAVSEGGQKSEYTLSPPCADSAF--SEAAQQR  355
Db      337  KLLAALQGDPG-----TPSGTEPEPPSPAAAGPLRLR--PPTSSAATYGAAAREG  386
OY      354  PVHPASVPSPVSVQPSILDEDSPLYVALSGHLMSADRLDEDSNKLKRSFELDKSVSYGASM  413
Db      387  GLGAGEPAPRPTRPA---TSAIQGLAGHLHSBRLODYNRLKRSFSLDKSA-----  437
OY      414  AASLHGFSSEDALEYKKESTLLDGTN-----KLQCF-SP---VOELSEQTPETSPD  461
Db      438  -----YAPSMRPDPGPDPDPCGAAPKCKLSPGALGLSSPIPD-SPD  480
OY      462  KERASTPKTLQTRAPSDSGSKRLHSVTRISSGSTAQRSLSLPLHSGSVEDNYHTSFLG-  520
Db      481  AADPAAPRRRRRRP-----PAGSPAR--SPAHSLG-----LNFQD  514
OY      521  --LTSQQLHTSAGLGLGK-----WMSDLAPQTSRPLSTSSWYFATSGSHFYSA  569
Db      515  AANQTRHGLSALSNAPGLPFGQPAQPGAMAPPLDPS--GTSPDGCWCTSPF-----  565
OY      570  SAIVGGSASVAYSVCOLPTCGDQYVSVRRQKPSDRADSRSHWEESSPEKOPFKRSCQ  629
Db      566  GAQGAAGVLFAPFGRAGAPGCGSGDLARRBAABAEPDRATGMPPEAPETQPKRRSCQ  625
OY      630  MEGESIMSENSR--ELGKVGSGSGSPGSGWEITVGS  665
Db      626  MEFEERG-IVTEGRARGEEIALAGKQASPFSGSVEIVGS  661

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```

RESULT 3
US-09-544-716-14
: Sequence 14, Application US/09544716
: Patent No. 6492157
: GENERAL INFORMATION:
: APPLICANT: Lucne, Ralf M.
: APPLICANT: Wei, Bo
: TITLE OF INVENTION: DSP-9 DUAL-SPECIFICITY PHOSPHATASE
: FILE REFERENCE: 200125.415
: CURRENT APPLICATION NUMBER: US/09/544,716
: CURRENT FILING DATE: 2000-04-10
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 14
: LENGTH: 170
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-544-716-14

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Query Match	19.1%	Score 654.5;	DB 4;	Length 170;
Best Local Similarity	72.5%	Pred. No. 5.6e-49;		
Matches 121;	Conservative 27;	Mismatch 18;	Indels 1;	Gaps 1
QY	134	GLCEKQ-STLVPCTISQPCPLPVANIGPTRLIPMLYLGCQDRVANKELIIONGIGYLTNAS	192	
Db	1	GLCEKQPAALLPMLSGQPCPLPVESVGLTRLLPHLYLGSQCDVANKDLMQNGSTYLTNAS	60	
QY	193	YTCPRPDFIPESHPLRYPVANDSFCEKILLPWLDKSVDFIEKAKASNCQVLVHCIAGISRSA	252	
Db	61	NSCPKPDFICSSRRFVAVINDNYCEKLLPWLDKSIETPRDKAKLSCQVIVHCIAGISRSA	120	
QY	253	TALAIYIMKRDMSIDENRYFVYEKARTTISPNPNFGLDLHYKKIK	299	
Db	121	TALAIYIMKTGMSDDAIFYVQDRAISIPNPNFGLLEHYERTLAK	167	

RESULT 4
US-09-557-921-15
; Sequence 15, Application US/09557921
; Patent No. 6551810
; GENERAL INFORMATION:
; APPLICANT: Lucbe, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE


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/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8486
/ LENGTH: 491
/ TYPE: PRT
/ ORGANISM: Human
US-09-949-016-8486
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Query Match          13.8%; Score 470.5; DB 4; Length 491;
Best Local Similarity 34.0%; Pred. No. 3.4e-32;
Matches 113; Conservative 63; Mismatches 107; Indels 49; Gaps 8;
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QY 19 LESGTEKVLIDSRPVEYNTSHILBAININCSKLMKRLOQDKVLTTELIOHSA-KHKY 77
DB 137 LELGNERLLMDRCPELYESSHIESAINVAIPGIMLRLOKGNLFVRALFTRGEDRKF 196
QY 78 DIDC-SQKVVYDQSSOD-VASISSDCEFTVLIGKLEKSPNSVHLLAGFAEFSRCFGL 135
DB 197 TRRCGDTVVLVDESSDMNMENTGESVLGLLKLKDKGCAFYLEGGFSKFOAEFSIH 256
QY 136 CECKSTLVPTC-ISOCPCLPVANIG----- 158
DB 257 CE--TULDSGSSSPPLVVLGIGRISDSSDIESLDNDPNSATDSDGSPLSNSQP 314
QY 159 --PTRLIPNLYIGCORVINKELIQONGIGVYNLSYTPKPK-DPIESHPLRVPVNDSP 215
DB 315 SEFVEILPFLYIGACADSTNLDVLEBFGIKYILNVTNPLNLFENAGFEKYQIPISDHM 374
QY 216 CEKILPMDKSVDFLEKAKASNGCVVHCLAGISRSATITAIYIMKMDMSLDEAYRPVK 275
DB 375 SGNLSQFPPEALSFIDEARGKCGVAVHCLAGISRSVTVTAIYMQKMLSMNDAYDIYK 434
QY 276 EKRPITSPNFNLGOLLDEYKKIKNOTGASGP 307
DB 435 MKSNISPPNFNMGQLDPERTL-----GLSSP 462
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RESULT 9
US-09-557-921-2
/ Sequence 2, Application US/09557921
/ Patent No. 6551810
/ GENERAL INFORMATION:
/ APPLICANT: Lucne, Ralf M.
/ TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
/ FILE REFERENCE: 200125.416
/ CURRENT APPLICATION NUMBER: US/09/557,921
/ CURRENT FILING DATE: 2000-04-20
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 482
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-557-921-2
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Query Match          13.7%; Score 469; DB 4; Length 482;
Best Local Similarity 35.9%; Pred. No. 4.5e-32;
Matches 107; Conservative 65; Mismatches 96; Indels 30; Gaps 7;
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QY 27 LLIDSRPVEYNTSHILBAININCS-KLMKRLOQDKVLTTELIO-HSAKHKVIDSCQK 84
DB 173 VILDRPMEYNTSHILBAININCS-KLMKRLOQDKVLTTELIO-HSAKHKVIDSCQK 232
QY 85 VVVYDOSQDVASISDCEFTVLIGKLEKSPNSVHLLAGFAEFSRCFGLCECK----- 139
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DB 233 IIVYDENTNPSRVMSPQPIHIVLESIKREGEPLVIAKGGLSFFKQNHENLNDNLQLOE 292
QY 140 -----STVPTCISQPCLP-VANIGETRLIPNLYIGCORVINKELIQONGIGY 187
DB 293 CREVGCGASASLSLPOPI--PTPDINAEILTPILPFLIGNEQDADQDLDMQNLINIGY 350
QY 188 VNAS-----YTCPPDPFPESHFLRPVNVNSFCCKILPMDKSVDFLEKAKASNGCVLV 242
DB 351 VINVTTHPLHYEKGFL---NYKRLPATYDSNNKQMLQYFEAEFTLBEARQCKGLIT 406
QY 243 HCLAGISRSATITAIYIMKMDMSLDEAYRPVKEKRPITSPNFGOLLDEYKKIRN 300
DB 407 HCOAGVSRSATIVIAVLMKHTMTWTDAYKFKYGRRPITSPNLMGQLLEBEDLNN 464
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RESULT 10
US-09-702-705-805
/ Sequence 805, Application US/09702705
/ Patent No. 6504010
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Lodes, Michael A.
/ APPLICANT: Fanger, Gary
/ APPLICANT: Vedvick, Tom
/ APPLICANT: Carter, Darlick
/ APPLICANT: Retter, Marc
/ APPLICANT: Mannion, Jane
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.478C14
/ CURRENT APPLICATION NUMBER: US/09/702,705
/ CURRENT FILING DATE: 2000-10-30
/ NUMBER OF SEQ ID NOS: 1833
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 805
/ LENGTH: 394
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-702-705-805
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Query Match          13.3%; Score 453; DB 4; Length 394;
Best Local Similarity 31.4%; Pred. No. 8e-31;
Matches 120; Conservative 73; Mismatches 143; Indels 46; Gaps 13;
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QY 19 LESGTEKVLIDSRPVEYNTSHILBAININCSKLMKRLOQDKVLTTELIO-HSAKHK 76
DB 39 LPSG-GKCLLDRCRFLAHSGYILGSVNRCNTIVRR-AKGSVSLQIILPAEEYVAR 96
QY 77 VDIDCSQKVVYDOSQDVASISDCEFTVLIGKLEKSF--NSVHLLAGFAEFSRCFPG 134
DB 97 LRSGLYANVIVYDERSRASLSRSDSVSLVQALRNARRTDICLKGYERFSSEYPE 156
QY 135 LCEGKSTL-----VPTCISQPCLPVA-----NIGETRLIPNLYIGCORVINKEL 179
DB 157 FCSKTALAAIPRPVPASATEPLDLDSCSGTPLHDEGEVLEILPFLYLSAVHAARDM 216
QY 180 IQONGIGVYNLSYTPKPKDPIESHFLRPVNDSPCEKILPMDKSVDFLEKAKASNGC 239
DB 217 LDALGITALLNVSSDCN-HFEGHYQKCIPEVDNHRADISSWMEIIEYIDAVKOCGR 275
QY 240 VLVHCLAGISRSATITAIYIMKMDMSLDEAYRPVKEKRPITSPNFGOLLDEYKKIR 299
DB 276 VLVHCGAGISRSATITAIYIMKMDMSLDEAYRPVKEKRPITSPNFGOLLDEYKKIR 335
QY 300 NQTAGSGPKSKLKLHLEKNEPVPVAVSEGGQKSETPLSPPCDSATSEAAQRPVHPAS 359
DB 336 ATSCAAEAS-----PSGPL-----GERGKTPATP-----TSQVFSEFPV-SVG 373
QY 360 VPVAVSVPGLSDPLVQALS 381
DB 374 VHSAPSSLPYL--HSPITTSPS 393
```

```

RESULT 11
US-09-736-457-805
; Sequence 805, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darlick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 805
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-805

Query Match      13.3%; Score 453; DB 4; Length 394;
Best Local Similarity 31.4%; Pred. No. 86-31;
Matches 120; Conservative 73; Mismatches 143; Indels 46; Gaps 13;

QY 19 LESGTEKVLIDSRPVEYNTSHILEAININCSKLMKRLQODKYLITELI--QHSARKK 76
DB 39 LPSSG-GKCLLDRCRFLAHASAGYILGSVNVRCNTIVRR-AGSVSLQILPAEEVRAR 96
QY 77 VDIDCSQKVVYDOSQDVASLSDPCFLTVLLGKLEKSF--NSVHLAAGFAEFRCRPG 134
DB 97 LRSGLYSAVIYDERSPRAESLREDSTVSLVVALRRNAERTDICKKGYERFSSEYPE 156
QY 135 LCEGKSTL-----VPTCISQP-----CLPVA-----NIGPTRILPNLYGQORDVYNKEL 179
DB 157 FCSKTKALAAIPPPVPSPATEBLDDCSCGTPHLDQEPVILPFLYIGSAVYHARRDM 216
QY 160 IQQNGIGVYLNASTYCPKPDPIPESHFLRPVNDSCFCEKILPWLKSDVFIKAKASNGC 239
DB 217 LDALGITLALNVSDCPN-HFEGHYQYKCIPVEDNHKADISSMFEALREYIDAVKDCGR 275
QY 240 VLVHCLAGISRSATTAIAYIMKRMMSLDEAVRFYKEKRPITSPPNPNFLGQLLDYEKKIK 299
DB 276 VLVHCOAGISRSATTCIAVIMMKKRVRLAEAFYKORRSITSPNFSFGQLQFESQVL 335
QY 300 NOTGASGPKSKLKLHLKRPNEVPVAVSEGGQKSTPLSPPCADATSEAAQRPVHPAS 359
DB 336 ATSCAAEAS-----PSCPL-----GERGKTPTAT-----TSQFVFSFPV-SVG 373
QY 360 VPSVPSVOPSLLEDSPLYQALS 381
DB 374 VHSAPSSLPYL--HSPITTSPS 393

```

```

; APPLICANT: Carter, Darlick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 805
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-614-124B-805

Query Match      13.3%; Score 453; DB 4; Length 394;
Best Local Similarity 31.4%; Pred. No. 86-31;
Matches 120; Conservative 73; Mismatches 143; Indels 46; Gaps 13;

QY 19 LESGTEKVLIDSRPVEYNTSHILEAININCSKLMKRLQODKYLITELI--QHSARKK 76
DB 39 LPSSG-GKCLLDRCRFLAHASAGYILGSVNVRCNTIVRR-AGSVSLQILPAEEVRAR 96
QY 77 VDIDCSQKVVYDOSQDVASLSDPCFLTVLLGKLEKSF--NSVHLAAGFAEFRCRPG 134
DB 97 LRSGLYSAVIYDERSPRAESLREDSTVSLVVALRRNAERTDICKKGYERFSSEYPE 156
QY 135 LCEGKSTL-----VPTCISQP-----CLPVA-----NIGPTRILPNLYGQORDVYNKEL 179
DB 157 FCSKTKALAAIPPPVPSPATEBLDDCSCGTPHLDQEPVILPFLYIGSAVYHARRDM 216
QY 160 IQQNGIGVYLNASTYCPKPDPIPESHFLRPVNDSCFCEKILPWLKSDVFIKAKASNGC 239
DB 217 LDALGITLALNVSDCPN-HFEGHYQYKCIPVEDNHKADISSMFEALREYIDAVKDCGR 275
QY 240 VLVHCLAGISRSATTAIAYIMKRMMSLDEAVRFYKEKRPITSPPNPNFLGQLLDYEKKIK 299
DB 276 VLVHCOAGISRSATTCIAVIMMKKRVRLAEAFYKORRSITSPNFSFGQLQFESQVL 335
QY 300 NOTGASGPKSKLKLHLKRPNEVPVAVSEGGQKSTPLSPPCADATSEAAQRPVHPAS 359
DB 336 ATSCAAEAS-----PSCPL-----GERGKTPTAT-----TSQFVFSFPV-SVG 373
QY 360 VPSVPSVOPSLLEDSPLYQALS 381
DB 374 VHSAPSSLPYL--HSPITTSPS 393

RESULT 13
US-09-671-325-805
; Sequence 805, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darlick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 805
; LENGTH: 394
; TYPE: PRT

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/ ORGANISM: Homo sapiens
US-09-671-325-805

Query Match      13.3%; Score 453; DB 4; Length 394;
Best Local Similarity 31.4%; Pred. No. 8e-31;
Matches 120; Conservative 73; Mismatches 143; Indels 46; Gaps 13;

QY 19 LESGTEKVLIDSRPFVEYNTSHILEAININCSKLMKRRLOQDKVLTIELI--QHSARKH 76
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39 LPBG-GKCLLDRCRFLAHAGYILGSVNVRCNTIVRR-AGKSVLEQLIPAEVEVAR 96
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 77 VDIDCSQKVVYDQSSQDVASLSDCFVLVLGLKLEKSF--NSVHLLAGGAERFCRPG 134
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 97 LRSGLYSAVIYDERSPPRAESLREDSTVSLVQALRRNAERTDCLLKGYERFSSEYPE 156
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 135 LCEGKSTL-----VPTCISQP-----CLPVA-----NIGPTRILPNLYLGGQRDVUNKEL 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 157 FCSKTKALAAIPPPVPSATEPDLDDCSSCGTPHLHDQEGPVEILPFLYLSAYHAARRDM 216
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 180 IQONGIGVYLNASYTCRPFDPFIPESHFLRPVNDSCFCEKILPWLKSDVDFIEKAKASNGC 239
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 217 LDALGITALLNVSSDCPN-HFEGHYQKCIPIVEDNHKADISSWFMALIEYIDAVDCRGR 275
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 240 VLVHCLAGISRSATTAIAYIMKMDMSLDEAYRVEKRPPTISPNFNLGQLLDYEKKIK 299
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 276 VLVHCOAGISRSATTCIAYIMMKRVRLBEAFEFVKORRSIISPNFSFMGQLLOFESQVL 335
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 300 NOTGASGPKSKLHLKRNPEVPVAVSBGQKSETPLSPPCADSATSSAAGQRPVHPAS 359
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 336 ATSCAAEAS-----PSGFL-----GERGKTPATP-----TSQFVPFSFPV-SVG 373
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 360 VPSVPSVOPSLLEDSPVLQALS 381
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 374 VHSAPSLPYL--HSPITTSPS 393
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-09-589-184-805
/ Sequence 805, Application US/09589184
/ Patent No. 6686447
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Lodes, Michael A.
/ APPLICANT: Fanger, Gary
/ APPLICANT: Vedvick, Tom
/ APPLICANT: Carter, Darrick
/ APPLICANT: Retter, Marc
/ APPLICANT: Mannion, Jane
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
/ FILE REFERENCE: 210121.478C8
/ CURRENT APPLICATION NUMBER: US/09/589,184
/ CURRENT FILING DATE: 2000-06-05
/ NUMBER OF SEQ ID NOS: 827
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 805
/ LENGTH: 394
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-589-184-805

Query Match      13.3%; Score 453; DB 4; Length 394;
Best Local Similarity 31.4%; Pred. No. 8e-31;
Matches 120; Conservative 73; Mismatches 143; Indels 46; Gaps 13;

QY 19 LESGTEKVLIDSRPFVEYNTSHILEAININCSKLMKRRLOQDKVLTIELI--QHSARKH 76
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39 LPBG-GKCLLDRCRFLAHAGYILGSVNVRCNTIVRR-AGKSVLEQLIPAEVEVAR 96
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 77 VDIDCSQKVVYDQSSQDVASLSDCFVLVLGLKLEKSF--NSVHLLAGGAERFCRPG 134
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 97 LRSGLYSAVIYDERSPPRAESLREDSTVSLVQALRRNAERTDCLLKGYERFSSEYPE 156
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 135 LCEGKSTL-----VPTCISQP-----CLPVA-----NIGPTRILPNLYLGGQRDVUNKEL 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 157 FCSKTKALAAIPPPVPSATEPDLDDCSSCGTPHLHDQEGPVEILPFLYLSAYHAARRDM 216
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 180 IQONGIGVYLNASYTCRPFDPFIPESHFLRPVNDSCFCEKILPWLKSDVDFIEKAKASNGC 239
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 217 LDALGITALLNVSSDCPN-HFEGHYQKCIPIVEDNHKADISSWFMALIEYIDAVDCRGR 275
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 240 VLVHCLAGISRSATTAIAYIMKMDMSLDEAYRVEKRPPTISPNFNLGQLLDYEKKIK 299
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 276 VLVHCOAGISRSATTCIAYIMMKRVRLBEAFEFVKORRSIISPNFSFMGQLLOFESQVL 335
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 300 NOTGASGPKSKLHLKRNPEVPVAVSBGQKSETPLSPPCADSATSSAAGQRPVHPAS 359
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 336 ATSCAAEAS-----PSGFL-----GERGKTPATP-----TSQFVPFSFPV-SVG 373
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 360 VPSVPSVOPSLLEDSPVLQALS 381
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 374 VHSAPSLPYL--HSPITTSPS 393
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
QY 135 LCEGKSTL-----VPTCISQP-----CLPVA-----NIGPTRILPNLYLGGQRDVUNKEL 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 157 FCSKTKALAAIPPPVPSATEPDLDDCSSCGTPHLHDQEGPVEILPFLYLSAYHAARRDM 216
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 180 IQONGIGVYLNASYTCRPFDPFIPESHFLRPVNDSCFCEKILPWLKSDVDFIEKAKASNGC 239
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 217 LDALGITALLNVSSDCPN-HFEGHYQKCIPIVEDNHKADISSWFMALIEYIDAVDCRGR 275
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 240 VLVHCLAGISRSATTAIAYIMKMDMSLDEAYRVEKRPPTISPNFNLGQLLDYEKKIK 299
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DB 276 VLVHCOAGISRSATTCIAYIMMKRVRLBEAFEFVKORRSIISPNFSFMGQLLOFESQVL 335
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 300 NOTGASGPKSKLHLKRNPEVPVAVSBGQKSETPLSPPCADSATSSAAGQRPVHPAS 359
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 336 ATSCAAEAS-----PSGFL-----GERGKTPATP-----TSQFVPFSFPV-SVG 373
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 360 VPSVPSVOPSLLEDSPVLQALS 381
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 374 VHSAPSLPYL--HSPITTSPS 393
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RESULT 15
US-09-658-824-805
/ Sequence 805, Application US/09658824
/ Patent No. 6746846
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Lodes, Michael A.
/ APPLICANT: Fanger, Gary
/ APPLICANT: Vedvick, Tom
/ APPLICANT: Carter, Darrick
/ APPLICANT: Retter, Marc
/ APPLICANT: Mannion, Jane
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
/ FILE REFERENCE: 210121.478C11
/ CURRENT APPLICATION NUMBER: US/09/658,824
/ CURRENT FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 1788
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 805
/ LENGTH: 394
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-658-824-805

Query Match      13.3%; Score 453; DB 4; Length 394;
Best Local Similarity 31.4%; Pred. No. 8e-31;
Matches 120; Conservative 73; Mismatches 143; Indels 46; Gaps 13;

QY 19 LESGTEKVLIDSRPFVEYNTSHILEAININCSKLMKRRLOQDKVLTIELI--QHSARKH 76
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39 LPBG-GKCLLDRCRFLAHAGYILGSVNVRCNTIVRR-AGKSVLEQLIPAEVEVAR 96
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 77 VDIDCSQKVVYDQSSQDVASLSDCFVLVLGLKLEKSF--NSVHLLAGGAERFCRPG 134
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 97 LRSGLYSAVIYDERSPPRAESLREDSTVSLVQALRRNAERTDCLLKGYERFSSEYPE 156
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 135 LCEGKSTL-----VPTCISQP-----CLPVA-----NIGPTRILPNLYLGGQRDVUNKEL 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 157 FCSKTKALAAIPPPVPSATEPDLDDCSSCGTPHLHDQEGPVEILPFLYLSAYHAARRDM 216
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 180 IQONGIGVYLNASYTCRPFDPFIPESHFLRPVNDSCFCEKILPWLKSDVDFIEKAKASNGC 239
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 217 LDALGITALLNVSSDCPN-HFEGHYQKCIPIVEDNHKADISSWFMALIEYIDAVDCRGR 275
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 240 VLVHCLAGISRSATTAIAYIMKMDMSLDEAYRVEKRPPTISPNFNLGQLLDYEKKIK 299
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 276 VLVHCOAGISRSATTCIAYIMMKRVRLBEAFEFVKORRSIISPNFSFMGQLLOFESQVL 335
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 300 NOTGASGPKSKLHLKRNPEVPVAVSBGQKSETPLSPPCADSATSSAAGQRPVHPAS 359
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 336 ATSCAAEAS-----PSGFL-----GERGKTPATP-----TSQFVPFSFPV-SVG 373
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 360 VPSVPSVOPSLLEDSPVLQALS 381
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 374 VHSAPSLPYL--HSPITTSPS 393
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Qy 300 NOTGASGPKSLKLLHLEKNEPVPAVSEGGOKSETPLSPPCADSATSEAGORPVHPAS 359
Db 336 ATSCAAEAAS-----PSGFL-----GERGKTPTATP-----TSQFVFSFPV-SVG 373
Qy 360 VPSVPSVOPSLLEDSPPLVQALS 381
Db 374 VHSAPSSLPLYL--HSPITTSPS 393

Search completed: February 9, 2005, 12:13:08
Job time : 43.637 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: February 14, 2005, 09:42:14 / Search time 293.645 Seconds
(without alignments)
3705.573 Million cell updates/sec

Title: US-10-029-345A-109
Perfect score: 3418
Sequence: 1 MAHEMIGQIVTERLVALL.....LGKVGSGSFGSGMEIIEVS 665

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1202784 seqs, 81813359 residues
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=445 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pcio -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10029345@cgn2_1.141@rnuc_09022005_091208_25808 -NCPU=6 -ICPU=3
-NO_MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- Issued_Patents_NA:*
- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
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 - 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3406	99.6	1998	4	US-09-816-494-3
2	3406	99.6	3544	4	US-09-816-494-1
3	1326	38.8	2377	4	US-09-920-668-3
4	1324	38.7	2351	4	US-09-949-016-14992
5	799.5	23.4	13782	4	US-09-949-016-14992
6	480	13.0	2109	4	US-09-016-434-1135
7	480	13.0	2109	4	US-09-023-655-946
8	475	13.0	2475	4	US-09-949-016-2615
9	475	13.9	333	4	US-09-513-999C-2877
10	469	13.7	1830	4	US-09-557-921-1
11	453	13.3	1238	4	US-09-702-705-803
12	453	13.3	1238	4	US-09-736-457-803

13	453	13.3	1238	4	US-09-614-124B-803	Sequence 803, App
14	453	13.3	1238	4	US-09-671-325-803	Sequence 803, App
15	453	13.3	1238	4	US-09-589-184-803	Sequence 803, App
16	453	13.3	1238	4	US-09-658-824-803	Sequence 803, App
17	451.5	13.2	2240	4	US-09-016-434-1100	Sequence 1100, App
18	450.5	13.2	2064	4	US-09-702-705-825	Sequence 825, App
19	450.5	13.2	2064	4	US-09-736-457-825	Sequence 825, App
20	450.5	13.2	2064	4	US-09-614-124B-825	Sequence 825, App
21	450.5	13.2	2064	4	US-09-671-325-825	Sequence 825, App
22	450.5	13.2	2064	4	US-09-589-184-825	Sequence 825, App
23	450.5	13.2	2064	4	US-09-658-824-825	Sequence 825, App
24	450.5	13.2	2109	4	US-09-702-705-826	Sequence 826, App
25	450.5	13.2	2109	4	US-09-736-457-826	Sequence 826, App
26	450.5	13.2	2109	4	US-09-614-124B-826	Sequence 826, App
27	450.5	13.2	2109	4	US-09-671-325-826	Sequence 826, App
28	450.5	13.2	2109	4	US-09-589-184-826	Sequence 826, App
29	450.5	13.2	2109	4	US-09-658-824-826	Sequence 826, App
30	450.5	13.2	2109	4	US-09-949-016-2210	Sequence 2210, App
31	447	13.1	1993	2	US-08-990-379-2	Sequence 2, App1
32	445	13.0	1238	2	US-08-530-290-11	Sequence 11, App1
33	428.5	12.5	2000	4	US-09-016-434-1291	Sequence 1291, App
34	428.5	12.5	2000	4	US-09-919-497-10	Sequence 10, App1
35	428.5	12.5	2015	4	US-09-949-016-4369	Sequence 4369, App
36	427.5	12.5	2283	4	US-09-949-016-4617	Sequence 4617, App
37	427.5	12.5	2303	4	US-09-922-146-3	Sequence 3, App1
38	425	12.4	944	4	US-09-371-671B-10	Sequence 10, App1
39	405.5	11.9	1987	2	US-08-990-379-1	Sequence 1, App1
40	384	11.2	2473	4	US-09-949-016-623	Sequence 623, App
41	382.5	11.2	1619	4	US-09-702-705-801	Sequence 801, App
42	382.5	11.2	1619	4	US-09-736-457-801	Sequence 801, App
43	382.5	11.2	1619	4	US-09-614-124B-801	Sequence 801, App
44	382.5	11.2	1619	4	US-09-671-325-801	Sequence 801, App
45	382.5	11.2	1619	4	US-09-589-184-801	Sequence 801, App

ALIGNMENTS

RESULT 1
US-09-816-494-3
; Sequence 3, Application US/09816494
; Patent No. 6664089
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-816-494-3

Alignment Scores:
Pred. No.: 0
Score: 3406.00
Percent Similarity: 99.85%
Best Local Similarity: 99.70%
Query Match: 99.65%
DB: 4
Length: 1998
Matches: 663
Conservative: 1
Mismatch: 1
Indels: 0
Gaps: 0

US-10-029-345A-109 (1-665) x US-09-816-494-3 (1-1998)

QY 1 MetAAHsgLMeIILgLYThrgInIleValThrgIuWAgLgLeuValAlaIleuLgU 20
DB 1 ATGGCCATGTGAGATGATTGGAATCTCAATTTGTACTGAGAGGTGTGGCTCTGTGGAA 60
QY 21 SerGIYThrgIuLyValIleuLeuIleAsSerArpPropheValGIuYrAnThrSer 40

Db 61 AGTGAACGGAAAAAGTGTGTAATTGATAGCCGGCAATTGTGGAAATACATACTCC 120
Qy 41 HIIILILEUGLUALALEANILEANCYSERILEUWELIYARGATLEUGLNGIN 60
Db 121 CACATTTTGGAAACCATTAATATCACTGCTCCAACTTAATGAAGGAAGTTGCAACG 180
Qy 61 APLYSVALLEULIETHRGULEULIENHISERIALYSHISLYSVALAEPILAEAP 80
Db 181 GCAAAAGTGTATTCACAGAGCTCATCCAGCATTCAGCCAAACATTAAGATTGACTTGA 240
Qy 81 CYSSEGLNLYSVALYVALTYRAEPGINSESSERGLNASPVALLASERLEUSERS 100
Db 241 TGCAGTCAGAGAGGTGTAGTTACGATCAAAAGCTCCCAAGATGTCTCTCTCTTCA 300
Qy 101 AEPQVSPHELEUTHRALLEULEUGLYLYSLEUGLULYSSESPHEANSERVALHISLE 120
Db 301 GACTGTTTCTCATCTACTCTGGGTAACTGGAGAGAGCTTCAACTCTGTTCACCTG 360
Qy 121 LEUVALGLYGYPHALAGLUPHESERARGPHEPROGLYLEUCYSGIUGLYLSER 140
Db 361 CTTCAGAGTGGGTTTCTGAGTTCTCTCGTTGTTCCCTGGCTCTGTAAAGAAATCC 420
Qy 141 THRLEUVALPROTHRYSILSESGINPROCYSELEUPROVALALASANTLEGLYPROTHR 160
Db 421 ACTCTAGTCCCTACGCACTTCTCAGCCTTGCTTACCTGTTGCCAACATGGGCCAAC 480
Qy 161 ARGILILEUPROASNLEUTHRYLEUGLYCYSGINARGASPVALLASANTLEGLYLEU 180
Db 481 CGAATCTTCCCAATCTTAATCTGGCTCCAGCGAGATGCTCTCAACAAAGAGCTGAG 540
Qy 181 GINGINASNGIYILEGLYTYRVALLEUASNALASERTYTHR CYSPROLYSPROASPHE 200
Db 541 CAGCAAGATGGGATTTGTTATGTAAATGCCAGCAATCTGTCCAAAGCTGACTTT 600
Qy 201 ILEPROGLUSERHISPHLEUARGVALPROVALASNASPSPHECYSGIULYSILEU 220
Db 601 ATCCCCGAGTCTCATTTCTCGGTGGTGGCTGAGATGACAGCTTTGTGAGAAATTTTG 660
Qy 221 PROTPLEUASPLYSSEVALASPHLEILEGLIULYSVALALYSERASNGIYCYVAL 240
Db 661 CCGTGTGGACAAATCATTAATTTTCATTGAGAAAGCAAAAGCCCTCCATGGAAGTGT 720
Qy 241 LEUVALHISCYSELEUVALAGIYILESERARGSERALATHRIEALILEALTYRIEMET 260
Db 721 CTAGAGCACTGTTTAGCTGAGATCTCCGCTCGGCAACATGCTATGCTCACTCATG 780
Qy 261 LYSARGMETASPMESERILEUASPGIUALITYRARGPHEVALLYSGIULYARGPROTHR 280
Db 781 AAGAGATGACATGTCTTTAGATGACAGCTTACAGATTTGTGAAAAAGAAAGACCTTCT 840
Qy 281 ILESERPROASNPHASNPHELEUGLYGINLEUASAPTYRGLULYLYSRIEYASN 300
Db 841 ATATCTCCAACTTCAATTTTCTGGGCAACTCTCGAGACTATGAGAAAGATTAAAGAC 900
Qy 301 GINTHRGIALASERGLYPROLYSERLYSLEULYSLEUHLISLEUGLULYSERPROASN 320
Db 901 CAGACTGGAGCATCGGGCCAAAGAGCAAACTCAAGCTGCTGCACTGGAGAGCAAT 960
Qy 321 GLUPROVALPROLAVASERIGLYGLYGINLYSSEGLIUTHRPROLEUSERPROPRO 340
Db 961 GAACTGTGCTCGCTGCTCAGAGGTGAGACGAAAAAGAGACCCCTCAGTCCACCC 1020
Qy 341 CYSALASPSERALATHSERGLUALALAGIYGINARGPROVALHISPROLISERVAL 360
Db 1021 TGTGCGCACTGTCTACTCAGAGGCAAGAGCAAAAGCCCGTGCATCCGCGCAGCTG 1080
Qy 361 PROSERVALPROSERVALGINPROSERLEUENGUJASPSERPROLEUVALGINALAEU 380
Db 1081 CCCAGCGTGGCCAGGCGTCAAGCCGTGCTGTTAGAGGACAGCCGCTGTCAGGCGCTC 1140
Qy 381 SERGLYLEUHLISLEUSERALASPARGLEUGLUPSPSERANLYSLEULYARGSERPHE 400

Db 1141 AGTGGGCTGCACTGTCCGACAGACAGCTGGAGAGACAGCAATTAAGCTCAAGGTTCCCTTC 1200
Qy 401 SERLEUASPILELYSSERVALSERTYSERALASERMETCALALASERLEUHLISGLYPHE 420
Db 1201 TCTCTGGATATCAAAATCAGTTTCATATTCAGCCAGACATGAGCATCTCTTACATGGCTTC 1260
Qy 421 SERSESGIUAASVALALEUGLUTYTYRILYSPROSETRHTRHLEUASPGIYTHIRASN 440
Db 1261 TCTCATACAGAAAGATGCTTTGGAAATCTACAAACCTTCACTACTCTGATGGAGCCAAC 1320
Qy 441 IYLSLEUCYSGINPHESESPROVALGINLULEUSERGINUTHRPROGLIUTHRSESPRO 460
Db 1321 AAGCTATGCCAGTTCTCCCTGTTTCAAGAACTATCGAGAGACTCCGAAACAGTCTCT 1380
Qy 461 APLYSGLIUGLUALASERTILEPROLYSILEUGLINTHRAALARGPROSERASPSEGIN 480
Db 1381 GATTAAGAGAGAGCCAGCATCCCAAGAGCTGCAGACCCGAGGCTTTCAGACAGCGAG 1440
Qy 481 SERLYSARGLEUHLISERVALARGTHRSESSERGLYTHRALAGINARGSERLEUEN 500
Db 1441 AGCAAGCATTTGCATTCGGTACAGAACAGAGCATGGGCAACCGCCAGAGTCTCTTTTA 1500
Qy 501 SERPROLEUHLISARGSERGLYSERVALGLUASPARNTYRHSRTHSERPHELEUPHEGLY 520
Db 1501 TCTCCACTGCATTCGAAGTGGAGCGTGGAGAGACATTCACACACAGCTTCTTTTGGGC 1560
Qy 521 LEUSERTHRSERGINGINHISLEUTHRILYSERVALAGIYLEUGLYLEULYGLIYTPHIS 540
Db 1561 CTYTTCACACACCGACAGACACCTCAGCAAGTCTGCTGCGCTTAAAGGCTGGGAC 1620
Qy 541 SERASPILEUVALAPROGLINTHRSERTHRPROSERLEUTHRSESSERTYRYPHEALA 560
Db 1621 TCGAATATCTTGGCCCCCACAACCTTACCCCTTCCCTGACACAGCTGATTTTGCC 1680
Qy 561 THRGLUSERSERHISPHETYSERVALASERLALILEYRGILYSERALASERTYSER 580
Db 1681 ACAGAGTCTTCACTTACTGCTGCTCAGCCCATCTTAACGAGGACAGTCCAGTTACTCT 1740
Qy 581 ALATYRSERCYSSERGINLEUPROTHR CYSGIYASPGIUNVALTYRSEVALARGARG 600
Db 1741 GCCTACAGCTCAGCCAGCTGCCCCCACTTGGGAGAACCAAGTATTTCTGTGCGAGCGG 1800
Qy 601 GINLYSPROSEARPARALASPSERARGHRSERTPHISGLIUGLUSERPROPHGLU 620
Db 1801 CAGAAAGCAATGTGACAGAGCTGACTCGCGGAGAGCTGGATGAGAGAGCCCTTTGAA 1860
Qy 621 LYSGLINPHELYSARGARGSERCYSGIMETGLUPHEGLYGLUSERIILEMETSERGLUASN 640
Db 1861 AAGCAGTTTAAACGACAGAGCTGCCAAATGGAATTTGAGAGAGCATCATGTCAAGAAC 1920
Qy 641 ARGSEARPGIUGLULEUGLYLYSVALGLYSERGINSESPHESESGIYSEMETGGLU 660
Db 1921 AGGTCAAGGAGAGCTGGGGAAAGTGAGGAGTCAAGTCTTGTGGGAGCATGAAA 1980
Qy 661 ILEILEGLIUNVALSER 665
Db 1981 ATCATTTAGAGTCTCC 1995

RESULT 2

US-09-816-494-1

; Sequence 1, Application us/09816494

; Patent No. 6664089

; GENERAL INFORMATION:

; APPLICANT: Meyers, Rachel A.

; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY

; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR

; FILE REFERENCE: 10448-030002

; CURRENT APPLICATION NUMBER: us/09/816,494

; PRIOR FILING DATE: 2001-03-23

; PRIOR APPLICATION NUMBER: US 60/191,858

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 4.0

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/ SEQ ID NO 1
/ LENGTH: 3544
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (589) ... (2583)
US-09-816-494-1

Alignment Scores:
Pred. No.: 0 Length: 3544
Score: 3406.00 Matches: 663
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.65% Indels: 0
DB: 4 Gaps: 0

US-10-029-345A-109 (1-665) x US-09-816-494-1 (1-3544)
QY 1 MetAlaHlAgLueMeTllegLyThrgInIleValThrgLuArgLeuValAlaLeuEngIn 20
DB ATGGCCCATGAGATGATGAACTGAACTCAATGTTACTGAGAGGTGGTGGCTGCTGGAGA 648
QY 21 SerGlyThrgLulYleuValleuLeuIleApsSerArgProPheValGluTyzAsnThrSer 40
DB 649 AGTGAAGCGAAAGAGTGTCTGCTAATTGATACCGGCAATTGTGGAAATACATACATCC 708
QY 41 HisIleLeuGluAlaIleAsnIleApsCySerLybLeuMeLyArgArgLeuEngIn 60
DB 709 CACATTTTGAAGCATTAATATCAATGCTCCAAAGCTTATGAAACGAAAGTTGCACACG 768
QY 61 AspLybValleuIleThrgLueuIleGInHlSerArgAlaPheHlAlaValApsIleAps 80
DB 769 GACAAAGGTTATATACAGAGCTCAATCCAGCATTCAGCAACATTAAGGTTGACATGAT 828
QY 81 CysSerGInLybValIleValTyzApsInSerSerGInApsValAlaSerLeuSerSer 100
DB 829 TGCACATCGAAGGTTGTTAGTTACATCAAAAGCTCCAAAGATGGTCCCTCTCTTCA 888
QY 101 ApsCyPheLeuThrValleuLeuGluTybLeuGluTybSerPheApsSerValHlApsLeu 120
DB 889 GACTTTTCTCAGCTGATCTTCTGGGTAAACTGAGAAAGAGCTTCAACTCTTTCACCTG 948
QY 121 LeuAlaGlybPheAlaGluPheSerArgCyPheProGlyLeuCyGInGlyTybSer 140
DB 949 CTGAGAGGTGGTGTGCTGAGTCTCTCTGTGTTCCTGGGCTCTGTAAGAAATATCC 1008
QY 141 ThrLeuValProThrCyAlaSerGInProCybLeuProValAlaAsnIleGlyProThr 160
DB 1009 ACTCTAGTCCCTACCTGATTTCTAGCTTCTTACCTGTTGCCAACATTTGGGCAAC 1068
QY 161 ArgIleLeuProApsLeuTybLeuGluTybGInArgApsValleuApsLybGluLeuIle 180
DB 1069 CGAATTTCTCCCAATCTTATCTTGGCTGCCAGAGATGTCTCTCAACAGAGAGCTGAT 1128
QY 181 GInGInaangLyIleGlyTybValleuApsAlaSerTybThrCybProLybProApsPhe 200
DB 1129 CAGCGAATGGGATGGTATGTGTAAATGACACATTAACCTGTCCAAAGCTTACTT 1188
QY 201 IleProGInSerHlApsPheLeuArgValProValApsApsPheCybGluTybIleLeu 220
DB 1189 ATCCCGAGTCTCATTTCTGGGTGGTGGCTGCGAATGACAGCTTTTGGAGAAATTTTG 1248
QY 221 ProTPLeuApsLybSerValApsPheIleGluTybAlaTybAlaSerApsnGlyCybVal 240
DB 1249 CCGTGTGTGCAATCAATCAATGATTTCAATTGAGAAAGCAAAAGCTCCCAATGATGTGT 1308
QY 241 LeuValHlApsCybLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTybIleMet 260
DB 1309 CTAGTGCACGTGTTAGTGGATCTCCGCTCCGACCATGCTATGGCCCTACATCATG 1368
QY 261 LysArgMetApsMetSerLeuApsGluAlaTybArgPheValGluTybArgProThr 280
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DB 1369 AAGAGATGACATGTCTTAGATGAGCTTACAGATTTGTGAAGAAAAAGACCTACT 1428
QY 281 IleSerProApsPheApsPheLeuGluTybIleLeuApsTybGluTybLybAla 300
DB 1429 ATATCTCAAACTTCAATTTTCTGGGCCAACTCTGAGCTATGAGAAAGATTAAGAAC 1488
QY 301 GInThrgLulAAsGlyProLybSerLybLeuIleLeuGluTybApsProAps 320
DB 1489 CAGACTGAGATCAAGGCGCAAGAGCAAACTCAAGCTGTCTGACCTGAGAGAGCCAAAT 1548
QY 321 GluProValProAlaValSerGluGlyGInLybSerGInThrProLeuSerProPro 340
DB 1549 GAACCTGTCCCTGCTGTCTCAGAGGGTGAGACGAAAGAGAGACCCCTCAGTCAACC 1608
QY 341 CybAlaApsSerAlaThrSerGluAlaAlaGlyGInArgProValHlProAlaSerVal 360
DB 1609 TGTGCCACTGTGCTACCTCAGAGGACAGAGCAAAAGCCCGTCAATCCCGCAGCCGG 1668
QY 361 ProSerValProSerValGInProSerLeuGluApsSerProLeuValGInAlaLeu 380
DB 1669 CCCAGCTGCCCAGGCTGACGCTGCTGTTAGAGACAGCCCGCTGTACAGGCGCTC 1728
QY 381 SerGlyLeuHlApsSerAlaApsArgLeuGluApsSerApsLybLeuLybArgSerPhe 400
DB 1729 AGTGGCTGACACTGTCCGACAGACAGGCTGGAAAGACAGCAATTAAGCTCAAGGCTTCC 1788
QY 401 SerLeuApsIleLybSerValSerTybSerAlaSerMetAlaAlaSerLeuHlApsPhe 420
DB 1789 TCTCGAATATCAATCAATGATTCAATTCAGGACAGCATGAGCATCTTCAATGAGCTTC 1848
QY 421 SerSerSerGluApsAlaLeuGluTybTybLybProSerThrThrLeuApsGluThyrAsn 440
DB 1849 TCTCATATCAAGATGCTTTTGAATATCAAACTTCACTCACTGTGATGGAGCAAC 1908
QY 441 LysLeuCybGInPheSerProValGInLybLeuSerGInThrProGluThrSerPro 460
DB 1909 AAGCTATCCAGTCTTCCCTGTTGAGAACTATGAGAGACATCCCGAAACAGTCTCT 1968
QY 461 AspLybGluGluAlaSerIleProLybLybLeuGInThrAlaArgProSerApsSerGIn 480
DB 1969 GATAAGGAGGAAGCCAGCATCCCAAGAGCTGACAGCCGCGCATTCACACAGCCAG 2028
QY 481 SerLybApsLeuHlApsSerValArgThrSerSerSerGlyThrAlaGluSerLeuLeu 500
DB 2029 AGCAGACATTCATTCCTGCTCAAGACAGCACTGAGCAACGCGGCAAGGTCCTTTTA 2088
QY 501 SerProLeuHlApsSerGlySerValGluApsApsTybHlApsThrPheLeuPheGly 520
DB 2089 TCTCATGATCGATCGAAGTGGAGGCTGAGAGCAATTAACAACACAGCTTCTTTTCCGG 2148
QY 521 LeuSerThrSerGInGInHlApsLeuThrLybSerAlaGlyLeuGlyLeuLybGlyTybHis 540
DB 2149 CTTTCACACAGCCAGCACACTCAAGAGTCTGCTGCGCTTGAAGGGCTGGCAC 2208
QY 541 SerApsIleLeuAlaProGInThrSerThrProSerLeuThrSerSerTybTybPheAla 560
DB 2209 TGGATATCTTGGCCCCCAAGCCCTTACCCCTTCTGACCAAGAGCTGGAATTTTGC 2268
QY 561 ThrGInSerSerHlApsPheTybSerAlaSerAlaIleTybGlyGlySerAlaSerTybSer 580
DB 2269 ACAAGTCTCACTCACTTACTTGTCTGCTCAAGCATTAAGGAGGAGGAGGAGGAGTACT 2328
QY 581 AlaTybSerCybSerGInLeuProThrCybGluApsGluValTybSerValArgArgArg 600
DB 2329 GCTTACAGCTCAGCAGCTCCCACTTGGAGAGCCAAAGCTATTTCTGTGGGCGGCGG 2388
QY 601 GInLybProSerApsApsAlaApsSerArgArgSerTybHlApsGluGluSerProPheGlu 620
DB 2389 CAGAGCCCAAGTGAAGAGTGAATCTCGGCGGAGAGCTGGCATGAAGAGAGCCCTTTGAA 2448
QY 621 LysGInPheLybApsArgSerCybGInMetGluPheGlyGInSerIleMetSerGluAps 640
DB 2449 AAGCATTTTAAACGAGAGAGCTGCCAAATTGAAATTTGAGAGAGCATCATGTCAAGAAC 2508
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QY 641 ArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGln 660
DB 2509 AGGTCAAGGAAAGAGCTGGGGAAAGTGGGAGTCACTAGCTTTTCGGGACAGTGGAA 2568
QY 661 IleIleGluValSer 665
DB 2569 ATCATGAGGCTCTCC 2583

RESULT 3
US-09-920-668-3
; Sequence 3, Application US/09920668
; Patent No. 6482644
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 8 EXPRESSION
; FILE REFERENCE: RUS-0246
; CURRENT APPLICATION NUMBER: US/09/920,668
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 3
; LENGTH: 2377
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)...(2012)
US-09-920-668-3

Alignment Scores:
Pred. No.: 1,38e-126 Length: 2377
Score: 1326.00 Matches: 314
Percent Similarity: 58.54 Conservative: 94
Best Local Similarity: 45.05 Mismatches: 185
Query Match: 38.79 Indels: 104
Gaps: 21

US-10-029-345A-109 (1-665) x US-09-920-668-3 (1-2377)
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QY 20 GlnSerGlyThrGluLysValLeuLeuLeuSerSerArgProPheValGlnIleValThr 39
DB 195 CGGGGGGGGCTGGGGGGCGCGCTGATCAACAGCGCGCTCTTGTGGAGTACAAACAGC 254
QY 40 SerHisIleLeuGluAlaIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIle 59
DB 255 TGGCATGTGCTCAGCTCCGCTCAACATCTGCTCTCCAGCTGTGTAAAGCGGGCTGCAG 314
QY 60 GlnAspLysValLeuIleThrGluLeuIleGlnHisSerAlaLysHisLysValAspIle 79
DB 315 CAGGGCAAGTACCATTCGAGCTCATCCAGCGGCTGCACAGCAGCAGGTGAGGCT 374
QY 80 AspCysSerGlnLysValValValIleValIleValIleValIleValIleValIleVal 99
DB 375 ACGGAGCCACAGGAGTGGTGTATGACAGACAGCGGAGACGACAGCTGTGCGC 434
QY 100 SerAspCysPheLeuThrValLeuLeuGlnIleLysLeuGlnIleLysSerPheAsnSerValHis 119
DB 435 GAGAGACAGCTCTCTCAATCTGCTGAGCAAGCTGAGCGCTGCTTGACAGCGTGGCC 494
QY 120 LeuLeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyLys 139
DB 495 ATCTCACTGGGGGGTTCGACACCTTCTCTCTGCTTCCCGGCTCTGGAGGGCAG 554
QY 140 ---SerThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGly 158
DB 555 CCGTGTGCTGCTGCTCAACCATGAGCTCTCCAGCGCTGCTGCTGCTGCTGCTGCTG 614
QY 159 ProThrArgIleLeuProAsnLeuThrLeuGlnCysGlnArgAspValLeuAsnLysGlu 178
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DB 615 CTGACCCGATCTGCTCACTCACTTACCTGGGCTGGCAGAGAGCTCTTAACAGGAT 674
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DB 675 CTGATGAGCAGAAATGATATAGCTACGCTCCAAAGCAGCACTCTGCCCCAAGCT 734
QY 199 AspPheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluLys 218
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QY 219 IleLeuProThrLeuAspLysSerValAspPheIleGlnLysAlaLysAlaSerGlnIle 238
DB 795 CTGCTGCCCTGGCTGGAGCAATGCAATCAAGTTCATCAATTAAGCAAGCTCTCCAGCTGC 854
QY 239 CysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaThr 258
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DB 915 ATCATGAAGACCATGGCATGCTCTCCGACAGCGCTTACAGATTCTGTGAAGAGACAGCGGC 974
QY 279 ProThrIleSerProAsnPheAsnPheLeuGlnIleLeuLeuAspIleValLysIle 298
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QY 299 LysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeuGlnLys 318
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QY 319 ProAsn-----GluProValProAlaValSerGluGlnIleLysSerGluThr 335
DB 1071 CCTTCAGGAGAGCGGAGGCTCCGCTCAATCTGCTGCGCGGAGCGGCTGCCAGCGCTG 1130
QY 336 ProLeuSerProProCysAlaAspSerAlaThr-----SerGlnAlaGlyGlnArg 353
DB 1131 CCA-----CCACTTACTCAGAGAGCGCTGCCAGAGAAATGGGCTGCCAGGAGAGGC 1184
QY 354 ProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuAsp 373
DB 1185 GGCCTGAGCGGGGCGGAGAGCCCGCGCGCCCGCCAGCGCGCGCGGCG-----ACC 1235
QY 374 SerProLeuValGlnAlaLeuSerGlyLeuHisSerSerAlaAspArgLeuAspSer 393
DB 1236 AGCGCATGTCAGCAGAGGCTGCGGCTGCACTTCTTCGACCCGCTGCAGAACT 1295
QY 394 AsnLysLeuLysArgSerPheSerLeuAspIleLysSerValSerTyrsSerAlaSerMet 413
DB 1296 AACCGCTCAAGCGCTCTCTCTCCCTGGAATCAAGCTGCC----- 1337
QY 414 AlaAlaSerLeuHisGlyPheSerSerSerGlnAspAlaLeuGlnIleTyrsProSer 433
DB 1338 -----TACGCCCTTAGC 1349
QY 434 ThrThrLeuAspGlyThrAsn-----LysLeuCysGlnPhe 445
DB 1350 AGGGAGGCCAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 1409
QY 446 ---SerPro-----ValGlnGluLeuSerGlnIleThrProGluThrSerProAsp 461
DB 1410 GACAGCGCGTGGGGGGCGGCGGCTGCTGCTGCGCGCGCGCGCGAG--AGCCCGGAC 1466
QY 462 LysGluGlnLysSerIleProLysLysLeuGlnThrAlaArgProSerAspSerGlnSer 481
DB 1467 GCGCGCGCTAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1511
QY 482 LysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeuSer 501
DB 1512 -----CCGCGCGGCTCCCGCGCGCG-----TCC 1535
QY 502 ProLeuHisArgSerGlySerValGluAspAsnTyrsHisThrSerPheLeuPheGly--- 520
```

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Db      1536 CCGCGGCACAGCTCGGC-----CTGAACCTCGCGAT 1568
Qy      521 -----LeuSerThSerGInGInIaLeuThrLySerAlaGlyLeuGlyLeuGly 538
Db      1569 GCGGCCCGGCAGACTCGCGGCACGGCCTCTCGGCGCTTGCGCGCCCGGCGTGC 1628
Qy      539 -----TrpHisSerAspIleuAlaProGInThrSer 549
Db      1629 CTTGGCCAGCCGCGCGCCCGGGGCTTGAGCACCGCGCGTTAATCTCCA-----GGC 1682
Qy      550 ThrProSerLeuThrSerSerTrpTyRpeAlaThrGluSerGInAspHetyrSerAla 569
Db      1683 AGCGCGTCCCGCAGCGGCGCCCTGTGCTTCAGCCCGAG----- 1721
Qy      570 SerAlaIleTyGlyGlySerAlaSerTyRserAlaTyRserCySerGInLeuProThr 589
Db      1722 GCGCGCACAGGGGCGCGGGGCTGTGTTCGCCCTTCGCGCGGCGGCGCGCCGCGGA 1781
Qy      590 CySGlyAspGlnValTyRserValArgArgArgGlnIlySerProSerAspAlaAspSer 609
Db      1782 CCAGGCGCGCGCAGCAGCCTGCGCGCGCGGAGGACAGCGAGGCGCTGAGCCCCGAGCGC 1841
Qy      610 ArgArgSerTrpHieGluGluSerProPheGluLyGlnPheLyAsArgArgSerCyGln 629
Db      1842 CCGACCGCGCTGCGCCGAGGAGCGCGGCCCGCGAGACCGAGTTCAAGCCCGCACTGCGAG 1901
Qy      630 MetGluPheGlyGluSerIleMetSerGluAsnArgSerArg--GluGluLeuGlyLyAs 648
Db      1902 ATGGAGTTCTGAGAGAGGCGC--ATGGTGTGAGGGGCGCGCGCGCGAGGAGCTGCGCGCC 1958
Qy      649 ValGlySerGlnSerSerPheSerGlySerMetGluIleLeuValSer 665
Db      1959 CTGGCGACAGCGCGAGCTTCTCGGGCAGCGTGAAGTCAATCAGAGGTCTC 2009

RESULT 4
US-09-949-016-3250
; Sequence 3250, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3250
; LENGTH: 2351
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3250

Alignment Scores:
Pred. No.:      2,18e-126      Length:      2351
Score:          1324.00      Matches:      314
Percent Similarity: 58.39%      Conservative: 93
Best Local Similarity: 45.05%      Mismatches: 186
Query Match:      38.74%      Indels:      104
DB:              4      Gaps:      21

US-10-029-345A-109 (1-665) x US-09-949-016-3250 (1-2351)
Qy      1 MetAlaHisGluMetIleGlyThrGlnIleVal---ThrGluArgLeuValAlaLeuLeu 19
Db      109 ATGGCTGGGGAGCCGCGTCCCGAGAGAGGATGATGATCCAGAGAGCTGGCCAGCCTGCTG 168

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[illegible]

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Db      1210 AGGCACTGACAGAGGCGCTGCGGCGCTGACCTCTCTCGACCGCCCTGACGAGCACT 1269
Qy      394 AsnlyleuLysArgSerPheSerLeuAspIleLysSerValSerYrSerAlaSerMet 413
Db      1270 AACCGCTCAAGGCGCTCTCTCTCTCGACATCAAGCTCC----- 1311
Qy      414 AlaAlaSerLeuHisGlyPheSerSerSerGluAspAlaLeuGluYrYrLysProSer 433
Db      1312 -----TACGCCCTTAGC 1323
Qy      434 ThrThrLeuAspGlyThrAsn-----LysLeuCysGlnPhe 445
Db      1324 ATGCGGCGCCAGCGCGCCCGGCGCCCGACCGCGCGAGGCGCCGGAAGCTCTGCAAGCTG 1383
Qy      446 ---SerPro-----ValGlnGluLeuSerGluGlnThrProGluThrSerProAsp 461
Db      1384 GACAGCGCTGTGGGGCGCGCGCTGGGCGCTGTCTCGCCCATCCCGGAC--ACCCCGGAC 1440
Qy      462 LysGluGluLysSerIleProLysLysLeuGlnThrAlaArgProSerAspSerGlnSer 481
Db      1441 GCGCGCGCTGATGCGCGCGCCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1485
Qy      482 LysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeuSer 501
Db      1486 -----CCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1509
Qy      502 ProLeuHisArgSerGlySerValGluAspAsnYrHisThrSerPheLeuPheGly--- 520
Db      1510 CCGCGCGACAGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1542
Qy      521 ---LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGly 538
Db      1543 GCGCGCGCGGACACTCGCGCGGACGCGCGCTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1602
Qy      539 -----TrpHisSerAspIleLeuAlaProGlnThrSer 549
Db      1603 CTTGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1656
Qy      550 ThrProSerLeuThrSerSerTrpYrPheAlaThrGluSerSerHisPheYrSerAla 569
Db      1657 ACGCCGTCGCCGACGCGCGCGCTGTGCTTCAAGCCCGAG----- 1695
Qy      570 SerAlaIleTyrGlyLysSerAlaSerYrSerAlaTyrSerCysSerGlnLeuProThr 589
Db      1696 GCGCGCGAGGCGCGCGCGCGCGCGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1755
Qy      590 CysGlyAspGlnValTyrSerValArgArgGlnLysProSerAspArgAlaAspSer 609
Db      1756 CCAAGCGCGGCGAGCGACTGCGCGCGCGGAGCGAGCGAGCGAGCTGAGCCCGGAGCGCG 1815
Qy      610 ArgArgSerTrpHisGluGluSerProPheGluLysGlnPheLysArgArgSerCysGln 629
Db      1816 CCGAGCGCGCTGCGCGCGAGAGCGCGCGCGCGAGACGACGATCAAGGCGCGAGCTGCCAG 1875
Qy      630 MetGluPheGlyLysSerIleMetSerGluAsnArgSerArg---GluLysLeuGlyLys 648
Db      1876 ATGAGATTGAGAGGCG---ATGATGAGAGGCGCGCGCGCGCGCGAGAGGCTGGCGCGC 1932
Qy      649 ValGlySerGlnSerSerPheSerGlySerMetGluIleGluValSer 665
Db      1933 CTGGGCGAAGCGAGCTTCTCTCGGCGAGCTGAGAGTCATCAGAGTGTCC 1983

RESULT 5
US-09-949-016-14992
; Sequence 14992, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
```

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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 14992
; LENGTH: 13782
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14992

Alignment Scores:
Pred. No.: 1,366-70 Length: 13782
Score: 799.50 Matches: 254
Percent Similarity: 34.53% Conservative: 63
Best Local Similarity: 27.67% Mismatches: 154
Query Match: 23.39% Indels: 449
DB: 4 Gaps: 23

US-10-029-345A-109 (1-665) x US-09-949-016-14992 (1-13782)
Qy      123 GlyGlyPheAlaGluPheSerArgCysPheProGlyLeuGlyLys---SerThr 141
Db      8879 GAGGAGCTTCGACCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8938
Qy      142 LeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThrArg 161
Db      8939 CTGCTACCATGAGGCTCTCCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 8998
Qy      162 IleLeuProAsnLeuTyrLeuGlyCysGlnArgPheValLeuAsnIleGly 178
Db      8999 ATCTGCTCACTTACTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 9057
Qy      178 ----- 178
Db      9058 GTGAGTTCGAGGAGGTGATGAGGAAAGGCGAGAGCTCCAGAGCAGCTTGCGACG 9117
Qy      178 ----- 178
Db      9118 GAGAGCGGAGATGAGAGGAGAAAGAGCTGAAGGAGTGAAGTGTGTGGAGAA 9177
Qy      178 ----- 178
Db      9178 GCATGTGGGGGCCAGAGAGAGACCCAGGCTCCCAACCATGCCCCTGAAAGACACA 9237
Qy      178 ----- 178
Db      9238 GCAAGGCTTGGGAGAGGCGCGGAGGCGCTGCGGGAGAGAGCGGGAGCTGGCATGCCAA 9297
Qy      178 ----- 178
Db      9298 GCTGGGATGTCACTGGGCTCTGGCGAGCTGTGAAGAAATCCATGTTTAAATAATGT 9357
Qy      178 ----- 178
Db      9358 GACGAGGAAAGGATAAAGCAACCAACGAGCAATCAATAAATTCCTAGAGCCCAAC 9417
Qy      178 ----- 178
Db      9418 ACCAGCGTGGGTGGGCTTGAGTCGAGAGCCAGCGGTGCCACCCCGCGACGAGGCC 9477
Qy      178 ----- 178
Db      9478 CAGGATCGAAGGTGACACAGAGAGGCTCTTGAGGCTCTCCCTGTGATACATGAGATCT 9537
Qy      178 ----- 178
Db      9538 GAGCAAAATTCAGAGCTCCAGGATTCATAAGGCTCTGTACGCGAGGCGAGGAGAAAG 9597
```

OY	178	-----	178
Db	9588	CCTCACCCTTCACTCCGCCCGCCAGCTTCTCCACCCTTCCACCCTCCCGGCC	9657
OY	179	-----LeuIleGlnIleAsnGlyIleGlyTyrValIleuAsnIleSerThrCys	195
Db	9658	CTCCAGGATCTGATGACGCAAAATGAAATAGTACGTCTCTCAACGCAAGCACTCTCCG	9717
OY	196	ProTyrProAlaPheIleProGluSerHisPheLeuArgValProValAsnAspSerPhe	215
Db	9718	CCCAAGCTGTGACTTCATCTGCGAAGCGGCTTCAATGGGGTCTCCCATCAACGCACTAC	9777
OY	216	CysGluTyrValIleuProTyrPheAspTyrSerValAspPheIleGlu-----	231
Db	9778	TGTAAAAAATGCTGCTGCTGGCTGGACAGTCCATGAGTTCATCGG-TGAGTCTGGCT	9836
OY	231	-----	231
Db	9837	GAGGAGAGGAGGAGGAGCCTGGCTAGAGAAAGGCTAGAGCTGTGTGTGGCCACAGACAG	9896
OY	231	-----	231
Db	9897	GAGGAGGATCCCGAGAGATAGCCGGAAGCTGTGGCATGGGCGGGTCCCTCACT	9956
OY	231	-----	231
Db	9957	GAGCCAGGAGAGACTGTGCAGTCTTAGCCCTCACTGGCCCCCATGGCCCACTGGCCA	10016
OY	232	---LysAlaIleValAspSerAsnGlyCysValIleuValHisCysLeuAlaGlyIleSerArg	250
Db	10017	GATAAAGCCAAAGCTCTCAGCTGCGCAAGTATGTCATCTGTGCTGGCTGGCATCTCCGC	10076
OY	251	SerAlaThrIleAlaIleAlaTyrIleMetLysArgMetAspMetSerLeuAspGlnAla	270
Db	10077	TCTGCACACATCGCCATCGCTACATCATATGAAAGCATGGGCAATGTCCTCCAGCAGCGCC	10136
OY	271	Tyr-----	271
Db	10137	TACAGGATACCACTTCCCGAGTGGCGCATTTGGCTCAAGCGTGCCTTCCCTCCCC	10196
OY	271	-----	271
Db	10197	GGCTGGCCCACTGCACCAAGATATGACCCCACTGCACAGACCCGTGGCAAGAGAGAGGC	10256
OY	271	-----	271
Db	10257	CTGAGACACAGCTGGCGCACAATGAGCTGCGGGTGCCAGCGGGTGCCTCAGGTGGCAG	10316
OY	272	-----ArgPheValIleGluTyr	277
Db	10317	CCTGGCCCGCGCGGCGCTGGAGCTGAGCCTCTCCCGCGGTTCTGTGAAGGACAGG	10376
OY	278	ArgProThrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGlnTyrLys	297
Db	10377	CGCCGCTCATCTGCGCAACTTCTCTGGCGCAGGTGGAGTACAGAGCGCAGC	10436
OY	298	IleLysAsnGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeuGln	317
Db	10437	CTGAAGCTGCGCGCGCCCTGCAGAGGACCGCGGC-----	10472
OY	318	LysProAsn-----GluProValProAlaValSerGluGlyGlnLysSerGln	334
Db	10473	ACCCCTTCAGAGACCGCGAGAGCTCCCGCCAGTCTGCGCCGCGGCCCGCGTGCACAG	10532
OY	335	ThrProLeuSerProProCysAlaAspSerAlaThr-----SerGlnAlaIleGln	352
Db	10533	CTGCCA-----CCACTTACTCTGAGAGGCGTGCACACAGGAAATCGGCTGCAGAGAG	10586
OY	353	ArgProValHisProAlaSerValProSerValProSerValGlnProSerLeuLeuGln	372
Db	10587	GGCGGCGTGAAGCGCGGGGAGAGCCCGCGGCCCCCAAGCGCCCGCGC-----	10637
OY	373	AspSerProLeuValGlnAlaLeuSerGlyLeuHisLeuSerAlaAspArgLeuLysP	392

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Db      10698  ACCAGGCCACTGCAAGCAGGGGCTGCGGCGCTGCACCTCTCTCCGAGCCGCTGCAGAGC 106997
Oy      393  SerAnlybLeuLybArgSerPheSerLeuAerLysSerValSerTySerAlaSer 412
Db      10698  ACTAAACGGCTCAAGCGCTCTCTCTCCCTGACATCAAGTCTGCC----- 10742
Oy      413  MetAlaIaSerLeuHnISGLYPheSerSerSerGluAerAlaLeuGluTyTyTyPro 432
Db      10743  -----TACGCCCTT 10751
Oy      433  SerThrThrLeuAerGlyThraan-----LysLeuCybGln 444
Db      10752  AGCATGGGGCCCAACGAGCCCCGGGGCCCCCGAGCCCCGGGAGAGGCCCGAAAGCTCTGCAG 10811
Oy      445  Phe---SerPro-----ValGlnGluLeuSerGluGlnThrProGluThrSerPro 460
Db      10812  CTGGACAGCCCGTCGGGGGGCGGGCGCTGGAGCTGTGCTCTCCGCCCATCCCGAGC---AGCCGG 10868
Oy      461  AepLybGluGluAlaSerLLeProlYbLybLeuGlnThrAlaArgProSerAerSerGln 480
Db      10869  GACCCCGCGCTGATGGCGCCCAACGAGCCCCCGCGCGGCGCCCGGCC----- 10916
Oy      481  SerLybArgLeuHnISerValaArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500
Db      10917  -----CCGCGAGCTCCCGCGCGC----- 10937
Oy      501  SerProLeuHnIaArgSerGlySerValGluAerAerTyHnIaThrSerPheLeuPheGly 520
Db      10938  TCCCCCGCGCAAGCGCTCGGC-----CTGAACCTTCGCG 10970
Oy      521  -----LeuSerThrSerGlnGlnHnISLeuThrLysSerAlaGlyLeuGlyLeuYb 537
Db      10971  GATCGCGCCCGGACAGACTCCGCGGACAGCGCTCTCTCCGCGCTCGCGCGCGCCGCGCGCC 11030
Oy      538  Gly-----TrpISerAerLLeuAlaProGlnThr 548
Db      11031  GGCCCTGGCAAGCCCGCGCGCCCGGAGGCTGGGACAGCCGCGCTGACATCCCA----- 11084
Oy      549  SerThrProSerLeuThrSerSerLTPYrPheAlaThrGluSerSerHnIaPheTySer 568
Db      11085  GGCACGCGCTGCGCCAGCGGCGCTGTGCTTCAAGCCCGAG----- 11126
Oy      569  AlaSerAlaLLeTyGlyGlySerAlaSerTySerAlaTySerCySerGlnLeuPro 588
Db      11127  ---GGCGCAGAGGAGGCGGGGCGGGTGTGTCGCGCTTCGCGCGGCGGAGCGCGCCG 11183
Oy      589  ThrCybGlyAerGlnValTySerValaArgAlaArgGlnLybProSerAerArgAlaAer 608
Db      11184  GAGCAGAGCGCGCGAGCGACTGCGCGCGCGGAGAGCAGAGGAGCTAAGCCCCGGAGC 11243
Oy      609  SerArgArgSerThrHnISGLuGluSerProPheGlnLybLeuLybArgArgSerCyb 628
Db      11244  GCGGAGACCGGCTGGCCCAAGAGCCGGCGCCCGGAGACGCACTTCAAGCGCGCGACGTCC 11303
Oy      629  GlnMetGluPheGlyGluSerLLeMetSerGluAerAerSerArg---GlnGluLeuGly 647
Db      11304  CAGATGAGATTCAAGAGGAGC---ATGATGAGAGGGGCGCGCGCGCGAGAGACTGGGC 11360
Oy      648  LysValGlySerGlnSerSerPheSerGlySerMetGluLLeLLeGluValSer 665
Db      11361  GCCCTGGGCAAGCAGCGAGCTTCTCGGCAAGGTGAGATCATCAAGGTCTCC 11414

RESULT 6
US-09-016-434-1135
; Sequence 1135, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Selhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490

```


Qy 31 rArgProPheValGluTyr-AsnThrSerHisIleuGluAlaIleAsnIleAsnCy5 51
Db 59 CCGGCATTTTGGAATACCAATACATCCACATTTTGGAGCCATTATATACATGCT 118
Qy 51 erIleuWeclybAgaGleuGlnIleAspIlyValIleuIlethrgIleuIleGln 71
Db 119 CCAGCTTATGAAGCAGAGGTCGCAACAGCAAGGTTATTAACAGAGCTCATCAGC 178
Qy 71 fAserAlaIlybIlyValAspIleAspCySerGlnIlyValIleValIleAspGlns 91
Db 179 ATTACGCGAACTAAGTTAGTTCATTCAGTCAGTCAAGAGTTGATTCAGATCAMA 238
Qy 91 eSerGlnAspValAlaSerIleuSerSerAspCySpheleuThrValIleuGlyVal 111
Db 239 GCTCCCAATGTTGCTCTCTCTCTTCAGACGTTTTCATCTGACTTCTGGTAAAC 298
Qy 111 euGluIlySerPheAsnSerValHisIleuAla 122
Db 299 TGGAGAAAGCTTCACTCTGTTCACTGCTTGA 333
RESULT 10
US-09-557-921-1
/ Sequence 1, Application US/09557921
/ Patent No. 6551810
/ GENERAL INFORMATION:
/ APPLICANT: Lucbe, Ralf M.
/ APPLICANT: Wei, Bo
/ TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
/ FILE REFERENCE: 200125.416
/ CURRENT APPLICATION NUMBER: US/09/557,921
/ CURRENT FILING DATE: 2000-04-20
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 1830
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-557-921-1
Alignment Scores:
Pred. No.: 6,04e-38 Length: 1830
Score: 469.00 Matches: 107
Percent Similarity: 57.72% Conservative: 65
Best Local Similarity: 35.91% Mismatches: 96
Query Match: 13.72% Indels: 30
Gaps: 7
US-10-029-345A-109 (1-665) x US-09-557-921-1 (1-1830)
Qy 27 LeuIleuIleAspSerArgProPheValGluTyrAsnThrSerHisIleuGluAlaIle 46
Db 603 GTCATTCATTCGTCGAGGCTTCATTCAGTACACAAAGAGTACATCCAGAGGCTGTC 662
Qy 47 AsnIleAsnCySer---LysIleuWeclybAgaGleuGlnIleAspIlyValIleuIle 65
Db 663 CACATTAACGTGCGCATTAAGATACAGCGCGAGAGCTCAGAGGCAAGATCACTGTC 722
Qy 66 ThrGluIleuIleGln---HisSerAlaIlybIlyValAspIleAspCySerGlnIly 84
Db 723 CTAGACTTGATTTCTGTAGGAGGAGCAAGCACTCTTCAGAGATCTTTTCCAAAGAA 782
Qy 85 ValIleValIleAspIleSerGlnAspValAlaSerIleuSerSerAspCySpheleu 104
Db 783 ATTATAGTTTATGATAGATACCAATACCAAGCGAGTATGCTCCCAAGCCACTT 842
Qy 105 ThrValIleuGlyIlybIleuGluIlySerPheAsnSerValHisIleuAlaGlyIly 124
Db 843 CACATAGCTCTGAGTCCCTGAAGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 902
Qy 125 PheIleGluIlyPheSerArgSpheProGlyLeuCyGluGlyIlyb----- 139
Db 903 CTTAGTAGTTTAAAGCAGAAACATGAAACCTCTGTGACAACTCCCTCCAGCTCCAAAG 962

Qy 140 -----SerThrIleuValProThrCySileser 148
Db 963 TGGCGGAGAGTGGGGGGCGCGCATCCGGGCTGAGGCTGTGACTTCAGGCCATC--- 1019
Qy 149 GlnProCyLeuPro---ValAlaAsnIleGlyProThrArgIleuProAsnLeuTyr 167
Db 1020 ---CCACACACCCCTGACATCGAGAAAGCTGAGCTCACCCCACTCTGCTTC 1076
Qy 168 LeuGlyCyGlnArgAspValIleuAsnIlybGlnIleGlnIleAsnGlyIly 187
Db 1077 CTGGATATAGAGAGATGCTCAGACCTGACACCATGAGCGGTGAACAGGCTAC 1136
Qy 188 ValIleuAsnAlaSer-----TyrThrCybProIlybAspPheIlePro 202
Db 1137 GTCATACAGTACACCATGATCTCCCTCTACCATATAGAGAAAGCCCTTTC----- 1190
Qy 203 GluSerHisPheIleuArgValProValAsnAspSerPheCyGluIlybIleuProTyr 222
Db 1191 -----ACTACAGAGGCTGCGCAGCAGCTGACAGCAAGAGAACTGCGGAGTAC 1244
Qy 223 LeuAspIlySerValAspPheIleGluIlybAlaIlybAlaSerAsnIlyCyValIleuVal 242
Db 1245 TTTGAAGAGGCTTTGAGTTCAITGAGGAAGCTCACAGCTGAGAGGCTTCTCATC 1304
Qy 243 HisCyLeuAlaGlyIlySerArgSerAlaThrIleAlaIleAlaTyrIleWeclybArg 262
Db 1305 CACTGCGAGCTGGGTGTCCTCCGCTCCGACCATGTGATCCCTTACTTGAAGAGCAC 1364
Qy 263 MetAspMetSerIleuAspGluAlaTyrArgPheValIlybGluIlybArgProThrIleSer 282
Db 1365 ACTCGATGACCATGATGATGCTTAAATTTGCAAGAGCAAGCAAGCAATATATCTCC 1424
Qy 283 ProAsnPheAspPheIleuGluIlybIleuAspIlybGluIlybIleAsn 300
Db 1425 CCAAACCTTAACTCATGGGCGAGTTGCTAGAGTTGAGAGAAAGCACTAAACAC 1478
RESULT 11
US-09-702-705-803
/ Sequence 803, Application US/09702705
/ Patent No. 6504010
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tonglong
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Lodes, Michael A.
/ APPLICANT: Ranger, Gary
/ APPLICANT: Vedvick, Tom
/ APPLICANT: Carter, Darlick
/ APPLICANT: Retter, Marc
/ APPLICANT: Mannion, Jane
/ APPLICANT: Pan, Lidun
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.478C14
/ CURRENT APPLICATION NUMBER: US/09/702,705
/ CURRENT FILING DATE: 2000-10-30
/ NUMBER OF SEQ ID NOS: 1833
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 803
/ LENGTH: 1238
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-702-705-803
Alignment Scores:
Pred. No.: 1.34e-36 Length: 1238
Score: 453.00 Matches: 120
Percent Similarity: 50.52% Conservative: 73
Best Local Similarity: 31.41% Mismatches: 143
Query Match: 13.25% Indels: 46
Gaps: 13
US-10-029-345A-109 (1-665) x US-09-702-705-803 (1-1238)


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Db      999 ATCATCTCGCCCACTTCAAGCTTCATGGGCGACCTGCTGCAGTTCCAGTCTGCTG 1058
Qy      300 AaenGlnThrGlyValAserGlyProlysSerLysLeuLysLeuLysLeuLysPro 319
Db      1059 GCCACGCTCTGCTGCTCGAGGCTGCTAGC-----CCG 1091
Qy      320 AaenGlnProValProAlaValSerGlnGlyGlnLysSerGlnThrProLeuSerPro 339
Db      1092 TCGGACCCCTG-----GGGAGCGGGCGAAGACCCCGCCACCCG 1133
Qy      340 ProCysAlaAspSerAlaThrSerGlnAlaAlaGlyGlnArgProValHisProAlaSer 359
Db      1134 -----ACCTCGCAGTTCTGCTTTCAGCTTTTCCGGTC--TCCGTGGGC 1172
Qy      360 ValProSerValProSerValGlnProSerLeuLeuGlnAspSerProLeuValGlnAla 379
Db      1173 GTGCACCTCGGCCCCCGACGACCTGCTTACTG-----CACAGCCCATCACCACCTCT 1226
Qy      380 LeuSer 381
Db      1227 CCCAGC 1232

RESULT 14
US-09-671-325-803
; Sequence 803, Application US/09671325
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongrong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: DIAGNOSIS OF LUNG CANCER
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 803
; LENGTH: 1238
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-671-325-803

Alignment Scores:
Pred. No.: 1,34e-36 Length: 1238
Score: 453.00 Matches: 120
Percent Similarity: 50.52% Conservatve: 73
Best Local Similarity: 31.41% Mismatches: 143
Query Match: 13.25% Indels: 46
Db: 4 Gaps: 13

US-10-029-345A-109 (1-665) x US-09-671-325-803 (1-1238)
Qy      19 LeuGlnSerGlyThrGlnLysValLeuLeuLysAspSerArgProPheValGlnLysr 38
Db      168 CTGCCGAGCGGC--GGCAAGTCCCTGCTGCTGCACTGCAGACCGTTCTGGCGACAGC 224
Qy      39 ThrSerHisLeuGlnAlaLeuAsnLeuAsnLeuAsnLeuAsnLeuMetLysArgLysLeu 58
Db      225 GCGGCTACATCTTACGTTCCGCTCAACGCGCCTGAACACCATGCTGCGCGCGG--- 281
Qy      59 GlnGlnAspLysValLeuLysLeuThrGlnLeuLys-----GlnHisSerAlaLysHisLys 76
Db      282 GCTAAGGCGCTCGTGAAGCTGAGAGATCTGCGCGCGAGAGAGAGATACGCGCCGCG 341
Qy      77 ValAspLysLeuAspCysSerGlnLysValValValLysArgGlnSerSerGlnAspValAla 96
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Db      342 TTGCGCTCCGCGCTTACTCGCGGCTCATCTGCTACAGACGAGCGACGCCGCGCGAG 401
Qy      97 SerLeuSerSerAspCysPheLeuThrValLeuLeuGlyLysLeuGlnLysSerPhe--- 115
Db      402 AACCTCCGAGAGACAGCAGCTGTGCTGGTGGGAGAGCGCTGCGCGAGCGCGAG 461
Qy      116 ---AaenSerValHisLeuLeuAlaGlyGlyPheAlaGlnPheSerArgCysPheProGly 134
Db      462 CGCACCGACATCTGCTGCTCAAGCGCGCTATGAGAGTTTCTCCAGATACCCAGAA 521
Qy      135 LeuCysGlnGlyLysSerThrLeu-----ValProThrCysLysSer 148
Db      522 TTCTGTTTAAACCAAGCGCTCGCAGCCATCCACCCCGCGTTCCCGCCAGCCACA 581
Qy      149 GlnPro-----CysLeuProValAla-----AsnLleGlyPro 159
Db      582 GAGCCCTTGAGACCTGAGCTGCTCTGTGGAGACCCCATACAGACAGAGAGAGTCTT 641
Qy      160 ThrArgLysLeuProAsnLeuLysLeuGlyCysGlnArgAspValLeuAsnLysGlnLeu 179
Db      642 GTGAGATCTCTTCCCTTCTACTCGGAGTGCCTACACATGCTGCCCGGAGAGACATG 701
Qy      180 lIeGlnGlnAaenGlyTlIeGlyTyValLeuAsnAlaSerTyThrCysProLysProAsp 199
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Qy      200 PheLleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGlnLysIle 219
Db      759 TTGGAAGACACTATCATGATCAAGTCAATCCAGTGAAGATATACACAGCCGACATC 818
Qy      220 LeuProTyrLeuAspLysSerValAspPheIleGlnLysAlaLysAlaSerAsnGlyCys 239
Db      819 AGCTCTGGTTCATGAGAGCCATAGATACATCATGATGCCGTGAAGAGACTGCCGTGGCGC 878
Qy      240 ValLeuValHisCysLeuAlaGlyLysSerArgSerAlaThrIleAlaIleAlaTyrIle 259
Db      879 GTGCTGTGCACTGCAGCGCGGCACTCTCGGCTGGCCACCATCTGCTGCTTACTG 938
Qy      260 MetLysArgMetAspMetSerLeuAspGlnAlaTyrArgPheValLysGlnLysArgPro 279
Db      939 ATGATGAAGAAACGGGTGAGGCTGAGAGAGGCTTCGAGTTCTTTAAGACGCGCGCAGC 998
Qy      280 ThrLysSerProAsnPheAsnPheLeuGlnLysLeuLeuAspTyArgLysLysLysLys 299
Db      999 ATCATCTCGCCCACTTCAAGCTTCATGGGCGACGCTGCTGAGATGCCACAGTCTG 1058
Qy      300 AaenGlnThrGlyValAserGlyProlysSerLysLeuLysLeuLysLeuLysPro 319
Db      1059 GCCACGCTCTGCTGCTCGAGGCTGCTAGC-----CCG 1091
Qy      320 AaenGlnProValProAlaValSerGlnGlyGlnLysSerGlnThrProLeuSerPro 339
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Qy      340 ProCysAlaAspSerAlaThrSerGlnAlaAlaGlyGlnArgProValHisProAlaSer 359
Db      1134 -----ACCTCGCAGTTCTGCTTTCAGCTTTTCCGGTC--TCCGTGGGC 1172
Qy      360 ValProSerValProSerValGlnProSerLeuLeuGlnAspSerProLeuValGlnAla 379
Db      1173 GTGCACCTCGGCCCCCGACGACCTGCTTACTG-----CACAGCCCATCACCACCTCT 1226
Qy      380 LeuSer 381
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RESULT 15
US-09-589-184-803
; Sequence 803, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongrong
; APPLICANT: Bangur, Chaitanya S.
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GenCore version 5.1.6
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Run on: February 14, 2005, 10:56:55 ; Search time 887.813 Seconds

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Title: US-10-029-345A-109

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Searched: 5378673 seqs, 2950229984 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	3406	99.6	1998	17	US-10-377-072-27
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6	3406	99.6	3496	9	US-09-964-273-1
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35	1262	36.9	2476	17	US-10-220-120-28
36	1075.5	31.5	2039	17	US-10-072-012-265
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38	724	21.2	461	18	US-10-357-930-12416
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ALIGNMENTS

RESULT 1
US-09-816-494-3
Sequence 3, Application US/09816494
Patent No. US20020034807A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USBS THEREFOR
FILE REFERENCE: 10448-030002
CURRENT APPLICATION NUMBER: US/09/816,494
PRIOR APPLICATION NUMBER: 2001-03-23
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens
US-09-816-494-3

Alignment Scores:

Pred. No.:	0	Length:	1998
Score:	3406.00	Matches:	663
Percent Similarity:	99.85%	Conservative:	1
Best Local Similarity:	99.70%	Mismatches:	1
Query Match:	99.65%	Indels:	0
DB:	9	Gaps:	0

US-10-029-345A-109 (1-665) x US-09-816-494-3 (1-1998)

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QY      1 MetAlaHisGluMetIleGlyThrGluIleValThrGluArgLeuValAlaLeuLeuGlu 20
DB      1 ATGGCCCATGAGATGATGGAATCAAAATGTTACTGAGAGGTGGTGGCTCTGCGTGGAA 60

QY      21 SerGlyThrGluValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40
DB      61 AGTGGAAACGGAAAAAGGTGCTTAATGATAGCCGGCCATTGTGGAAATACATACATCC 120

QY      41 HisIleLeuGluValAlaIleAsnIleAsnCysSerLysLeuMetLysArgLeuGln 60
DB      121 CACATTTTGGAAACCATTAATATCAACTGCTCCAGCTTATGAAAGGAGTTGCAACG 180

QY      61 AspLysValLeuIleThrGluLeuIleGlnHisSerAlaLysHisLysValAspIleAsp 80
DB      181 GACAAAGTGTATATACAGAGCTCATCCAGCATTCAGCGAAACATAGGTGACATTTGAT 240

QY      81 CysSerGluValValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
DB      241 TGGAGTCAGAAAGGTGTAGTTACGATCAAAAGCTCCCAAGATGTTCCCTCTCTCTTCA 300

QY      101 AspCysPheLeuThrValLeuLeuGlyLysLeuGluLysSerPheAsnSerValHisLeu 120
DB      301 GACTGTTTCTCATCTTACTCTCGGGTAACTGGAAAGAGCTTCAACTCTGTTCACCTG 360

QY      121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyLysSer 140
DB      361 CTTCGAGGTGGGTGTTCTGAGTTCCTCGTGTGTTCCCTGGGCTCTGTGAAAGGAAATCC 420

QY      141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
DB      421 ACTCTAGTCCCTACCTGCAATTTCTCAGCTTGTCTTACCTGTGCCAACTTGGGCCAAC 480

QY      161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnLysGluLeuIle 180
DB      481 CGAATCTTCCCAATCTTATATCTTGGCTCCAGCGAGATGCTCTCAACAGAGAGCTGATG 540

QY      181 GlnGlnAsnGlyTyrIleGlyTyrValLeuAsnAlaSerTyrThrCysProLysProAspPhe 200
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QY      221 ProTyrLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsnGlyCysVal 240
DB      661 CGGTGGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCCCTCCAAATGGAATGTT 720

QY      241 LeuValHisCysLeuAlaGlyTyrSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
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QY      261 LysArgMetAspMetSerIleAsnArgValAlaTyrArgPheValLysGluLysArgProThr 280
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QY      281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysLysIleLysAsn 300
DB      841 ATATCTCCAAACTTCAATTTTCTGGGCCCAACTCTCGAGCTATGAGAAAGATTAAAGAAC 900

QY      301 GlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeuGluLysProAsn 320

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QY      321 GluProValProAlaValSerGluGlyGlyLysSerGluThrProLeuSerProPro 340
DB      961 GAACCTGTCCTCGCTGCTCTCAGAGGGTGGACAGAAAAGCAGAACCCCTCAGTCCACCC 1020

QY      341 CysAlaAspSerAlaThrSerGluValAlaGlyGlnArgProValHisProAlaSerVal 360
DB      1021 TGTGCCACTCTGTACTTACCTCAGAGGACAGGACAAAGGCCCTGTGATCCGCCAGCGTG 1080

QY      361 ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380
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QY      381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLysArgSerPhe 400
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QY      401 SerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaIleSerLeuHisGlyPhe 420
DB      1201 TCTCTGATATCAATCAAGTTTCATATTCAGCCAGCATGGCAGCATCTTACATGGCTTC 1260

QY      421 SerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAspGlyThrAsn 440
DB      1261 TCTCATCAGAAAGATGCTTTGGAATATCAAAACCTTCCACTACTCTGGATGGAGCCAAC 1320

QY      441 LysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerPro 460
DB      1321 AAGCTATCCAGATTTCTCCCTGTTCAGGAACATATCGAGAGCACTCCGAAACCGACTCT 1380

QY      461 AspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerGln 480
DB      1381 GATTAAGAGAAAGCCAGCATCCCAAGAGCTGCAGACCGCCAGCTTCCAGACAGCCAG 1440

QY      481 SerLysArgLeuHisSerSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
DB      1441 AGCAAGCATATTCATTCGCTCAGAAACAGACAGAGTGGACACCGCCAGAGGTCCCTTTTA 1500

QY      501 SerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheGly 520
DB      1501 TCTTCACGTCATCCAAAGTGGAGCGGTGGAGACAAATTAACAACACAGCTTCCCTTTTCGGC 1560

QY      521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTyrHis 540
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QY      541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheAla 560
DB      1621 TCGATATCTTGGGCCCCCAAGACCTTACCTTCCCTGACCAAGCAGCTGGTATTTGGCC 1680

QY      561 ThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyLysSerAlaSerTyrSer 580
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QY      581 AlaTyrSerCysSerGlnLeuProThrCysGlyLysAspGlnValTyrSerValArgArg 600
DB      1741 GCTTACAGCTCAGCCAGACCTGCCACTTGGCGGAACCAAGCTATTTCTGTGCGAGCGG 1800

QY      601 GlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSerProPheGlu 620
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QY      621 LysGlnPheLysArgArgSerCysGluMetGluPheGlyGluSerIleMetSerGluAsn 640
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QY      641 ArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGlu 660
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QY      661 IleIleGluValSer 665
DB      1981 ATCATTTGAGGTCTCC 1995

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RESULT 2

US-10-377-072-27

Sequence 27, Application US/10377072

Publication No. US2004009501A1

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals Inc.

APPLICANT: Curtis, Rory A.J.

APPLICANT: Logan, Thomas Joseph

APPLICANT: Glucksmann, Maria A.

APPLICANT: Meyers, Rachel E.

APPLICANT: Williamson, Mark J.

APPLICANT: Rudolph-Owen, Laura A.

APPLICANT: Chun, Miyoung

APPLICANT: Tsai, Peng-Ying

TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,

TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES

FILE REFERENCE: MPIO3-0180NM

CURRENT APPLICATION NUMBER: US/10/377,072

CURRENT FILING DATE: 2003-02-27

PRIOR APPLICATION NUMBER: US 09/895,860

PRIOR FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US 60/215,370

PRIOR FILING DATE: 2000-06-29

PRIOR APPLICATION NUMBER: US 09/723,806

PRIOR FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: US 60/187,455

PRIOR FILING DATE: 2000-03-07

PRIOR APPLICATION NUMBER: US 09/843,297

PRIOR FILING DATE: 2001-04-25

PRIOR APPLICATION NUMBER: US 60/199,801

PRIOR FILING DATE: 2000-04-26

PRIOR APPLICATION NUMBER: US 09/861,801

PRIOR FILING DATE: 2001-05-21

PRIOR APPLICATION NUMBER: US 60/205,508

PRIOR FILING DATE: 2000-05-19

PRIOR APPLICATION NUMBER: US 09/816,494

PRIOR FILING DATE: 2001-03-23

PRIOR APPLICATION NUMBER: US 09/815,419

PRIOR FILING DATE: 2001-03-22

Remaining Prior Application data removed - See File Wrapper or PAM.

NUMBER OF SEQ ID NOS: 114

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 27

LENGTH: 1998

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)... (1998)

US-10-377-072-27

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QY	41	HsIlleLeuGIuAlaleuAnIleAenCySerIYleuMeIYarIgrLeugIn	60

DB	121	CACATTTGGAGCCATTATATCAATGCTCCAAAGCTTATGAGGAAAGTTGCAACAG	180
QY	61	AapIYValleuIlethrgInleuIleGIInHlSerAlaleuHlSerValAapIleAap	80
DB	181	GACAAAGTTATATACAGAGCTCAATCCAGCAATTCAGCAAAACATAGGTGACATTGAT	240
QY	81	CySerGIuYValleuValIYarApsInSerSerGIuApsValAlaSerleuSerSer	100
DB	241	TGCAGTCAGAAAGTTGTAGTTTACATCAACACTCCAAAGATGTGCCCTCTCTTCA	300
QY	101	AapCySphleuThValleuLeuGIYleuLeuGIuYSerPheApsSerValHleu	120
DB	301	GACTTTTCTCAGTACTTCTGGGTAACTGAGAAAGCTTCAACTCTTCCACTG	360
QY	121	LeuAlaGIYIYphAlGIuPheSerAryCySphPheProGIYleuCySgIuGIYIYSer	140
DB	361	CTTGACAGGGGTTGTGATGTTCTCTGTTTCCCTGAGGCTCTGTAAAGAAATTC	420
QY	141	ThrlEuaIProThrCySIlleSerGIuProCySleuProValAlaAnIleGIYProThr	160
DB	421	ACTGATGCTTCACTGATCTTCTCAAGCTTCACTGCTTCACTGAGCAATGGCCAAAC	480
QY	161	ArgIleleuProApsleuYrleuGIYCySgInArApsValleuAnIYsgIuLeuIle	180
DB	481	CGAATTTCTCCAAATCTTATCTTGAGTCCAGCAGAGATGCTCAACAGAGAGCTGAG	540
QY	181	GIuGIuAnGIYIleGIYrValleuAnIleAserYrThrCySProIYsProApsPhe	200
DB	541	CAGCAGAAATGGATGTGTATGTGTAATGACACAAATACCTGTCCAAAGCTGACTT	600
QY	201	IleProGIuSerHlAphleuAryValProValApsApsPheCySgIuYsIleu	220
DB	601	ATCCCCGATCTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	660
QY	221	ProIYleuApsIYSerValApsPheIleGIuYValAlaYsIleAserAnGIYCyVal	240
DB	661	CCGTGTTGACAAATCAATGATTTCAATGTAGAAAGCAAAAGCTCCAAATGAGATGT	720
QY	241	LeuValHlAryleuValagIYleSerArySerAlaThrlleAlaIleAlaYrIleMe	260
DB	721	CTAGTGCACTGTTTGTGCTGATCTCCGCTCCGCAACATGCTATGCTTCAATCAAC	780
QY	261	LyAryMetApsMeSerleuApsGIuAlaYrArApsPheValIleGIuYsAryProThr	280
DB	781	AMAGAGATGACATGCTTTAGATGAAGCTTCAAGTTTGTGAAAGAAAGAAAGCTTACT	840
QY	281	IleSerProApsPheApsPheleuGIYleuLeuApsYrGIuYsIleYsIleYsAps	300
DB	841	ATATCTCCAAATCTCAATTTCTGGGCCAACTCTGACTATGAGAAAGATTAAGAAC	900
QY	301	GIuThrgIYAlaSerGIYProIYsSerIYleuYsleuHlSerleuGIuYsProAps	320
DB	901	CAGACTGAGCATCGAGGCCAAAGCAAACTCAAGCTGCTCAGCTGAGAAAGCCAAAT	960
QY	321	GIuProValProAlaValSerGIuGIYGIuYsSerGIuThrProleuSerProPro	340
DB	961	GAACTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1020
QY	341	CysAlaApsSerAlaThrSerGIuAlaAlaGIYGIuAryProValHlApsValAserVal	360
DB	1021	TGTGCCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1080
QY	361	ProSerValProSerValGIuProSerleuLeuGIuApsSerProleuValGIuAla	380
DB	1081	CCACAGGCTCCAGAGGTGACGCTGCTGTTAGAGCAAGCCCTGCTGACAGGCTC	1140
QY	381	SerGIYleuHlAserSerAlaApsAryleuGIuApsSerApsIYleuYsArySerPhe	400
DB	1141	AGTGGCTGCACTTCTGCAAGAGCTGAGAGCAAGCAATAGCTCAAGCTTCTTCT	1200
QY	401	SerleuApsIleYsSerValSerYrSerAlaSerMetValAserleuHlGIYpHe	420
DB	1201	TCTTGATATCAATCAATGATTTCAATTCAGCAGCAATGAGCATCTTACATGGCTTC	1260

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QY 421 SerSerSerGluAlaLeuGluTyrTyrTyrProSerThrThrLeuAspGlyThrAsn 440
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Db 1261 TCTTCATCAGAAAGTGTGGAAATCTACAAACCTTCCACTCTGGATGGAGCAAC 1320
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QY 441 LysLeuGlnGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerPro 460
| | | | |
Db 1321 AAGCTATGCCAGTTCTCCCTGTTTCAAGAACTATCGAGAGAGACTCCCGAAACCAAGTCTCT 1380
| | | | |
QY 461 AspLysGlnGluAlaSerLysLeuPheGlnThrAlaArgProSerAspSerGln 480
| | | | |
Db 1381 GATTAAGAGAGAACCCAGCATCCCAAGAAAGCTCAGACCCGCGCTTCAAGACACGAC 1440
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QY 481 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
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QY 501 SerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheGly 520
| | | | |
Db 1501 TCTCCACTGCATCGAAGTGGAGCGTGGAGAGCAATTTACACACAGCTTCTTTTCGGC 1560
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QY 521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyThrHis 540
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Db 1561 CTTTCACACGACGACGACGACCTCAGAAAGTCTGCTGGCGCTTAAAGGCTGAC 1620
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QY 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerThrTyrPheAla 560
| | | | |
Db 1621 TCGGATATCTTGGCCCCCGACGCTTACCCCTTCCCTGACGACGCTGGATTTTGGC 1680
| | | | |
QY 561 ThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyLysSerAlaSerTyrSer 580
| | | | |
Db 1681 ACAGAGTCTCTCACTTACTCTGCTGCTCAGCATCTACGAGGAGGAGTGCAGTTACTCT 1740
| | | | |
QY 581 AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgArg 600
| | | | |
Db 1741 GCTTACAGCTGACGACGACGCTCCCTGCTGGAGACCAAGTCTATCTTGGCAGACGCG 1800
| | | | |
QY 601 GlnLysProSerSerAspArgAlaAspSerArgTyrSerThrHisGluGluSerProPheGlu 620
| | | | |
Db 1801 CAGAGCCAGATGACAGAGCTGACTGCGCGCGAGAGCTGGCATGAAAGAGCCCTTTGAA 1860
| | | | |
QY 621 LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerLysLeuSerGluAsn 640
| | | | |
Db 1861 AAGCGATTAAACGCGAAGCTGCCAAATGGAATTTGAGAGGACATCATGTCAGAGAAC 1920
| | | | |
QY 641 ArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGlu 660
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Db 1921 AGGTACGGGAAAGCTGGGAAAGTGGGCACTGACTTTCGGGCGACAGATGAA 1980
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QY 661 IleIleGluValSer 665
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Db 1981 ATCATTTGAGGTCTCC 1995
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PRIOR APPLICATION NUMBER: US 09/895,860
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,370
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/723,806
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/187,455
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/843,297
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199,801
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: US 09/861,801
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205,508
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/816,494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/815,419
PRIOR FILING DATE: 2001-03-22
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1998)
US-10-377-072-27

Alignment Scores:
Pred. No.: 0 Length: 1998
Score: 3406.00 Matches: 663
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.65% Indels: 0
DB: 18 Gaps: 0

US-10-029-345A-109 (1-665) x US-10-377-072-27 (1-1998)
QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuGln 20
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Db 1 ATGGCCCATGAGATGATTTGGAATCTCAATTTTACGAGAGTTGGTGGCTCTGCGAA 60
| | | | |
QY 21 SerGlyThrGluLysValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40
| | | | |
Db 61 AGTGGAAAGGAAAAAGTGTCTTAATGATGACCGGCGCATTTGGAAATACAAATCATCC 120
| | | | |
QY 41 HisIleLeuGluAlaIleAsnIleAsnCysSerLysLeuMetLysArgArgLeuGln 60
| | | | |
Db 121 CACATTTGGAAGCCATTATATATCACTGCTCAAGCTTATGAAAGCGAAGSTTCAACAG 180
| | | | |
QY 61 AspLysValLeuIleThrGluLeuIleGlnHisSerAlaLysHisLysValAspIleAsp 80
| | | | |
Db 181 GACAAAGTGAATTAACAGAGCTCATTCAGCATTCAGGAAACGTAAGTTGACATGAT 240
| | | | |
QY 81 CysSerGlnLysValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
| | | | |
Db 241 TGCAGTCAGAAAGTTGATGATTACATCAAAAGCTCCCAAGATGTTGGCTCTCTCTTCA 300
| | | | |
QY 101 AspCysPheLeuThrValIleLeuGlyLysLeuGlyLysSerPheAsnSerValHisLeu 120
| | | | |
Db 301 GACTGTTTCTCATCTGATCTTCTGGGTAACCTGGAAGAAAGCTTCAACTCTGTTCACTG 360
| | | | |
QY 121 LeuAlaGlyLysPheAlaGluPheSerArgCysPheProGlyLeuGlyGlyLysSer 140
| | | | |
Db 361 CTTCAGAGTGGGTTTGGCTGAGTTCTCTGTTGTTTCCCTGGCCCTGTAAGGAAATCC 420
| | | | |
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
| | | | |
Db 421 ACTCTAGTCCCTACTGCTCAATTTTCAGACCTTGTCTTACTGTTGCAACATTTGGGCAAC 480
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QY 161 Arg1LeuProAsnLeuTyrLeuGIYCySGInARgAPValLeuAsnLysGIuLeu180
 DB 481 CGAATTCCTCCCAATCTTATCTGGCTGCACCGAGATGCTCTCAACAAAGAGCTGAAG 540
 QY 181 GInGInAsnGIY1LeGIYTYrValLeuAsnA1SerTYrThrCyAProLysProAspPhe 200
 DB 541 CAGCAAGATGGAGTTGGTTATGTTAAATGCCAGCAATACCGTCCAAAGCCTGACTTT 600
 QY 201 I1eProG1uSerThiAPheLeuARgVALProVALAsnAPSerPheCySG1uLys1Leu 220
 DB 601 ATCCCCGAGCTCATCTTCTGGCTGTGCTGTGAATGACAGCTTTGTGTGAGAAATTTTG 660
 QY 221 ProTPLeuAspLysSerValAspPhe1LeGIuLysVALAsnAsnGIYCySVAL 240
 DB 661 CCGTGGTTGACAAATCAGTATGATTTCTTGAAGAAAGAAAGCCCTCCATGGATGTGTT 720
 QY 241 LeuVALAsCyLeuVALGIY1LeSerARgSERVALThr1LeA1LeA1LeA1TYr1LeMeC 260
 DB 721 CTAGTGCATGTTTATGCTGGATCTCCGCTCCGCCACATGGCTATGCCCTACATCATG 780
 QY 261 LysAPMetAspMetSerLeuAspGIUALATYrARgPheVALysGIuLysARgProThr 280
 DB 781 AAGAGGATGACATGCTTTAGATGAAGCTTACAGATTGTGAAAGAAAAAGACCTACT 840
 QY 281 I1eSerProAsnPhAsnAPheLeuGIYGIuLeuLeuAspTYrGIuLysVALLeuAsn 300
 DB 841 ATATCTCCCAACTTCAATTTTCTGGGCCAACTCTGGACTATGAGAAAGATTAAGAAC 900
 QY 301 G1nThrGIYALAsGIYProLysSerLYLeuLYLeuLeu1eLeuGIuLysProAsn 320
 DB 901 CAGACTGGAGCATCAGGGCCAAAGCAATCTCACTGCTGACCTGAGAAAGCAAT 960
 QY 321 GIuProVALProALAsGIuLysGIYGIuLysSerGIuThrProLysSerProPro 340
 DB 961 GAACCTGTCCCTGCTGTCTCAGAGGGGTGACAGAAAGAGAGCGCCCTCAGTCCACCC 1020
 QY 341 CySVALAsPserALeThSerGIUALAAGIYGIuLysARgProVALAsnAsnAsnVAL 360
 DB 1021 TGTGGCGACTGTGCTACCTCAAGAGGAGAGCAAAAGGCCGTGATCCCGCAGCGTG 1080
 QY 361 ProSerVALProSerVALGIuProSerLeuLeuGIuAspSerProLeuVALGIUALAsn 380
 DB 1081 CCCACGCTGCCAGCGCTGACCGCTGCTTATGAGAGACAGCCCGCTGTTACAGGGCTTC 1140
 QY 381 SerGIYLeuH1eLeuSERALAsAPARgLeuGIuAspSERAsnLYLeuLYAsrSerPhe 400
 DB 1141 AGTGGGCTGCACCTGTCCGACAGAGGTGAAAGACAGCAATTAAGCTCAAGCGTTCCTTC 1200
 QY 401 SerLeuAsp1LeLysSerVALSerTYrSERALAsSerMetALAsSerLeuH1eGIYpHe 420
 DB 1201 TCTCTGGAATATCAATACAGTTCATATTCAGCCAGATGGCAGCATCTTACATGGCTTC 1260
 QY 421 SerSerSerGIUALAsPVALeug1uTYrTYrLysProSerThrThreAspGIYThraAsn 440
 DB 1261 TCTCTATCAGAAAGATCTTTGAAATPCTCAAACTTCCACTACTGTGATGGAGCAAC 1320
 QY 441 LysLeuCySGInPheSerProVALGIuLysLeuSerGIuLysGIuThrProGIuThrSerPro 460
 DB 1321 AAGCTATGCGCAATTCCTCCCTGTTCAGAACTATGAGACAGACTCCGAAACCACTCT 1380
 QY 461 ARpLYGIuLysLAsSer1LeProLYsLYLeuGIuThRALAsrProSerAspSerGIu 480
 DB 1381 GATTAAGAGAGAAAGCCAGCATCCCAAGAGCTGCACACCGCTTCAAGACGCCAG 1440
 QY 481 SerLYsARgLeuH1eSerVALArGTThrSerSerSerGIYThRALGIuARgSerLeuLeu 500
 DB 1441 AGCAAGCGATTCATTCGCTCAGAACCAACAGAGGAGACCGCCCAAGAGTCCCTTTTA 1500
 QY 501 SerProLeuH1eARgSerGIYSerVALGIuAspAsnTYrH1eThrSerPheLeuPheGIY 520
 DB 1501 TCTCCACTGCATCGAAGTGGAGCGGTGAGAGCAATTAACACACCGACTTCTTTCGGCG 1560

QY 521 LeuSerThrSerGIuH1eSLeuThrLYsSERALAGIYLeuGIYLeuLYsGIYTrPHis 540
 DB 1561 CTTTCCACAGCCAGCAGACAGACTTCAAGAGTCTGCTGGCTTAAAGGCTTGAC 1620
 QY 541 SerAsp1LeuALAProGIuThrSerThrProSerLeuThrSerSerTrpTYrPheA1 560
 DB 1621 TCGGATATCTGGCCCCCAGACCTTACCCCTTCCCTGACACAGCAGTGTATTTTGGC 1680
 QY 561 ThrGIuSerSerThiAPheTYrSerALAsSerA1LeTYrGIYGIYSerLAsSerTYrSer 580
 DB 1681 ACAGAGTCTCCACACTTCTACTCTGCTCAGGCATCTAGAGGAGAGTCCAGTTACTCT 1740
 QY 581 ALATYrSerCySGInLeuProThrCySGIYAspGIYVALTYrSERVALArGAGAG 600
 DB 1741 GCCTACGCTGCAGCCAGCTGCCACTTGGAGAGACCAAGTCTATTTCTGCGCAGCG 1800
 QY 601 GIuLYsProSerAspARg1AspSERARgARgSerTrpH1eGIuLysSerProPheGIu 620
 DB 1801 CAGAGCCAAAGTACAGAGACTGACCTGCGCGAGCTGGCATGAGAGAGCCCTTTGAA 1860
 QY 621 LysGIuPheLYsARgARgSerCySGInMetGIuPheGIYGIuSer1LeMetSerGIuAsn 640
 DB 1861 AAGCAGTTTAAACGAGAAAGCTGCCAAATGGAATTTGAGAGAGCATCTGTCAGAGAAC 1920
 QY 641 ARgSERARgGIuLysLeuGIYLYsVALGIYSerGIuSerSerPheSerGIYSerMetGIu 660
 DB 1921 AGCTACGGGAAAGAGCTGGGAAAGTGGGAGTCACTGCTTTCGGGACAGATGAA 1980
 QY 661 I1e1eGIuVALSer 665
 DB 1981 ATCATTTGAGGTCTCC 1995

RESULT 4

US-10-168-506-2
 ; Sequence 2, Application US/10168506
 ; Publication No. US20040053229A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PLOMAN, GREGORY D.
 ; APPLICANT: MARTINEZ, RICARDO
 ; APPLICANT: WHITE, DAVID
 ; APPLICANT: MANNING, GERARD
 ; APPLICANT: SUDARSANAM, SUCHA
 ; APPLICANT: HILL, RON
 ; APPLICANT: FLANAGAN, PETER
 ; TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
 ; FILE REFERENCE: 038602/1351
 ; CURRENT APPLICATION NUMBER: US/10/168,506
 ; CURRENT FILING DATE: 2002-06-21
 ; PRIOR APPLICATION NUMBER: PCT/US00/34736
 ; PRIOR FILING DATE: 2000-12-21
 ; NUMBER OF SEQ ID NOS: 76
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 2732
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-168-506-2

Alignment Scores:

Pred. No.: 0 Length: 2732
 Score: 3406.00 Matches: 663
 Percent Similarity: 99.85% Conservative: 1
 Best Local Similarity: 99.70% Mismatches: 1
 Query Match: 99.65% Indels: 0
 DB: 17 Gaps: 0

US-10-029-345A-109 (1-665) x US-10-168-506-2 (1-2732)

QY 1 MetALAH1eGIuMeC11eGIYThrGIu1LeVALThrGIuARgLeuVALA1LeuLeuGIu 20
 DB 538 ATGGCCCATGAGATATTGGAATCAAAATTGTACTGAGAGGTTGGTGTCTGTGGAA 597
 QY 21 SerGIYThrGIuLYsVALLeuLeu1eAsPserARgProPheVALGIuLYsAsnThrSer 40

Db 598 AGTGGAAACGGAAGAGTCTAATTGATGACGGCATTCTTGGAATTCATATCATCTCC 657
Qy 41 HisIleuEnglualalleasnilleasnYserLysLeuMetLysArgIleuEngln 60
Db 658 CACATTTTGGAAACCATTAATATCACTGCTCCAGCTTATGAAGGAGGTGGCAACAG 717
Qy 61 AspLysValIleuIleThrgIleuIleGlnHisSerAlaLysHisLysValAspIleAsp 80
Db 718 GACAAAGTGTATTTACAGAGCTCATCCACATTCCAGCAACATAGGTTGACATTGAT 777
Qy 81 CysSerGlnLysValValValYrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db 778 TGCAGTCAGAAAGGTGTAGTTACGATCAAAAGCTCCCAAGATGTTGCTCTCTCTTCA 837
Qy 101 AspCysPheLeuThrValIleuLeuEngLysLysLeuGlnLysSerPheAsnSerValHisLeu 120
Db 838 GACTGTTTTCTCACTGACTTCTGGGTAACTGGAGAAAGCTTCAACTCTGTTCACTG 897
Qy 121 LeuAlaGlyValYpheaIleuPheSerArgCysPheProGlyLeuCysGlnGlyLysSer 140
Db 898 CTTCGACGTGGGTTTGTCTGAGTTCTCTGTTGTTTCCCTGCTCTGTGAAAGAAATCC 957
Qy 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Db 958 ACTCTAGTCCCTACGCAATTTCTCAGCCTTGCTTACGTTGCAACATGGGCCAAC 1017
Qy 161 ArgIleLeuProAsnLeuYrLeuEngLysGlnArgAspValLeuAsnLysGlnLeuIle 180
Db 1018 CGAATTTCTCCCAATCTTATCTGTGGCTGCAGCGAGATGCTCTCAACAGAGCTGAG 1077
Qy 181 GlnGlnAsnGlyIleGlyYrValLeuAsnAlaSerYrThrCysProLysProAspPhe 200
Db 1078 CAGCAAAATGGGATTTGTTATGTTAATGCCAGCAATACCTGTCCAAAGCTGACTTT 1137
Qy 201 IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGlnLysIleLeu 220
Db 1138 ATCCCGAGTCTCATTTCTCGCGTGTGCTGGAAGAAGACAGCTTTGTGAGAAATTTTG 1197
Qy 221 ProThrLeuAspLysSerValAspPheIleGlnLysAlaLysSerAsnGlyCysVal 240
Db 1198 CCGTGTGTGACAAATCACTAGATTTCAATTGAGAAAGCAAAAGCCCTCCAAATGATGTGT 1257
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Db 1258 CTAAGTGCATGTTTACGTGGATCTCCCTCCGCCACATGCGTATGCCCTACATCATG 1317
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Qy 281 IleSerProAsnPheAsnPheLeuEngLysIleuLeuAspYrGlnLysLysIleLysAsn 300
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Qy 301 GlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeuGlnLysProAsn 320
Db 1438 CAGACTGGAGCATCGAGGCCAAAGCAAACTCAAGCTGCTGCACCTGGAAGAAGCAAAAT 1497
Qy 321 GlnProValProAlaValSerGlnGlyGlyLysSerGlnThrProLeuSerProPro 340
Db 1498 GAACCTGTCCCTGCTCTCAGAGGGGTGACAGAAAGAGAAAGCCCTCAGTCAACCC 1557
Qy 341 CysAlaAspSerAlaThrSerGlnAlaIleGlyGlnArgProValHisProAlaSerVal 360
Db 1558 TGTGCGCACTGTGTAACCTCAAGAGGAGAGCAAAAGCCCTGCTATCCCGCAGCGTG 1617
Qy 361 ProSerValProSerValGlnProSerLeuLeuGlnAspSerProLeuValGlnAlaLeu 380
Db 1618 CCCAGCGTGGCCAGGCGTGCAGCGCTGCTTAAAGAGACAGCCCGCTGTACAGCGCTC 1677
Qy 381 SerGlyLeuHisLeuSerAlaAspArgLeuGlnAspSerAsnLysLeuLysArgSerPhe 400

Db 1678 AGTGGGCTGCACCTGTCCGACAGAGCTGGAAGAAGCAATTAAGTCAAGGCTTCTTC 1737
Qy 401 SerLeuAspIleLysSerValSerYrSerAlaSerMetAlaIleSerLeuHisGlyPhe 420
Db 1738 TCTCTGATATCAAAATCAAGTTTCAATATTCAGCCACAGACATGGCAGCATCTTACATGCTTC 1797
Qy 421 SerSerSerGlnAspAlaLeuEngLysYrYrLysProSerThrThrLeuAspGlyThrAsn 440
Db 1798 TCTCTATCAAGAAATGCTTTGGAAATCTAACAACTTCCATCTCTGATGGAGCCAAAC 1857
Qy 441 LysLeuCysGlnPheSerProValGlnLysLeuSerGlnGlnThrProGlnThrSerPro 460
Db 1858 AAGCTATGCAATGCTTCCCTGTTGAGAAATCATGAGAGACATCCCGAAACAGTCTCT 1917
Qy 461 AspLysGlnGlnAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerGln 480
Db 1918 GATTAAGAGAGAAAGCCAGATCCCAAGAGCTGCAGATGCGCAGGCTTCAGACAGCCAG 1977
Qy 481 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500
Db 1978 AGCAAGCATTCGATTCGCTCAGAACAGCAGCATGCGACCGCCAGAGTCTCTTTTA 2037
Qy 501 SerProLeuHisArgSerGlySerValGlnAspAsnYrHisThrSerPheLeuPheGly 520
Db 2038 TCTCCACTGCATCGAAATGGAGCGGTGAGAGCAATTACCAACAGAGCTTCTTTTCGCG 2097
Qy 521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuEngLysLeuLysGlyYrHis 540
Db 2098 CTTTCACACAGCAGACAGACCTCAGAAAGTCTGTGCTGGGCTTAAAGGCTGGGAC 2157
Qy 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerYrThrPheAla 560
Db 2158 TCGATATCTTGCGCCCCCAACACCTTACCTCCCTGACAGACAGCTGATTTTGGC 2217
Qy 561 ThrGlnSerSerHisPheYrSerAlaSerAlaIleYrGlyLysSerAlaSerYrSer 580
Db 2218 ACAGAGTCTCACTTCTACTGCTGCCTCACCAATCTACGAGAGGACAGTCCAGTTACTCT 2277
Qy 581 AlaYrSerCysSerGlnLeuProThrCysGlyLysAspGlnValYrSerValArgArgArg 600
Db 2278 GCTTACAGCTCAGCAGACCTCCCACTTGGCGAAGCAAAAGTCTATCTGTGCGAGGCGG 2337
Qy 601 GlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGlnGlnLysSerProPheGln 620
Db 2338 CAGAAAGCAATGACAGAGCTGACTCGCGCGAGAGCTGCATTAAGAGAGCCCTTTGAA 2397
Qy 621 LysGlnPheLysArgArgSerCysGlnMetGlnPheGlyLysSerIleMetSerGlnAsn 640
Db 2398 AAGCATTTTAAACGACAGAAAGCTGCCAAATGGAATTTGGAGAGACATCATGTACAGAGAC 2457
Qy 641 ArgSerArgGlnGlnLysGlyLysValGlySerGlnSerSerPheSerGlySerMetGln 660
Db 2458 AGGTACGAGAAAGAGCTGGGAAAGTGGGACGTACGTACTTTTGGGGCAGATGGA 2517
Qy 661 IleIleGlnValSer 665
Db 2518 ATCAATTGAGCTCTCC 2532

RESULT 5
US-10-257-026-1
; Sequence 1, Application US/10257026
; Publication No. US20040086859A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: New dual specificity phosphatase
; FILE REFERENCE: DOSPI0K0MS
; CURRENT APPLICATION NUMBER: US/10/257,026
; CURRENT FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3059
; TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (127)..(2121)
US-10-257-026-1

Alignment Scores:

Pred. No.:	0	Length:	3059
Score:	3406.00	Matches:	663
Percent Similarity:	99.85%	Conservative:	1
Best Local Similarity:	99.70%	Mismatches:	1
Query Match:	99.65%	Indels:	0
	17	Gaps:	0

US-10-029-345a-109 (1-665) x US-10-257-026-1 (1-3059)

QY 1 MetAlaHLeuMeTLeuGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
DB 127 ATGGCCCATGATGATGTAAGAACTCAATTGTACTGAGAGGTGGCTGCTGAGAA 186
QY 21 SerGlyThrGluValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
DB 187 AGTGAACGGAAGAAAGTGTCTGTAATGATGAGCCGCAATTTGTGAATACATATCATCC 246
QY 41 HisIleLeuGluAlaIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsn 60
DB 247 CACATTTTGGAGGCCATTAAATCAACTGCTCCAGCTTAATGAGCGAAGTTGCAACAG 306
QY 61 AspIleValIleuIleThrGluLeuIleGlnIleSerIleValIleValIleValIleAsp 80
DB 307 GACAAAGTGTATTAACAGAGCTCATCCAGCATTCAGCAAAACATTAAGTTGATGAT 366
QY 81 CysSerGlnIleValIleValIleValIleValIleValIleValIleValIleValIle 100
DB 367 TGCAGTCAGAAAGTGTATTAACAGATCAAGCTCCAGATGTTGCCCTCTCTCTTCA 426
QY 101 AspCysPheLeuThrValLeuLeuGlyIleValIleValIleValIleValIleValIle 120
DB 427 GACTGTTTCTCACTGTAATCTTCTGGGTAACCTGGAGAAAGCTTCACTCTGTTCACTG 486
QY 121 LeuAlaGlyIlePheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyIleVal 140
DB 487 CTTCAGAGGTGGTGTGCTGATGTTCTCTGTTTCTCTGCTGCTGCTGCTGCTGCTGCT 546
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
DB 547 ACTTAGTCCCTAACCTGCAATTTCTCAGCCTTCTTAACTGTTGCCAACTTGGGCCAAC 606
QY 161 ArgIleLeuProAsnLeuThrLeuGlyCysGlnArgAspValLeuAsnIleGlyLeuIle 180
DB 607 GCAATTTCTCCAAATCTTATCTTGGCTGCCAGCGAGATGCTCTCAACAGAGAGCTGATG 666
QY 181 GlnGlnAsnGlyIleGlyIleValLeuAsnAlaSerIleThrCysPheProLeuAspPhe 200
DB 667 CAGCAGAAATGGGATGTGTTATGTTAAATGCCAGCAATACCTGTCACAAAGCTGACTT 726
QY 201 IleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluIleValIle 220
DB 727 ATCCCCGAGTCAATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 786
QY 221 ProTribLeuAspIleSerValAspPheIleGluValAlaValAsnIleSerAsnIleCysVal 240
DB 787 CCGTGTGGTGGCAAAATCAATAGATTTCAATGAGAAAGCAAAAGCCCTCCATGAGATGTT 846
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIleAlaIle 260
DB 847 CTAAGTGCATGTTTATGCTGAGATCTCCGCTCCGCAACATGCTATGCTCAATCAATCA 906
QY 261 LysAlaGluMetAspMetSerLeuAspGluAlaIleValGluPheValIleGluIleVal 280
DB 907 AAGAGATGAGATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 966
QY 281 IleSerProAsnPheAsnPheLeuGlyIleLeuLeuAspIleValIleValIleValIle 300

DB 967 ATATCTCCAAACTTCAATTTTCTGGGCCAACTCTGAGCTATGAGAGAAATTAAAGAC 1026
QY 301 GlnThrGlyAlaSerGlyProIleSerIleValIleValIleValIleValIleValIle 320
DB 1027 CAGACTGGAGCATCAGGGCCAAAGAGCAAACTCAAGCTCTGCTCACTGAGAGCCAAAT 1086
QY 321 GluProValProAlaValSerGluGlyIleValIleValIleValIleValIleValIle 340
DB 1087 GAACTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1146
QY 341 CysAlaAspSerAlaThrSerGluAlaAlaGlyIleValIleValIleValIleValIle 360
DB 1147 TGTGCGACTGCTCAATCTCAAGGAGAGAGCAAAAGCCGCTGATCCCGCAGCGTG 1206
QY 361 ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380
DB 1207 CCCAGCGTCCAGAGGTGAGCGCTGCTGTTAGAGACAGCCGCTGCTGATAGAGCCAAAC 1266
QY 381 SerGlyLeuHisLeuSerAlaAspArgLeuIleValIleValIleValIleValIleVal 400
DB 1267 AGTGGGCTGACCTGTCCGAGACAGGCTGGAAGACAGCAATAGCTCAAGCGTCTTTC 1326
QY 401 SerLeuAspIleLeuSerValSerIleSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420
DB 1327 TCTCTGATATCAATCACTTCAATTCAGCCAGACATGAGCATCTTACATGCTTTC 1386
QY 421 SerSerSerGluAspAlaLeuGluIleValIleValIleValIleValIleValIleVal 440
DB 1387 TCTCATCAGAAAGATGCTTGGATATCAATCAATCTTCACTGATGAGGCAAC 1446
QY 441 LysLeuCysGlnPheSerProValGlnIleLeuSerGluGlnIleThrProGluThrSerPro 460
DB 1447 AAGCTATGCAATTTCTCCCTGTTGAGAACTATGAGACAACTCCGAAACCACTCT 1506
QY 461 AspIleGluGluAlaSerIleProIleValIleGlnIleThrAlaArgProSerAspSerGln 480
DB 1507 GATTAAGAGAAAGCAAGCATCCCAAGAAAGCTGAGACCGCCAGGCTTCAACAGCCAG 1566
QY 481 SerIleValGluHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
DB 1567 AGCAAGCAATTCATTCGGTCCAGAACCAAGCAAGATGGGACCGCCAGAGGTCCCTTTTA 1626
QY 501 SerProLeuHisArgSerGlySerValGluAspAsnIleThrSerPheLeuPheGly 520
DB 1627 TCTTCATGCAATCGAAGTGGAGCGTGGAGCAATTAACCAACAGCTTCTTTTCCGCG 1686
QY 521 LeuSerThrSerGlnGlnHisLeuThrIleValIleValIleValIleValIleValIle 540
DB 1687 CTTTCACAGCAGCAGACAGCATCTCAAGAGTGTCTGCTGCTGCTGCTTAAAGGCTGGCAC 1746
QY 541 SerAspIleLeuAlaProGlnIleThrSerThrProSerLeuThrSerSerIlePheAla 560
DB 1747 TCGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACAGCAGCTGATATTTTGGC 1806
QY 561 ThrGluSerSerHisPheThrSerAlaSerAlaIleIleIleIleIleIleIleIleIle 580
DB 1807 ACAAGTCTCACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1866
QY 581 AlaIleSerCysSerGlnLeuProThrCysGlyAspGlnValIleThrSerValArgArg 600
DB 1867 GCTTCAGCTGAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1926
QY 601 GlnIleProSerAspArgAlaAspSerArgArgSerIleGluGluIleValIleValIle 620
DB 1927 CAGAGCCAGTGAAGAGCTGATCGCGCGAGACTGCGATGAGAGAGCCCTTTTGA 1986
QY 621 LysGlnPheIleValArgSerCysGlnMetGluPheGlyIleGluIleIleIleIleIle 640
DB 1987 AAGCATTTAAACGAGAGCTGCCAAATGGAATTTGAGAGAGCATATGCAAGAAC 2046
QY 641 ArgSerArgGluGluLeuGlyIleValGlySerGlnSerSerPheSerGlySerMetGlu 660

Db 2047 AGGTCAAGGAGAGAGCTGGGAGAAAGTGGAGCTAGCTTAGCTTTTGGGACAGATGAA 2106
Qy 661 |||||
Db 2107 ATCATTTAGGCTTCC 2121

RESULT 6
US-09-964-277-1
; Sequence 1, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Lucche, Ralf M.
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-277-1

Alignment Scores:
Pred. No.: 0 Length: 3496
Score: 3406.00 Matches: 665
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.65% Indels: 0
Gaps: 0

US-10-029-345A-109 (1-665) x US-09-964-277-1 (1-3496)

Qy 1 MetAlaHiGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
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Qy 21 SerGlyThrGluValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
Db 622 AGTGGACCGAAGAAAGTCTGCTGTAATTAAGCCGCAATTTGGAAATACATTCATCC 681

Qy 41 HisIleLeuGluAlaIleAsnIleAsnCySerLysLeuMetLysArgArgLeuGln 60
Db 682 CACATTTTGGAGCCATTAATATCACTGCTCCAGCTTATGAGCGAAGGTTGCAACG 741

Qy 61 AspLysValLeuIleThrGluLeuIleGlnHisSerAlaLysHisLysValAsp 80
Db 742 GACAAAGTGTAAATACAGAGCTCATCCAGCATTCAGCGAACAATAGGTTGACATTCAT 801

Qy 81 CysSerGlnLysValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSer 100
Db 802 TCCAGTCAGAAAGTGTATGATTCATCAATCAAGCTCCCAAGATGTTGCTCTCTCTTCA 861

Qy 101 AspCysPheLeuThrValLeuLeuGlyLysLeuGluLysSerPheAsnSerValHis 120
Db 862 GACTTTTCTCAGTGTACTTCTGGGTAAACTGAGAAAGAGCTTCAACTCTGTCACCG 921

Qy 121 LeuAlaGlyLysPheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyLysSer 140
Db 922 CTTCGAGGCTGGTGGTGTGAGTTCCTCGTGTTCCTCGGCTCTGTAAGAAATCC 981

Qy 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Db 982 ACTCAAGTCCCTACCTGATTTCTCAGCTTCTTACCTGTTGCCAATTTGGGCAAC 1041

Qy 161 ArgIleLeuProAsnLeuLysLeuGlyCysGlnArgAspValLeuAsnLysGluLeu 180
Db 1042 CGAATTCCTCCCAATCTTATCTGTGGTCCAGCAGATGCTCTCAACAGAGAGCTGAT 1101

Qy 181 GlnGlnAsnGlyTyrIleGlyTyrValLeuAsnAlaSerTyrThrCysProLysProAsp 200

Db 1102 CAGCAGAAATGGGATTTGTTATGTAAATGCCAGCAATACCTGTCCAAAGCTGACTTT 1161
Qy 201 ILeProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIleLeu 220
Db 1162 ATCCCGAGTCCATTTCTGCTGCTGCTGGAATGACGCTTTTGTGAGAAATTTTGG 1221

Qy 221 ProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAspAsnGlyCysVal 240
Db 1222 CCGTGTGGACAAATCCATGATTTCAATTGAAAGCAAAAGCCCTCCAAATGATGTGTT 1281

Qy 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
Db 1282 CTAGTGCACTGTTTGTAGTGGATCTCCGCTCCGCCAACATCGCTATCGCTACATCAG 1341

Qy 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLysArgProThr 280
Db 1342 AAGAGAAAGCAATCTTTAGATGAACTTAAGATTTGTGAAGAAAGAAAGCACTACT 1401

Qy 281 ILeSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysIleLysAsn 300
Db 1402 ATATCTCCAACTTCAATTTTCTGGGCCCACTCTCGACCTATGAGAGAAATTTAGAAC 1461

Qy 301 GlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeuGluLysProAsn 320
Db 1462 CAGACTGGAGCATCAGGCGCAAGAGCAAACTCAAGCTGTGCACCTTGAGAGAGCAAT 1521

Qy 321 GluProValProAlaValSerGluGlyGlnLysSerGluThrProLeuSerProPro 340
Db 1522 GAACTGTCCCTGCTGTCTCAGAGGTGGAGCAAAAGCGAGAGCGCTTCAATGCCACC 1581

Qy 341 CysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSerVal 360
Db 1582 TGTGCCGACTGTGCTACTCAGAGGAGCAAGCAAAAGCCCGTGCATCCCGCAGAGGTG 1641

Qy 361 ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380
Db 1642 CCCAGCGGCCAGCGTGCACCGTCCGTGTAAAGACACCGCTGTGTAACAGCGCTTC 1701

Qy 381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLysArgSerPhe 400
Db 1702 AGTGGCTGCACTGTCCGAGACAGGCTGGAAAGCAATTAAGCTTCACCGTCTTC 1761

Qy 401 SerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420
Db 1762 TCTCGATATCAATCATGTTTCAATTAATTCAGCCAGCATGAGCATCTTATCATGGCTTC 1821

Qy 421 SerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAspGlyThrAsn 440
Db 1822 TCTCATCAGAAAGATGCTTGGAAATCTACAAACCTTCCACTCTGTGATGGAGCAAC 1881

Qy 441 LysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerPro 460
Db 1882 AAGCTATGCCAGTTCCTCCCTGTTCAAGAACTATCGAGAGACTCCCGAAACCAAGTCT 1941

Qy 461 AspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerGln 480
Db 1942 GATTAAGAGAAAGCAGACATCCCAAGAGCTGACAGCCGACAGCTTACAGACAGCAG 2001

Qy 481 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
Db 2002 AGCAAGGATTTGATTTGGTTCAGAACAGACAGCGTGCACCGCCAGAGGTCTCTTTTA 2061

Qy 501 SerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheGly 520
Db 2062 TCTCATCTGATCAAGTGGAGGTGGAAGCAATTTACACACAGCTTCTTTTGGCC 2121

Qy 521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTyrPhe 540
Db 2122 CTTCACACAGCGCAGACATTCACAGAAATGCTGTGCTGGGCTTTAAGGCGTGGCAC 2181

Qy 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheAla 560
Db 2182 TCGGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACAGCAGCTGTATTTTGGCC 2241

QY 561 ThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrSer 580
 DB 2242 ACAGAGTCTCTACACTTCTACTCTGCTCAGACCATTTACGAGAGCGAGTCCAGTTCTCT 2301
 QY 581 AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgArg 600
 DB 2302 GCTACAGCTGACGACGCTGCCCACTTGCGGAGACCAAGTCTATTCTGTGCGCAGCGCG 2361
 QY 601 GlnLysProSerAspArgAlaAspSerArgArgSerTTPHisGlnGluSerProPheGln 620
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 QY 621 LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMetSerGluAsn 640
 DB 2422 AAGCATTTAAACGACGAAAGCTGCCAAATGGAAATTTGGAGAGCATCTGTCAGAGAAC 2481
 QY 641 ArgSerArgGluGluLeuGlyValGlySerGlnSerSerPheSerGlySerMetGlu 660
 DB 2482 AGGTACCGGAGAGCTGGGAGAAAGTGGGCAAGTCAAGTTTTCGGGCGACATGAA 2541
 QY 661 IleIleGluValSer 665
 DB 2542 ATCATTTGAGTCTCC 2556
 RESULT 7
 US-10-370-715B-261
 ; Sequence 261, Application US/10370715B
 ; Publication No. US20040258678A1
 ; GENERAL INFORMATION:
 ; Patin Docket Preview
 ; APPLICANT: BODARY, SARAH C.
 ; APPLICANT: CLARK, HILLARY
 ; APPLICANT: BRISDELL, HUNTE
 ; APPLICANT: JACKMAN, JANET
 ; APPLICANT: SCHOENFELD, JILL R.
 ; APPLICANT: WILLIAMS, P. MICKEY
 ; APPLICANT: WOOD, WILLIAM I.
 ; APPLICANT: MU THOMAS D.
 ; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
 ; FILE OF INVENTION: Related Diseases
 ; FILE REFERENCE: P1948R1-US
 ; CURRENT APPLICATION NUMBER: US/10/370, 715B
 ; CURRENT FILING DATE: 2003-02-21
 ; NUMBER OF SEQ ID NOS: 742
 ; SEQ ID NO 261
 ; LENGTH: 3521
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-370-715B-261
 Alignment Scores:
 Pred. No.: 0 Length: 3521
 Score: 3406.00 Matches: 663
 Percent Similarity: 99.85% Conservative: 1
 Best Local Similarity: 99.70% Mismatches: 1
 Query Match: 99.65% Indels: 0
 DB: 18 Gaps: 0
 US-10-029-345A-109 (1-665) x US-10-370-715B-261 (1-3521)
 QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
 DB 564 ATGGCCCATGAGATGATGATGAACTCAATGTGTTACTGAGAGGTGGTGGCTGCTGGAGAA 623
 QY 21 SerGlyThrGluLysValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40
 DB 624 ATGGAGACGGAAGAAAGTGTGCTAATTGATGACCGCCCATTTGTGGAATACAAATCATCC 683
 QY 41 HisIleLeuGluAlaIleAsnIleAsnCysSerLysLeuMetLysArgArgLeuGln 60
 DB 684 CACATTTTGGAGCCATTAATATCACTCTCCAGCTTAATGAGGAGGAGTGGCAACAG 743

QY 61 AspLysValLeuIleThrGluLeuIleGlnHisSerAlaLysHisLysValAspIleAsp 80
 DB 744 GACAAAGTTTAAATACAGAGCTCAACAGCATTCAGCGAAACATAGGTTGACATTGAT 803
 QY 81 CysSerGlnLysValValIleTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
 DB 804 TGCAGTCAGAAAGTTGTATGATTAACATCAAACTCCCAAGATGTTCCCTCTCTTCA 863
 QY 101 AspCysPheLeuThrValLeuLeuGlyLysLysGluLysSerPheAsnSerValHisLeu 120
 DB 864 GACTGTTTCTACCTGACTTCTGGGTAACTGAGAAAGAGCTTCAACTCTGTTCACTCG 923
 QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyLysSer 140
 DB 924 CTTCAGAGTGGGTTTCTGAGTTCTCTGTTTCCCTGCTCTGTAAGGAAATCC 983
 QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
 DB 984 ACTTAAGTCCCACTGACATTCCTCAGCTTCTTCTGCTTCACTGTTGCCAAATGGCCAAAC 1043
 QY 161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnIleGlyLeu 180
 DB 1044 CGAATTTCTCCAAATCTTATCTTGCTGCGCAGCAGATGCTCTCAACAGAGCTGAAG 1103
 QY 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProLysProAspPhe 200
 DB 1104 CAGCAAAATGGAGATTTGTTATGTTAAATCCAGCAAAATCCTGTCCAAGCTGACTTT 1163
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 DB 1164 ATCCCGAGTCTCATTTCTGCTGCGCTGCGATGACAGCTTTGTGAGAAATTTTG 1223
 QY 221 ProThrLeuAspLysSerValAspPheIleGlyLysValAlaLysAsnGlyCysVal 240
 DB 1224 CCGTGTGGACAAATCAGTAAATTTCAATTGAGAAAGCAAAAGCTCCCAATGATGTT 1283
 QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
 DB 1284 CTAGTGCACTGTTTAGCTGGATCTCCGCTCCGACCAATGCTTATCCCTACATCAG 1343
 QY 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValIleGlyLysArgProThr 280
 DB 1344 AAGAGATGACATGCTTTAGATGAAAGCTTGTGTAAGAAAGAAAGAAAGAAAGAAAGCTTACT 1403
 QY 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGlnLysLysIleLysAsn 300
 DB 1404 ATATCTCCAAATCTCAATTTCTGGGCCCAACTCTGACTTATGAGAAAGATTAAGAAC 1463
 QY 301 GlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuLeuHisLeuGlnLysProAsn 320
 DB 1464 CAGACTGAGCATCAGGCGCCAAAGAGCAACTCAAGCTGCTGACCTGAGAGAACCAAT 1523
 QY 321 GluProValProAlaValSerGluGlyGlnLysSerGlyThrPheLeuSerProPro 340
 DB 1524 GAACCTGTCCTGCTGCTCAGAGGTGGAGCAAGAAAGAGAGAGCGCCCTCAGTCCACCC 1583
 QY 341 CysAlaAspSerAlaThrSerGlnAlaAlaGlyGlnArgProValHisProAlaSerVal 360
 DB 1584 TGTGCCGACTCTGCTAAGCTCAGAGGACAGAGCAAAAGCCCGTGTATCCGCCAGCGTG 1643
 QY 361 ProSerValProSerValGlnProSerLeuLeuGlnAspSerProLeuValGlnAlaLeu 380
 DB 1644 CCCAGCTGACCCAGCGTGCAGCGCTGCGCTGTTAGAGACAGCCCGCTGTACAGGCGCTC 1703
 QY 381 SerGlyLeuHisLeuSerAlaAspArgLeuGlnAspSerAsnLysLeuLysSerPhe 400
 DB 1704 AGTGGGCTGCACTGCTCGCAGACAGGCTGGAACAGCAATTAACCTCAAGCGTTCTTC 1763
 QY 401 SerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420
 DB 1764 TCTCTGAGATTCAAATCAGTTTCATATTCAGCCACATGCGACATCTTCAATGCTTTC 1823
 QY 421 SerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAspGlyThrAsn 440

Db 1824 TCCTCATCAGAAAGTCTTGGAACTTCAACAACTTCCACTCTGAGTGGAGCCAAAC 1883
Qy 441 LysLeuCyGlnPheSerProValGlnGluLeuSerGlnGlnThrProGlnThrSerPro 460
Db 1884 AAGCTATGCGAGGTTCTCCCTGTTCAAGAACTATCGAGAGAGACTCCCGAAACCAAGTCT 1943
Qy 461 AspArgGlnGlnAlaSerIleProValLeuGlnThrAlaArgProSerAspSerGln 480
Db 1944 GATTAAGAGAGACAGACATCCCGAAGAGCTGACGCCCGAGGCTTTCAGACAGCCAG 2003
Qy 481 SerIlyAspLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
Db 2004 AGCAAGGATTTGATTCGTCAGAACACGACAGACAGTGGACCCGCCAGAGTCCCTTTA 2063
Qy 501 SerProLeuHisArgSerGlySerValGluAspAsnTrpHisThrSerPheLeuPheGly 520
Db 2064 TCTCCACTGCATGAAAGTGGAGCGTGGAGACATTAACACACAGCTTCTTTTCGGC 2123
Qy 521 LeuSerThrSerGlnGlnHisIleuThrIlySerValGlyLeuGlyLeuIlySerGlyTrpHis 540
Db 2124 CTTTCCACGACGACGACGACCTCAAGAGTCTGCTGGCTTGAAGGCTGGAC 2183
Qy 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTrpIlyPheAla 560
Db 2184 TCGGATATCTTGGCCCCCGACGACTTACCCCTTCCCTGACGACAGCTGTATTTTGGC 2243
Qy 561 ThrGlnSerSerHisPheTrpSerAlaSerAlaIleTrpGlyGlySerAlaSerTrpSer 580
Db 2244 ACGAAGTCTCAACACTTCACTGCTCTCAGCCATCTACGAGAGAGTGGCAAGTTACTCT 2303
Qy 581 AlaTrpSerCySerSerGlnLeuProThrCySGlyAspGlnValTrpSerValArgAspArg 600
Db 2304 GCTTACAGCTGACGACGACGCTGACCTTGGGAGACCAAGTCTATTTCTGCGCAGGCGG 2363
Qy 601 GlnIlyProSerAspArgAlaAspSerArgArgSerTrpHisGlnGluSerProPheGln 620
Db 2364 CAGAACCCAAAGTACAGAGCTGACTCGCGCGGAGCTGGCATGAAGAGCCCTTTGAA 2423
Qy 621 LysGlnPheIlyArgArgSerCyGlnMetGluPheGlyGlnSerIleMetSerGluAsn 640
Db 2424 AAGCAATTTAAGCAGAAAGCTGCCAAATGGAAATTTGGAGAGCAATGTCAGAGAAC 2483
Qy 641 ArgSerArgGlnGluLeuGlyIlySerValGlySerGlnSerSerPheSerGlySerMetGlu 660
Db 2484 AGGTCAAGGGAAGAGCTGGGGAAGTGGGCAAGTCAAGTCTTTCGGGCAAGCATGGA 2543
Qy 661 IleIleGlnValSer 665
Db 2544 ATCATTGAGTCTCC 2558

RESULT 8
US-09-816-494-1
Sequence 1, Application US/09816494
Patent No. US20020034807A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
FILE REFERENCE: 10448-030002
CURRENT APPLICATION NUMBER: US/09/816,494
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,858
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3544
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (589)...(2583)

US-09-816-494-1
Alignment Scores:
Pred. No.: 0
Score: 3406.00
Percent Similarity: 99.85%
Best Local Similarity: 99.70%
Query Match: 99.65%
DB: 9
Gaps: 0

US-10-029-345A-109 (1-665) x US-09-816-494-1 (1-3544)

Qy 1 MetAlaHisGlnMetIleGlyThrGlnIleValThrGlyValAlaLeuLeuGln 20
Db 589 ATGGCCATGAGATTAATGGAACCTAAGATTTACTGAGAGGTGTGGCTCTGCTGAA 648
Qy 21 SerGlyThrGlnIlyValLeuLeuIleAspSerArgProPheValGluTrpAsnThrSer 40
Db 649 ACTGGAGCGAAGAAAGTCTGCTGCTATTAATGACCGGCAATTTGGATTAACATCATCC 708
Qy 41 HisIleLeuGlnAlaIleAsnIleAsnCySerIlyLeuMetIlyAspArgLeuGln 60
Db 709 CACATTTTGGAAAGCCATTAAATCAACTGCTCAAGCTTATGAAGCGAAGGTTGCAAG 768
Qy 61 AspIlyValIleuIleThrGlnLeuIleGlnHisSerAlaIlyHisIlyValAspIleAsp 80
Db 769 GACAAAGTTAATTAACAGAGCTCATCCAGATTCAGGAAACATTAAGTTGACATTGAT 828
Qy 81 CySerGlnIlyValIleValIlyTrpAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db 829 TGCAGTCAGAAAGTTGTAGTTTACATCAAGAGCTCCCAAGATGTTGCTCTCTCTTCA 888
Qy 101 AspCyPheLeuThrValLeuLeuGlyIlyIleuGlyIlySerPheAsnSerValHisIleu 120
Db 889 GACTGTTTTCACGTAACCTTCTGGGTAACTGGAGAAAGACCTTCACCTGTTCACTG 948
Qy 121 LeuAlaGlyIlyPheAlaGluPheSerArgCyPheProGlyLeuCyGlnGlyIlySer 140
Db 949 CTTCAGAGTGGGTTTGTGCAATTTCTCTGTTGTTTCCCTGGCTCTGTGAAGGAAATCC 1008
Qy 141 ThrLeuValProThrCysIleSerGlnProCyLeuProValAlaAsnIleGlyProThr 160
Db 1009 ACTTAGTCCCTTACCTGATTTCTCAGGCTGTTACTCGTTGCAACATTGGGCAACC 1068
Qy 161 ArgIleuProAsnLeuTrpLeuGlyCyGlnTrpAspValLeuAsnIleGlnIle 180
Db 1069 GCAATTTTCCCAATCTTATCTTGGCTGCCAGAGATGTCCTCAACAAAGAGCTGATG 1128
Qy 181 GlnGlnAsnGlyIleGlyTrpValLeuAsnAlaSerTrpThrCySProIlyProAspPhe 200
Db 1129 CAGCAGAAATGGGATTTGGTTATGTATTAATCCAGCAATACCTGTCCAAAGCTGACTTT 1188
Qy 201 IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCySGluIlyIleu 220
Db 1189 ATCCCGAGTCTCAATTTCTGCTGCTGCTGTGAATACAGCTTTTGGAAATTTTGG 1248
Qy 221 ProTrpLeuAspIlySerValAspPheIleGluIlyValIlyAsnAlaSerAsnGlyCyVal 240
Db 1249 CGTGGTTTGACAAATCATGATTAATTAATGAAGAAACCAAGCTCCCAATGGATGGTT 1308
Qy 241 LeuValHisCySerLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTrpIleMet 260
Db 1309 CTATGGACAGCTTTAGCTGGGATTCGCCGCTCCGCCACATCGCTATCGCTCATCATG 1368
Qy 261 LysArgMetAspMetSerLeuAspGlnAlaTrpArgPheValIlyGlyIlyAspProThr 280
Db 1369 AAGAGATGACATGCTTTAAGATGAAGCTTACAGATTTGGAAGAAAGAAAGACTTA 1428
Qy 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuAspTrpGlyIlyIlySerIleValAsn 300
Db 1429 ATATCTCCAAATCTTCAATTTCTGGGCAACTCTGACATATGGAAGAAAGATTAAGAAC 1488
Qy 301 GlnThrGlyAlaSerGlyProIlySerIlyLeuIlySerIlyLeuGlnIlyProAsn 320

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Db      1489 CAGACTGGAGCATCAGGCGCAAGAGCAAACTCAACTCTGTGACCTGGAGAAAGCCAAAT 1548
Qy      321 GUPProval1ProAlaValSerGluGlyGlyGlnLysSerGluThrProLysSerProPro 340
Db      1549 GAACTGTCTCTGTCTCTCAGAGGGTGGACAGAAAAGAGAGAGCGCCCTCAGTCCAGCC 1608
Qy      341 CysAlaAspSerLalaThrSerGluAlaGlyGlnArgProValHisProAlaSerVal 360
Db      1609 TGTGGCGACTGTCTACCTCAGAGGAGAGCAAGCAAGGCGCTGTGATCCCGCAGCGTG 1668
Qy      361 ProSerVal1ProSerVal1GlnProSerLeuLysAspSerProLeuVal1GlnAlaLeu 380
Db      1669 CCCAGGTGCCAGCGCTGACGCGCTGTGATGAGAGACAGCCGCTGTGATGAGCGGCTC 1728
Qy      381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAluLysLeuLysArgSerPhe 400
Db      1729 AGTGGGCTGACCTGTCTCCGACAGAGGCTGAAAGACAGCAATAGCTCAAGCGCTTCTTC 1788
Qy      401 SerLeuAspTleLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420
Db      1789 TCTCTGGAATACAAATCAGTTTCAATTCAGCCAGATGGCAGCATCTTACATGGCTTC 1848
Qy      421 SerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAspGlyThrAsn 440
Db      1849 TCTCTATCAGAAAGATCTTGGAAATCTACAAACCTTCCACTCTCTGATGGAGACCAAC 1908
Qy      441 LysLeuCysGlnPheSerProValGlnLysLeuSerGluGlnThrProGluThrSerPro 460
Db      1909 AAGCTATGCGAGATTCTCCCTGTTCAGAACTATCGAGAGAGACTCCGAAACCAATGCTCT 1968
Qy      461 AspLysGluGluAlaSerTleProLysLysLeuGlnThrAlaArgProSerAspSerGln 480
Db      1969 GATTAAGAGAGAAAGCGAGCATCCCAAGAAAGCTGCAACCGCCAGGCTTTCAGACACCG 2028
Qy      481 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
Db      2029 AGCAAGCGATTGCTTCGCTGAGAACCAAGACAGAGAGGCGCCAGAGGCTTCTTTTA 2088
Qy      501 SerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheGly 520
Db      2089 TCTCCACTGATCGAAGTGGAGCGTGGAGAGCAATTAACACCGAGCTTCTTTTCGGC 2148
Qy      521 LeuSerThrSerGlnGlnHisLysLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTyrPhe 540
Db      2149 CTTTTCACAGCAGCAGACGACCTCAGAAAGTCTGCTGGCGCTTAAAGGCTTGGCAC 2208
Qy      541 SerAspTleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheAla 560
Db      2209 TCGGATATCTTGGCCCCCGACAGCTTACCTTCCCTGACCGACGCTGTATTTTGGC 2268
Qy      561 ThrGluSerSerHisPheTyrSerAlaSerAlaLysTyrGlyLysSerAlaSerTyrSer 580
Db      2269 ACAGAGATCTCTACACTTCTGCTGCTCAGCATCTAAGAGGAGGAGTGGCAGATTACTCT 2328
Qy      581 AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgArg 600
Db      2329 GCTTACAGCTGACGAGCGCTGCCACTTCCGAGACCAAGTCTATTTCTGTGCGCAGCGG 2388
Qy      601 GlnLysProSerAspArgAlaAspSerArgArgSerTyrHisGlnGluLysSerProPheGlu 620
Db      2389 CAGAACCCAGTACAGAGCTGACCTGCGCGGAGGCTGGCAGTAAAGACCCCTTTGAA 2448
Qy      621 LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGlnSerTleMetSerGluAsn 640
Db      2449 AAGCAGATTAAACGAGAGAGCTGCCAAATGGAATTTTGGAGAGCATCATGTACAGAGAC 2508
Qy      641 ArgSerArgGluGluLeuGlyLysValGlyLysSerGlnSerSerPheSerGlySerMetGlu 660
Db      2509 AGCTACCGGAGAGAGAGCTGGGAGAAAGTGGCAGTCACTTTCGCGGCGACGATGAA 2568
Qy      661 IleIleGluValSer 665

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Db      2569 ATCATTTAGAGTCTCC 2583
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; Sequence 25, Application US/10377072
; Publication No. US20040009501A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Mayoung
; APPLICANT: Tsai, Feng-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MP103-01BOMNIM
; CURRENT APPLICATION NUMBER: US/10/377,072
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895,860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/843,297
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; PRIOR FILING DATE: 2001-03-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589) ... (2586)
US-10-377-072-25
Alignment Scores:
Pred. No.: 0 Length: 3544
Score: 3406.00 Matches: 663
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.65% Indels: 0
DB: 17 Gaps: 0
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Qy      1 MetAlaHisGluMetTleGlyThrGlnLysValThrGluArgLeuValAlaLeuLeuGln 20
Db      589 ATGGCCCAATGAGATGATTTGAACTCAAAATTTGTTACTGAGAGGTTGGTCTGCTGGA 648
Qy      21 SerGlyThrGlnLysValLeuLeuLysAspSerArgProPheValGluTyrAsnThrSer 40
Db      649 AGTGAACCGAAGAAAGTGTCTGCTAATTTGATACCGGCTTTTGTGAATATACATCATCC 708
Qy      41 HisIleLeuGluAlaIleAsnLysLeuMetLysArgArgLeuGlnGln 60

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Db 709 CACATTTGGAGGCAATTAATATCACTGCTCCAGGCTTATGAAGGAGGTTGGCAACAG 768
 Qy 61 AspIyValLeuIleThrGluLeuIleGlnHisSerAlaIySHisValAspIleAsp 80
 Db 769 GACAAAGTGTAAATTACAGAGCTCATCAGCATTCACGAAACATAAGTGTGACATTGAT 828
 Qy 81 CysSerGlnIyValValIyYrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
 Db 829 TGCAGTACGAAGGTGTAGTTTACGATCAAGCTCCCAAGATGTGCTCTCTCTTCA 888
 Qy 101 AspCysPheLeuThrValIleLeuGlyIyValLeuGlyIySerPheAsnSerValHisLeu 120
 Db 889 GACTGTTTCTCACTGACTTCTGGGTAACTGGAGAAAGACTTCAACTCTGTTTCACTG 948
 Qy 121 LeuAlaGlyIyGlyPheAlaGlyPheSerArgCysPheProGlyLeuCysGlyIyIySer 140
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 Qy 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
 Db 1009 ACTCTAGTCCCTTACCTGCAATTTCTCAGCCTTGCTTACTGTTGCAACATTTGGGCCAAC 1068
 Qy 161 ArgIleLeuProAsnLeuIyIyLeuGlyCysGlnArgAspValLeuAsnIyGlyLeuIle 180
 Db 1069 CGAATTCCTCCCAATCTTTATCTTGCGCTCCAGCGAGATGTCTCTCAACAAGAGCTGATG 1128
 Qy 181 GlnGlnAsnGlyIleGlyIyValIleAsnAlaSerIyThrCysPheProIyAspPhe 200
 Db 1129 CAGCAGAAATGGAGTTGGTTATGTTTAATGCCAGCAATTCCTGCCAAGGCTGACTT 1188
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 Db 1189 ATCCCGAGGCTCATTTCCGCTGCGTGCCTGATGAAGAGCTTTGTGAGAAAATTTTG 1248
 Qy 221 ProThrLeuAspIySerValAspPheIleGlnIyValAlaIySAsnGlyCysVal 240
 Db 1249 CCGTGTGTGACAAATCAGTAGATTCATTGAGAAAGCAAAAGCCCTCCATGATGTGTT 1308
 Qy 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIyIleMet 260
 Db 1309 CTAGTGCACGTGTTTACTGAGATCTCCGCTCCGCCAACATCCCTATCCGCTTACATCAG 1368
 Qy 261 LysArgMetAspMetSerLeuAspGlnAlaIyYrArgPheValIySglnIySArgProThr 280
 Db 1369 AAGAGATGACATGATCTTATGATGAAGCTTACAGATTTGTGAAAAGAAAGAAAGCTTACT 1428
 Qy 281 IleSerProAsnPheAsnPheLeuGlyIyGlnLeuLeuAspTyrGlnIySHisIleIyAsn 300
 Db 1429 ATATCTCCAAATTCATATTTCTGGGCCCAACTCTGACTATGAGAAAGATTGAAGAC 1488
 Qy 301 GlnThrGlyAlaSerGlyProIySerIySLeuIySLeuIleHisLeuGlyIySProAsn 320
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 Qy 321 GluProValProAlaValSerGlyIyGlnIySLeuIySLeuThrProLeuSerProPro 340
 Db 1549 GAACCTGTCTCCGTCTCTCAGAGGGGTGACAGAAAGAGAGAGCCCTCAGTCCACCC 1608
 Qy 341 CysAlaAspSerAlaThrSerGlnAlaIyGlnArgProValHisProIleAspVal 360
 Db 1609 TGTGCGACTTCTGCTACTCAGAGGAGAGAGCAAAAGGCCCGGTGATCCGCCAGCGTG 1668
 Qy 361 ProSerValProSerValGlnProSerLeuLeuGlnAspSerProLeuValGlnAlaLeu 380
 Db 1669 CCCAGGTCGCCAGGGTGCAGCGCTGCTTGAAGAGACAGCCCGCTGTTACAGCGCTC 1728
 Qy 381 SerGlyLeuHisLeuSerAlaAspArgLeuGlnAspSerAsnIySLeuIySArgSerPhe 400
 Db 1729 AGTGGGCTGCACCTGTCCGACAGCGCTGGAAGACAGCAATTAACCTCAAGGCTTCTTC 1788
 Qy 401 SerLeuAspIleIySerValSerIySerAlaSerMetAlaIleSerLeuHisIyGlyPhe 420

Db 1789 TCTCTGATATCAATACAGTTTCATATTCAGCGACAGATGGCAGCATCTTACATGGCTTC 1848
 Qy 421 SerSerSerGlnAspAlaLeuGlyIyYrIySProSerThrThrLeuAspGlyIyThrAsn 440
 Db 1849 TCTCATCAGAAAGATGCTTTGGATAATACAAACCTTCCATCTGATGGAGCCAAAC 1908
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 Db 1909 AAGCTATGCCAGTTCTCCCTCTCTCAGAACTATGAGACAGACATCCGAAACAGTCT 1968
 Qy 461 AspIySglnIyAlaSerIleProIySLeuGlnThrAlaArgProSerAspSerGln 480
 Db 1969 GATTAAGAGAGAGCCAGCATCCCAAGAAAGCTGAGACCGCCAGGCTTACAGAGCCAG 2028
 Qy 481 SerIySArgLeuHisSerValArgThrSerSerSerGlyIyThrAlaGlnArgSerLeu 500
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 Qy 501 SerProLeuHisArgSerGlySerValGlnAspAsnIySHisThrSerPheLeuPheGly 520
 Db 2089 TCTCAGCTGCATCGAAGTGGAGCTGGAGAGCAATTAACACACAGCTTCTTTCCGCG 2148
 Qy 521 LeuSerThrSerGlnHisLeuThrIySLeuAlaGlyLeuGlyIyLeuIySgIyYrIyHis 540
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 Qy 541 SerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerThrIyPheAla 560
 Db 2209 TCGAATCTTGGCCCCCAGACCTTACCCCTCCCTGACACAGAGCTGTATTTTGGC 2268
 Qy 561 ThrGlnSerSerHisPheThrSerSerAlaSerAlaIleIyGlyIySerAlaSerIySer 580
 Db 2269 ACAGAGTCTTCACATTCATCTGCTGCTCAGACATCTACGAGGAGGAGGCCAGTTACTCT 2328
 Qy 581 AlaIySerCysSerGlnLeuProThrCysGlyAspGlnValIySerValArgArgArg 600
 Db 2329 GCTTACAGCTCAGGACAGCTGCCCATCTTGCAGAGCCAAAGCTTATCTGTCGAGGCGG 2388
 Qy 601 GlnIySProSerAspArgAlaAspSerArgArgSerThrIySglnIySLeuSerProPheGln 620
 Db 2389 CAGAGCCAAAGTACAGAGCTGATCTCGCGGAGAGCTGGCATGAAAGAGGCCCTTTGAA 2448
 Qy 621 LysGlnPheIySArgArgSerCysGlnMetGlnPheGlyIyGlnSerIleMetSerGlnAsn 640
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 Qy 641 ArgSerArgGlnIyLeuGlyIyValAlaIySerGlnSerSerPheSerGlySerMetGln 660
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 Db 2569 ATCATTTAGGTCTCC 2583
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 US-10-377-072-25
 ; Sequence 25, Application US/10377072
 ; Publication No. US20040157221A9
 GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals Inc.
 ; APPLICANT: Curtis, Roy A.J.
 ; APPLICANT: Logan, Thomas Joseph
 ; APPLICANT: Glucksmann, Maria A.
 ; APPLICANT: Meyers, Rachel E.
 ; APPLICANT: Williamson, Mark J.
 ; APPLICANT: Rudolph-Owen, Laura A.
 ; APPLICANT: Chun, Myoung
 ; APPLICANT: Tsai, Fong-Ying
 ; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
 ; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
 ; TITLE OF INVENTION: AND USRS THEREFOR
 ; FILE REFERENCE: MP103-0180NMIM
 ; CURRENT APPLICATION NUMBER: US/10/377,072


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CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US 09/895,860
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,370
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/723,806
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/187,455
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/843,297
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199,801
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PRIOR APPLICATION NUMBER: US 09/861,801
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205,508
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/816,494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/815,419
PRIOR FILING DATE: 2001-03-22
Remaining prior Application data removed - See File Wrapper or PALM.
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SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 3544
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (589)...(2586)
US-10-377-072-25

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Score: 3406.00 Matches: 663
Percent Similarity: 99.854 Conservative: 1
Best Local Similarity: 99.704 Mismatches: 1
Query Match: 99.658 Indels: 0
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US-10-029-345A-109 (1-665) x US-10-377-072-25 (1-3544)

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QY 21 SerGlyThrGluLeuValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
DB 649 AGTGAACCGAAGAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
QY 41 HisIleLeuGluAlaIleHisLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
DB 709 CACATTTTGAAGCCATTATATCACTGCTCAAGCTTATGAGGGAAGGTTGGAACAG 768
QY 61 AspLeuValLeuIleThrGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
DB 769 GACAAAGGTATTAACAGAGCTCAATCCAGCAATTCAGCGAAACATTAAGTTGACAT 828
QY 81 CysSerGlnIleValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSer 100
DB 829 TCCAGTCAGAGAGTTGATGATTAACATCAAGCTCCCAAGATGTTGCTCTCTCTTCA 888
QY 101 AspCysPheLeuThrValLeuLeuGlyLeuLeuGlyLeuLeuLeuLeuLeuLeuLeu 120
DB 889 GACTGTTTCTCAGCTGATCTTCTGGGTAACTGAGAAAGAGCTTCAACTCTGTTCACTG 948
QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuGlyGlyGlySer 140
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QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160

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DB 1069 CGAATTTCTCCAACTTATATCTTGGCTGCGCAGCGAGATGCTCTCAACAGAGCTGAAG 1128
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DB 1609 TGTGCCGACTCTGCTACCTCAGAGGACAGCAAGCAAGCCCGTGCATCCCGCAGCGTG 1668
QY 361 ProSerValProSerValGlnProSerLeuGlyLysSerProLeuValGlnAlaLeu 380
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QY 381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnIleLeuLysArgSerPhe 400
DB 1729 AGTGGCTGCACTGCTCCGACAGACGCTGGAAGACAGCAATTAAGCTCAAGGCTTCTTC 1788
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QY 421 SerSerSerGluAspAlaLeuGlyTyrTyrLysProSerThrThrLeuAspGlyThrAsn 440
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QY 441 LysLeuCysGlnPheSerProValGlnIleLeuSerGlyGlnThrProGlnThrSerPro 460
DB 1909 AAGCTATGCGAGTTTCTCCCTGTTCAAGAACTATGAGACAGATCCGAAACAGTCTT 1968
QY 461 AspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerGln 480
DB 1969 GATTAAGAGAAAGCAGAGATCCCAAGAAAGCTGACAGACCGCTTCAACAGCGCAG 2028
QY 481 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500
DB 2029 AGCAAGCATTGCTATTCGATGAACACAGCACTGGACCGCCAGAGGCTCCCTTTA 2088
QY 501 SerProLeuHisArgSerGlySerValGlnAspArgTyrHisThrSerPheLeuPheGly 520
DB 2089 TCTCAGCTGATCGAAGTGGAGCGTGGAGGACATTTACACAGAGTCTCTTTTCCGC 2148

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Db      1832 AGTGGCTCACCTGTCCGACAGACAGCTGAAAGACAGCAATTAAGCTCAAGCTTCTTC 1891
Qy      |||||
Db      401 SerLeuAppliLeuSerValSerYrSerAlaSerMetAlaAlaSerLeuHISglYpHe 420
Qy      |||||
Db      1892 TCTCTGAATATCAAAATCAGTTTCAATATCAAGCCAGATGAGCATCTTACATGGCTTC 1951
Qy      |||||
Qy      421 SerSerSerGluApAlaLeuGluYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYr 440
Db      1952 TCTCTATCAAGAAAGATCTTGGAAATCTCAAACTTCCACTCTCTGATGGACCAAC 2011
Qy      |||||
Qy      441 LysLeuCyseGlnPheSerProValGlnGluLeuSerGlnGlnThrProGluThrSerPro 460
Db      2012 AAGCTATGCCAGTTCTCCCTCTTCCAGAACTATCCAGACAGACTCCCAACCAAGTCTCT 2071
Qy      |||||
Qy      461 ApblyGluGluAlaSerLeuLeuPheGlyLeuGlnThrAlaArgProSerApbSerGln 480
Db      2072 GATTAAGGAGAAAGCCAGCATCCCAAGAAAGCTGCAACCCGCGCTTCAAGACACAG 2131
Qy      |||||
Qy      481 SerLysArgLeuHISerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
Db      2132 AGCAAGCATTTGATTCGGTCAAGACACAGACAGACAGACAGCCCGCCAGAGTCCCTTTA 2191
Qy      |||||
Qy      501 SerProLeuHISerGlnSerGlySerValGluApbSerYrYrYrYrYrYrYrYrYrYrYr 520
Db      2192 TCTCCACTGCATCGAAGTGGAGCGTGGAGAGCAATTAACACACAGCTTCTTTCGGC 2251
Qy      |||||
Qy      521 LeuSerThrSerGlnGlnHISerLeuThrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYr 540
Db      2252 CTTTTCACAGCAGCAGACAGACCTCAGAAAGTGTGCTGGCTGGCTTAAAGGGCTGGCAC 2311
Qy      |||||
Qy      541 SerApbLeuAlaLeuAlaProGlnThrSerThrProSerLeuThrSerSerThrYrYrPheAla 560
Db      2312 TCGGATATCTTGGCCCCCAGACCTTACCCCTTCCCTCAACAGACGCTGATTTTGGC 2371
Qy      |||||
Qy      561 ThrGluSerSerHISerHISerYrSerAlaSerAlaIleYrGlyGlySerAlaSerYrSer 580
Db      2372 ACAGAGTCTCTACACTTACTGCTGCTCAGCATCTACGAGAGCGAGTCCAGTTACTCT 2431
Qy      |||||
Qy      581 AlaYrSerCyseSerGlnLeuProThrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYrYr 600
Db      2432 GCTTACAGCTGACAGCAGCTGCCACTTCCGAGACCAAGTCAATTCCTGCGCAGCGC 2491
Qy      |||||
Qy      601 GlnLysProSerApbArgAlaApbSerArgArgSerTrpHISgluGluSerProPheGlu 620
Db      2492 CAGAAAGCCAGATGACAGACTGACTGCGCGGAGCTGGCATGAGAGAGCCCTTTGAA 2551
Qy      |||||
Qy      621 LysGlnPheLysArgYrSerCyseGlnMetGluPheGlyGluSerIleMetSerGluAsn 640
Db      2552 AAGCATTTAAACGAGAAAGCTGCCAAATGGAATTTGAGAGAGCATGTCAGAGAAC 2611
Qy      |||||
Qy      641 ArgSerArgGluGluLeuGluLysValGlySerGlnSerSerPheSerGlySerMetGlu 660
Db      2612 AGTCAACGGGAAGAGCTGGGGAAAGTGGGAGAGTCAAGTCTTTCGGGCGAGCATGAA 2671
Qy      |||||
Qy      661 IleIleGluValSer 665
Db      2672 ATCATTGAGGTCTCC 2686

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; APPLICANT: KEARNEY, Liam
; TITLE OF INVENTION: PROTEIN PHOSPHATASES
; FILE REFERENCE: PI-0173 PCT
; CURRENT APPLICATION NUMBER: 2003-01-28
; PRIOR APPLICATION NUMBER: PCT/US01/23716
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 60/221,679
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/223,272
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/224,309
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 60/226,728
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/229,254
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: US 60/231,366
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 3766
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040058341A1 7480570CB1
US-10-343-357-17

Alignment Scores:
Pred. No.: 0 Length: 3766
Score: 3406.00 Matches: 663
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.65% Indels: 0
DB: 17 Gaps: 0

US-10-029-345A-109 (1-665) x US-10-343-357-17 (1-3766)
Qy      1 MetAlaHISgluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGln 20
Db      538 ATGGCCCATGAGATGATGGAATCAAAATGTTACTGAGAGGTGGCTGCTGCGAA 597
Qy      21 SerGlyThrGluLysValLeuLeuIleApbSerArgProPheValGluYrYrYrYrSer 40
Db      598 ACTGGAACGGAAAGAGTGTGCTTAATGATAGCCGCGCAATTTGGAAATACATCATCC 657
Qy      41 HISIleLeuGluAlaIleAsnIleAsnCyseSerLysLeuMetLysArgYrGluGlnGln 60
Db      658 CACATTTTGAAGCCATTATATCAACTGCTCCAGCTTATGAAAGCGAAGTTGCAACAG 717
Qy      61 ApbLysValLeuIleThrGluLeuIleGlnHISerAlaLysHISLysValAlaPhePhe 80
Db      718 GACAAAGTTAATTAACAGAGCTCATCCAGCATTCAGGAAACATTAAGTTGACATTAAT 777
Qy      81 CyseSerGlnLysValValValYrYrApbGlnSerSerGlnApbValAlaSerLeuSerSer 100
Db      778 TGCAGTCAAGAGTGTATGATTACATCAAACTCCCAAGAGTGGCTCTCTCTTCA 837
Qy      101 ApbCysePheLeuThrValLeuLeuGluLysLeuGluLysSerPheAsnSerValHISLeu 120
Db      838 GACTGTTTCTACGTAATCTTGGGTAACAGAGAGAGCTTCAACTCTGTCACTCG 897
Qy      121 LeuAlaGlyGlyPheAlaGluPheSerArgCysePheProGlyLeuCyseGluGlyLysSer 140
Db      898 CTGAGAGGTGGTTTGTGAGAGTTCTCGTGTGTTCCCTGGGCTCGTGAAGAAATCC 957
Qy      141 ThrLeuValProThrCyseIleSerGlnProCyseLeuProValAlaAsnIleGlyProThr 160
Db      958 ACTCTAGTCCCTCACTGATTTCTGAGCTTCTTCACTGTTGCCAACATTTGGGCAACC 1017
Qy      161 ArgIleLeuProAsnLeuYrIleuGlyCyseGlnArgApbValLeuAsnLysgluLeuIle 180

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1018 CGAATCTTCCCAATCTTATCTTGGCTGCAGAGATCTCTCAACAGAGCTGATG 1077
181 GlnGlnAsnGly111eglyTyValLeuAsnAspSerThrCysProlypProaspPhe 200
1078 CACAGAAATGGATGGTGTATGTGTAAATGCCAGCAATGCTGTCCAAAGCCTGACTTT 1137
201 ILAProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluys111eLeu 220
1138 ATCCCGAGTCTCAATTTCTGCGGTGCGTGAATGACAGCTTTGTGAGAAATTTTGG 1197
221 ProTrpLeuAspIysSerValAspPhe111eglyValLeuAsnAspSerAsnGlyCysVal 240
1198 CCGTGGTGGACAATCAGATGATTTTCATGAGAAAGCAAAACCTCCCAATGATGTGTT 1257
241 LeuValHisCysLeuAlaGly111eSerArgSerValThr111eAla111eAlaTy111eMet 260
1258 CTAGTGCACGTGTAGCTGGGATCTCCGCTCCGCACTCCCTATCGCTACATCATG 1317
261 LysArgMetAspMetSerLeuAspGluAlaTyArgPheValLysGluLysArgProThr 280
1318 AACAGATGACATGCTCTTATGATGAAGCTTACAGATTTGTGAAGAAAGAAAGACCTACT 1377
281 ILeserProAsnAspPheLeuGlyGluLeuLeuAspTyrgLulysLys111eLysAsn 300
1378 ATATCTCCAAATTCATATTTTCTGGGCAACTCTGGAATGAGAAAGATTAAGAAC 1437
301 GlnThrGlyAlaSerGlyProlypSerLysLeuLysLeuLeuHis111eGluLysProAsn 320
1438 CAGACTGGAGCATCAGAGCCAGCAAGCAAACTCAGCTGTGACCTGAGAGAGCCCAAT 1497
321 GluProValProAlaValSerGluGlyGluLysSerGluThrProLeuSerProPro 340
1498 GAACCTGTCTCTCTCTCTCAGAGGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1557
341 CysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSerVal 360
1558 TGTGCGCACTGTCTACTCAGAGGCGAGAGAGCAAAAGCCGTGATCCCGCAGCGTGG 1617
361 ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaLeu 380
1618 CCCAGGCTGCCAGCGCTGAGCGGTGCTGTGTGAAGAGAGCCCGCTGTGTACAGGGCGTC 1677
381 SerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLysArgSerPhe 400
1678 AGTGGCTGCACCTGTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1737
401 SerLeuAspI11eLysSerValSerTySerAlaSerMetAlaAlaSerLeuHis111eGlyPhe 420
1738 TCTCTGATATCAATCAGTTTCATATTCAGCCAGCATGGCAGCATCTTACATGGCTTC 1797
421 SerSerSerGluAspAlaLeuGluTyTyTyLysProSerThrThrLeuAspGlyThrAsn 440
1798 TCTCTATCAAGAAAGATCTTGAATATCAAACTTCCATCTGTGATGGAGCAAC 1857
441 LysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerPro 460
1858 AAGCTATGCAATTTCTCCCTGTTCAGAACTATCGAGACAACTCCGAAACCACTGCTT 1917
461 AspLysGluGluAlaSer111eProLysLysLeuGlnThrAlaArgProSerAspSerGln 480
1918 GATTAAG 1977
481 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
1978 ACAAAGCCATTCATTCGCTGAGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2037
501 SerProLeuHisArgSerGlySerValGluAspAsnTyHisThrSerPheLeuPheGly 520
2038 TCTCACTGCATCAGAGTGGAGCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2097
521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTrpHis 540

2098 CTTTCACACGAG 2157
541 SerAspI11eLeuAlaProGlnThrSerThrProSerLeuThrSerSerTrpTyPheAla 560
2158 TCGGATATCTTGGCCCGCCAG 2217
561 ThrGluSerSerHisPheTySerSerAlaSerAla111eTyrgLysLysSerAlaSerTySer 580
2218 ACAAAGTCTCACTTCTACTTCTGCTCAGCATCTACAGAGAGAGAGAGAGAGAGAGAGAG 2277
581 AlaTySerCysSerGlnLeuProThrCysGlyAspGlnValTySerValArgArg 600
2278 GCTTACAGTGCAGGAG 2337
601 GlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSerProPheGlu 620
2338 CAGAAAGCCAG 2397
621 LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSer111eMetSerGluAsn 640
2398 AAGCATTTTAAAGCAG 2457
641 ArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGlu 660
2458 AGGTACCGGAG 2517
661 IL11eGluValSer 665
2518 ATCATTTGAGGTCTCC 2532

RESULT 13
US-10-648-593-115
; Sequence 115, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648, 593
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 115
; LENGTH: 4790
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-648-593-115

Alignment Scores:
Pred. No.: 0 Length: 4790
Score: 3406.00 Matches: 663
Percent Similarity: 99.85% Conservative: 1
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 99.65% Indels: 0
DB: 18 Gaps: 0

US-10-029-345A-109 (1-665) x US-10-648-593-115 (1-4790)

1 MetAlaHisGluMet111eglyThrGln111eValThrGluArgLeuValAlaLeuLeuGlu 20
184 ATGGCCCATGATGATTTGAAATCAATGTTTATCTAGAGAGTTGGTGGCTGTGAGAA 243
21 SerGlyThrGluLysValLeuLeu111eAspSerArgProPheValGluTyArgThrSer 40
244 AGTGAAG 303
41 His111eGluGluAla111eAsn111eAsnCysSerLysLeuMetLysArgArgLeuGln 60
304 CACATTTTGGAG 363

QY 61 AapLyVaIleuIleThrgIleuIleGIInHleSeAlaIyBhIleYsVaIaApIleap 80
 DB 364 GACAAAGTGTATTCAGAGCTCATCCAGATTCAGCAACATTAAGTTGATTCAT 423
 QY 81 CysSeGIInHleYsVaIaIyIraApGIInSeSeGIInaSpVaIaIaSeIleuSeSer 100
 DB 424 TGCAGTCAGAAAGGTGATTAAGATTCAGATCCCAAGATGTCCTCTCTCTCA 483
 QY 101 AapCyPheIeUThrVaIleuIleuGIyIyIleuGIInuIySeSerPheanSeVaIaIleu 120
 DB 484 GACTGTTTCTCACTGACTCTGGGGTAACTGGAAAGAGCTTCAACTCTGTTCACTGG 543
 QY 121 LeuAaGIyGIyPheAaGIuPheSeArCySPheProGIyLeuCySgIuGIyIySeSer 140
 DB 544 CTTCAGAGTGGGTTCTGAGTTCTCTGTTGTTCTCTGGCTCTGTTGAAGGAATCC 603
 QY 141 ThrLeuVaIProThrCySIIeSeGIInProCySleuProVaIaIaAnIleGIyProThr 160
 DB 604 ACTCTAGTCCCTACCTGCATTTCTCAGCCTTGTCTCTGTTCCAACTTGGGCCAAC 663
 QY 161 ArgIleuProaInleuTyIleuGIyCySIIaArgaSpVaIleuAnIySeGIleuIle 180
 DB 664 CGAATTCCTCCAACTTTATCTTGGCTGCAGCGAGATGCTCTCAACAGAGAGCTGAG 723
 QY 181 GIInaInaNGIyIleGIyTyIraIleuAnIaSeTyIleThCySProIySProaPhe 200
 DB 724 CAGCAAAATGGAGTGTATTAAGTGAATGCCAGAAATCCGTCTCAAGAGCTGACTT 783
 QY 201 IleProGIuSeRhaIaPheIeUaIraVaIProVaIaAnASePheCySgIuIyIleu 220
 DB 784 ATCCCGAGTCTCATTTCTGGGTGGCTGCTGAATGACAGCTTTGTGAAGAAATTTTG 843
 QY 221 ProThrPheUaPlySeSeVaIaPheIleGIyIyVaIaIyVaIaSeRaNGIyCyVaI 240
 DB 844 CGGTGTTTGACAAATCAGTGAATTCATTTGAGAAAGCAAAAGCCCTCAATGATGTGT 903
 QY 241 LeuVaIHaCySeIeUaIaGIyIleSeRaGSeSeRaIaThIleAlaIleAlaTyIleMet 260
 DB 904 CTAGTGCATGTTTACGTGAGATCTCCCTCCGCCACCACTGCTATCCCTACATCAAG 963
 QY 261 LySaIraGMeCaSPMeSeSeIeUaPGLaIaTyIraIraPheVaIleGIyIyIyIyIyIy 280
 DB 964 AAGAGATGACATGCTTTAAGATGAAGCTTACAGTTTGTGAAGAAAAAGACTTACT 1023
 QY 281 IleSeProaInPheanPheIeUaGIyIleuIleuApyIyGIyIyIyIyIyIyIyIy 300
 DB 1024 ATATCTCCAACTTCATTTCTGGGCCCAATCTGAGCTATGAGAAAGATTAAAGAC 1083
 QY 301 GIInThrgIyAlaSeGIyIyProIySeIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 320
 DB 1084 CAGACTGGAGCATCAGAGGCCAAAGCAAACTCAAGCTCTGACTGAGAAAGCCCAAT 1143
 QY 321 GIuProVaIProAlaVaISeGIuGIyGIyIyIySeGIuThrProIeUSeProPro 340
 DB 1144 GAACCTGTCTCTCTCTCTCAGAGGTGACAGAAAGGAGAACGCCCTTCACTCAACC 1203
 QY 341 CyBaIaASeSeRaIaThSeGIuAlaIaGIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 360
 DB 1204 TGTGCGCACTGCTGCTCTCAGAGGTGACAGAAAGGAGAACGCCCTTCACTCAACC 1263
 QY 361 ProSeSeVaIProSeSeVaIaIInProSeIeUaIeUaIeUaIeUaIeUaIeUaIeU 380
 DB 1264 CCGAGGTCGCCAGCGCTGAGCGCTGCTGTTAGAGAACGCCCTGTTAAGAGGCTC 1323
 QY 381 SeGIyIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeU 400
 DB 1324 AATGGGCTGCACTGTCCGACAGAGCTGGAAGACAGAAATAGTCAAGCTTCTTC 1383
 QY 401 SeIleUaPlyIeUaSeSeVaISeTyISeRaIaSeMeRaIaIaSeIeUaIeUaIeUaIeU 420
 DB 1384 TCTCTGATATCAATCAAGTTTCATATTCAGCAGCATGAGCATCTTACATGCTTC 1443

QY 421 SerSeSeGIuAaPAlaIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeU 440
 DB 1444 TCTCTATCAAGAGATCTTTGGAATTAATCAAACTTCACTACTGTGATGGAGCAAC 1503
 QY 441 IyIeUaCySgIInPheSeProVaIaGIInIeUaSeGIuGIInThrProGIuThrSePro 460
 DB 1504 AAGCTATGCAATTCCTCCCTGTTCAAGAACTATCGAGACAGACTCCCAACACTCT 1563
 QY 461 AapLyGIuGIuAaSeIleProIyIyIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeU 480
 DB 1564 GATTAAGAGAGAACAGCATCCCAAGAGCTGACAGACCGAGCTTCAAGACACCGAG 1623
 QY 481 SeIySaIraGIInIeSeVaIaIraThSeSeSeSeGIyIyThraIaIaIraSeIeUaIeU 500
 DB 1624 AGCAAGCATTCATTCGCTGAGAACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1683
 QY 501 SeProIeUaIaIySeSeGIySeVaIaIaAaPaaTyIleThSePheIeUaPheGIy 520
 DB 1684 TCTCCACTGATCGAAGTGGAGCGTGGAGAGCAATTAACACAGCTTCTTTCGGC 1743
 QY 521 IeUSeThSeGIInIaIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeU 540
 DB 1744 CTTCACACAGACAGACAGACCTCAAGAGTGTGCTGGCTGGCTGCTTAAGGGCTGGCAG 1803
 QY 541 SeRaPlyIeUaIaProGIInThSeThrProSeIeUaIeUaIeUaIeUaIeUaIeUaIeU 560
 DB 1804 TCGATATCTTGGCCCCCAGACTCTTACCTTCTCTCAACAGAGCTGATTTTGGC 1863
 QY 561 ThrgIuSeSeRhaIaPheIySeSeRaIaIeIyIyGIyIySeRaIaSeTyIySeR 580
 DB 1864 ACAGAGTCTCTACACTTACTCTGCTCAGCATCTAAGAGAGAGAGAGAGAGAGAGAG 1923
 QY 581 AlaTyISeCySeGIInIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeUaIeU 600
 DB 1924 GCTTACAGTGGAG 1983
 QY 601 GIuIyProSeSaPArGaIaAaPSeRaIaIySeSeRaIaIySeSeRaIaIySeSeRaIaIy 620
 DB 1984 CAGAAAGCAAGTACAGAGACTGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2043
 QY 621 IySaIraGMeCaSPMeSeSeIeUaPGLaIaTyIraIraPheVaIleGIyIyIyIyIyIy 640
 DB 2044 AAGCATTTAAACGAGAAAGCTGCCAAATGAAATTTGAGAGAGATCATGTCAGAGAAC 2103
 QY 641 ArgSaIraGMeCaSPMeSeSeIeUaPGLaIaTyIraIraPheVaIleGIyIyIyIyIyIy 660
 DB 2104 AGGTACAGGAG 2163
 QY 661 IleIleGIuVaISeR 665
 DB 2164 ATCATTTAGAGTCTCC 2178
 RESULT 14
 US-10-357-930-20824
 ; Sequence 20824, Application US/10357930
 ; Publication No. US20040259086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Endege, Wilson
 ; APPLICANT: Monahan, John
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 ; TITLE OF INVENTION: HUMAN PROSTATE CANCER
 ; FILE REFERENCE: MRI-007BCN
 ; CURRENT APPLICATION NUMBER: US/10/357,930
 ; PRIOR FILING DATE: 2003-02-04
 ; PRIOR APPLICATION NUMBER: 09/785,276
 ; PRIOR FILING DATE: 2003-02-16
 ; PRIOR APPLICATION NUMBER: 60/183,319
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: 60/189,862
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/207,454

;; PRIOR FILING DATE: 2000-05-25
;; PRIOR APPLICATION NUMBER: 60/211,314
;; PRIOR FILING DATE: 2000-06-09
;; PRIOR APPLICATION NUMBER: 60/219,007
;; PRIOR FILING DATE: 2000-07-18
;; PRIOR APPLICATION NUMBER: 60/255,281
;; PRIOR FILING DATE: 2000-12-13
;; NUMBER OF SEQ ID NOS: 62232
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 20824
;; LENGTH: 5145
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1, 5144, 5145
;; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-20824

Alignment Scores:

Pred. No.:	0	Length:	5145
Score:	3406.00	Matches:	663
Percent Similarity:	99.85%	Conservative:	1
Best Local Similarity:	99.70%	Mismatches:	0
Query Match:	18	Indels:	0
DB:	18	Gaps:	0

US-10-029-345A-109 (1-665) x US-10-357-930-20824 (1-5145)

QY 1 MetAlaHISGLuMeTlEGlYthrgInIleValThrgIuArgLeuValAlaLeuEngIn 20
DB 589 ATGGCCATGATGATGATGAACTCAATTTGTTACTGAGAGGTGTGCTCGTGGAA 648
QY 21 SerGIYthrgInuYsValleuEnIleAspSerArgProPheValGIuYrAsnThrSer 40
DB 649 AGTGAACGAAAGTGTCTGCTAATGTATGACCGGCCATTGTGGAAATACATCATCC 708
QY 41 HisIleLeuGIuAlaIleAsnIleAsnCYsSerLYLeuMeLYsArgLeuEngIn 60
DB 709 CACATTTTGGAGCCATTATATCACTGCTCCAGCTTATGAGCGAAGTTGCACAG 768
QY 61 AspLYsValleuIleThrgIuLeuIleGIuHisSerAlaLYsIleValAspIleAsp 80
DB 769 GACAAAGTGTATATACAGAGCTCATCCAGATTGACGAAACATTAAGTTGACATTGAT 828
QY 81 CYsSerGIuLYsValValTYrAspGIuSerSerGIuAspValAlAserLeuSerSer 100
DB 829 TCCAGTCAGAGGTGTGTATTCATGATCAAAAGCTCCCAAGATGTGGCTCTCTCTTCA 888
QY 101 AspCYsPheLeuThrValleuLeuGIYsLeuGIuLYsSerPheAsnSerValHisLeu 120
DB 889 GACTGTTTCTCACTGTACTTCTGGGTAACTGGAGAAAGCTTCAACTCTTTCACTTG 948
QY 121 LeuAlaGIYGIYpHeAlaGIuPheSerArgCYsPheProGIYLeuCYsGIuGIYsSer 140
DB 949 CTGTGAGGTGGTGTGTGTCTGAGTTCTCTCGTTTCCCTGGCCCTGTGAAAGAAATCC 1008
QY 141 ThrLeuValProThrCYsIleSerGIuProCYsLeuProValAlaAsnIleGIYProThr 160
DB 1009 ACTCTAGTCCCTACCTGCACTTCTCAAGCTTCTTACCTGTGGCCAACTTGGCAACC 1068
QY 161 ArgIleLeuProAsnLeuTYrLeuGIYCYsGIuArgAspValLeuAsnIleGIuLeu 180
DB 1069 CGAATTTCTTCCAACTTTATTTCTGGCTGCCAGCAGATGCTCTCAACAAGAGCTGATG 1128
QY 181 GIuGIuAsnGIYIleGIYTYrValleuAsnAlaSerTYrThrCYsProLYsPheAspPhe 200
DB 1129 CAGCGAATGTGGATGTATGTGTAAATGCCCAATACCTGTCCAAAGCCTGACTTT 1188
QY 201 IleProGIuSerHisPheLeuArgValProValaAspSerPheCYsGIuLYsIleLeu 220
DB 1189 ATCCCCGAGTCTCATTTCTCGGTGTGCTGTGAATGACAGCTTTTGTGAGAAATTTTG 1248

QY 221 ProTrIleuAspLYsSerValAspPheIleGIuLYsAlaLYsAsnGIYCYsVal 240
DB 1249 CCGTGGTGGACAAATCGATGATTTCAATGGAAGCAAAAGCTCCAAATGAGATGT 1308
QY 241 LeuValHisCYsLeuAlaGIYIleSerArgSerAlaThrIleAlaIleAlaTYrIleMet 260
DB 1309 CTAGTGCACTGTTTATGCTGGATCTCCGCTCCGACCATCGCATATGCGCTACATCATG 1368
QY 261 LYsArgMetAspMetSerLeuAspGIuAlaTYrArgPheValLYsGIuLYsArgProThr 280
DB 1369 AAGAGATGTACATCTCTTGTATGATGACATTACAGATTTGTGAAGAAAGAAAGCTCTCT 1428
QY 281 IleSerProAsnPheAsnPheLeuGIYGIuIleuAspTYrGIuLYsIleIleYsAsn 300
DB 1429 ATATCTCCAACTTCAATTTTCTGGGCCAACTCTCGAGCTTGTAGAGAAAGATTAGAAC 1488
QY 301 GIuThrgIYAlaSerGIYProLYsSerLYsLeuLYsLeuHisIleuGIuLYsPheAsn 320
DB 1489 CAGACTGAGCATCGAGGCCCAAGAGCAAACTCAAGCTGTGCACCTGAGAGCCAAAT 1548
QY 321 GIuProValProAlaValaSerGIuGIYGIuLYsSerGIuThrProLeuSerProPro 340
DB 1549 GAACTGTCTCTGTCTCTCAAGGGTGTGACAGAAACGAGACGCCCTCAGTCCACC 1608
QY 341 CYsAlaAspSerAlaThrSerGIuAlaIleGIYGIuArgProValHisProAlaSerVal 360
DB 1609 TGTGCCACTCTGCTTACTCTCAGAGGACAGACAGCAAAAGCCGTGCACTCCGACGCTG 1668
QY 361 ProSerValProSerValGIuProSerLeuLeuGIuAspSerProLeuValGIuAlaLeu 380
DB 1669 CCNAGCTGCCCAAGGTGTGACCCGTGCTTTAGAGGACAGCCGCTGTACAGGCGCTC 1728
QY 381 SerGIYLeuHisIleuSerAlaAspArgLeuGIuAspSerAlaLYsLeuLYsArgSerPhe 400
DB 1729 AGTGGCTGCACCTGTCTCGACAGAGGTGTGAACAGCAATTAAGCTCAACGTTCTTC 1788
QY 401 SerLeuAspIleLYsSerValSerTYrSerAlaSerMetAlaAlaSerLeuHisGIYPhe 420
DB 1789 TCTCGATATCAATCATGCTTCAATTTCAAGCCAGCATGAGCATCTTTCATGCGCTTC 1848
QY 421 SerSerSerGIuAspAlaLeuGIuTYrTYrLYsProSerThrThrLeuAspGIYThrAsn 440
DB 1849 TCTCATACAGAAAGTGTGTGAATACATCAAACTTCACTCACTGAGAGGAGCAAC 1908
QY 441 LYsLeuCYsGIuPheSerProValGIuGIuLeuSerGIuGIuThrProGIuThrSerPro 460
DB 1909 AAGCTATGCCAGTCTCTCCCTGTTCAGAACTATTCGAGAGCACTCCGAAACCAAGTCT 1968
QY 461 AspLYsGIuGIuAlaSerIleProLYsLYsLeuGIuThrAlaArgProSerAspSerGIu 480
DB 1969 GATTAAGAGGAAGCCAGCATCCCAAGAGCTGCAGACCGCAGGCTTCAAGACGCCAG 2028
QY 481 SerLYsArgLeuHisSerValArgThrSerSerSerGIYThrAlaGIuArgSerLeuLeu 500
DB 2029 AGCAAGGCATTTGCAATGGTGTGACAAACAGCAGAGTGGACCGCCAGAGGTTCCCTTTTA 2088
QY 501 SerProLeuHisArgSerGIYSerValGIuAspAsnTYrHisThrSerPheLeuPheGIY 520
DB 2089 TCTCCACTGCATCCAAAGGTGGAGGCTGAGAGCAATTAACCAACACCACTTCTTTTGGCC 2148
QY 521 LeuSerThrSerGIuGIuHisIleuThrLYsSerAlaGIYLeuGIYLeuLYsGIYTYrPhe 540
DB 2149 CTTTCCACACCGACGACGACCTACAGATCTGTGCTGGCTCTTAAGGCTGTGCAC 2208
QY 541 SerAspIleLeuAlaProGIuThrSerThrProSerLeuThrSerSerTYrTYrPheAla 560
DB 2209 TCGGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACAGCACTGTGATTTTGGCC 2268
QY 561 ThrgIuSerSerHisPheTYrSerAlaSerAlaIleTYrGIYLYsSerAlaSerTYrSer 580
DB 2269 ACAGAGTCTTCACTTCTGCTGCTCAGCCATTCAGAGGCAATGTGCCAGATTACTCT 2328
QY 581 AlaTYrSerCYsSerGIuLeuProThrCYsGIYAspGIuValTYrSerValArgArgArg 600

Db 1729 AGTGGGCTGCCTGTCCTCCGACAGGCTGGAAGACAGCAATTAAGCTCAAGCTTCCTTC 1788
QY 401 SerLeuAsp1LeuSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPhe 420
Db 1789 TCTCTGGAATATCAATCAAGTTTCATATTCAGCCAGCATGGCAGCATCTTACATGCTTC 1848
QY 421 SerSerSerGluAspAlaLeuGluTyrTyrLeuProSerThrThrLeuAspGlyThrAsn 440
Db 1849 TCTCTCATTCAGAAATGCTTTGGAAATCTACAAACCTTCCACTACTCTGGATGGACCAAC 1908
QY 441 LysLeuCysGlnPheSerProValGlnGluLeuSerGlnGlnThrProGluThrSerPro 460
Db 1909 AAGCTATGCCAGTTCTCCCTGTTTCAGAACTATCGAGCAGACTCCCGAAACCACTCCT 1968
QY 461 AspLysGluGluAlaSer1LeuProLysLeuGlnThrAlaArgProSerAspSerGln 480
Db 1969 GATTAAGAGAGAAACCCAGCAATCCCAAGAAAGCTGCAGACCGCGCTTCAGACAGCCAG 2028
QY 481 SerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuLeu 500
Db 2029 AGCAACCGATTGATTCGCTCAGAACCAAGCAGCAGCTGGCACCGCCAGAGGTCCTTTTA 2088
QY 501 SerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheGly 520
Db 2089 TCTCCACTGCATCGAAGTGGAGCGTGGAGAGCAATTAACCAACAGCTTCCTTTCCGCG 2148
QY 521 LeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTyrHis 540
Db 2149 CTTTCCACCAAGCAGCAGCACTCAGAAAGTCTGCTGGCTGGCTTAAAGGCTGGCAC 2208
QY 541 SerAsp1LeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrTyrPheAla 560
Db 2209 TCGGAATCTTGGCCCCCAGACCTTACCCCTTCCCTGACAGACGCTGATTTTGGCC 2268
QY 561 ThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyLysSerAlaSerTyrSer 580
Db 2269 ACAGAGTCTTCACACTTACTCTGCTCAGCCATCTACGAGGAGGAGTGCCAGTTACTCT 2328
QY 581 AlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArg 600
Db 2329 GCCTACAGCTGCAGCCAGCTGCCACTTGCAGACCAAGTCTATCTGTGGCAGGCGG 2388
QY 601 GlnLysProSerAspArgAlaAspSerArgSerTyrHisGluGluSerProPheGlu 620
Db 2389 CAGAGCCAGTACAGAGCTGACTGCGCGGAGCTGGCATGAAGAGCCCTTTGAA 2448
QY 621 LysGlnPheLysArgSerCysGlnMetGluPheGlyGluSerIleMetSerGluAsn 640
Db 2449 AAGCAGTTTAAAGCAGAACTGCCAAATGGAATTGGAAGAGCATCATGTCAAGAAAC 2508
QY 641 ArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetGlu 660
Db 2509 AGGTACCGGGAAGAGCTGGGAAAGTGGAGTCACTTCTTTCGGGAGCATTGGAA 2568
QY 661 IleIleGluValSer 665
Db 2569 ATCATTTGAGGTCTCC 2583

Search completed: February 14, 2005, 14:04:12
Job time : 940.813 secs

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OM protein - protein search, using SW model

Run on: February 9, 2005, 12:00:17 ; Search time 19.363 Seconds
(without alignments)
1164.285 Million cell updates/sec

Title: US-10-029-345A-109_COPY_1_302
Perfect score: 1564
Sequence: 1 MAHEMIGTQVTERLVALL.....PNNFLAGQLDYKKIKKQT 302

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTCUTS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfilest.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1552	99.2	665	4	US-09-816-494-2
2	989	63.2	661	4	US-09-949-016-9121
3	654.5	41.8	170	4	US-09-544-716-14
4	654.5	41.8	170	4	US-09-557-921-15
5	654.5	41.8	170	4	US-09-564-357-17
6	654.5	41.8	170	4	US-09-619-380-16
7	619	39.6	155	4	US-09-955-732A-6
8	469	30.0	482	4	US-09-557-921-2
9	466.5	29.8	491	4	US-09-949-016-8486
10	425	27.2	314	4	US-09-371-671B-11
11	425	27.2	367	2	US-08-996-379-6
12	425	27.2	394	2	US-08-530-290-23
13	425	27.2	394	4	US-09-702-705-805
14	425	27.2	394	4	US-09-702-705-805
15	425	27.2	394	4	US-09-736-457-805
16	425	27.2	394	4	US-09-736-457-805
17	425	27.2	394	4	US-09-614-124B-805
18	425	27.2	394	4	US-09-614-124B-827
19	425	27.2	394	4	US-09-671-325-805
20	425	27.2	394	4	US-09-671-325-827
21	425	27.2	394	4	US-09-589-184-805
22	425	27.2	394	4	US-09-589-184-827
23	425	27.2	394	4	US-09-658-824-805
24	425	27.2	394	4	US-09-658-824-827
25	425	27.2	413	4	US-09-949-016-8081
26	423.5	27.1	395	2	US-08-990-379-5
27	415	26.5	367	2	US-08-530-290-24

28	415	26.5	367	4	US-09-919-497-60	Sequence 60, App1
29	415	26.5	449	4	US-09-949-016-10840	Sequence 10840, A
30	409.5	26.2	313	2	US-08-990-379-7	Sequence 7, App1
31	409	26.2	314	3	US-09-164-193-22	Sequence 22, App1
32	409	26.2	314	4	US-09-221-448A-22	Sequence 22, App1
33	408	26.1	421	4	US-09-949-016-10488	Sequence 10488, A
34	377.5	24.1	393	2	US-08-990-379-4	Sequence 4, App1
35	357	22.8	302	4	US-09-702-705-806	Sequence 806, App
36	357	22.8	302	4	US-09-736-457-806	Sequence 806, App
37	357	22.8	302	4	US-09-614-124B-806	Sequence 806, App
38	357	22.8	302	4	US-09-671-325-806	Sequence 806, App
39	357	22.8	302	4	US-09-589-184-806	Sequence 806, App
40	357	22.8	302	4	US-09-658-824-806	Sequence 806, App
41	351	22.4	384	4	US-09-949-016-6494	Sequence 6494, Ap
42	349.5	22.3	397	2	US-08-990-379-8	Sequence 8, App1
43	346.5	22.2	168	4	US-09-544-716-13	Sequence 13, App1
44	346.5	22.2	168	4	US-09-557-921-13	Sequence 13, App1
45	346.5	22.2	168	4	US-09-564-357-16	Sequence 16, App1

ALIGNMENTS

RESULT 1									
US-09-816-494-2									
; Sequence 2, Application US/09816494									
; Patent No. 6664089									
; GENERAL INFORMATION:									
; APPLICANT: Meyers, Rachel A.									
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY									
; FILE REFERENCE: 10448-030002									
; CURRENT APPLICATION NUMBER: US/09/816,494									
; PRIOR APPLICATION NUMBER: 2001-03-23									
; PRIOR FILING DATE: 2000-03-24									
; NUMBER OF SEQ ID NOS: 10									
; SOFTWARE: FASTSEQ for Windows Version 4.0									
; SEQ ID NO 2									
; LENGTH: 665									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-09-816-494-2									
Query Match 99.2%; Score 1552; DB 4; Length 665;									
Best Local Similarity 99.3%; Pred. No. 3.9e-161;									
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;									
QY	1	MAHEMIGTQVTERLVALL	ESGTEKVLIDSRPVEYNTSHIL	RAININCSKLMKRRLQ	60				
DB	1	MAHEMIGTQVTERLVALL	ESGTEKVLIDSRPVEYNTSHIL	RAININCSKLMKRRLQ	60				
QY	61	DKVLITELIHSARKYVD	ICDSQKVVYVYDSSQDVASIS	SDCFLTVLLGKLEKSFNSVHL	120				
DB	61	DKVLITELIHSARKYVD	ICDSQKVVYVYDSSQDVASIS	SDCFLTVLLGKLEKSFNSVHL	120				
QY	121	LAGFAERSRFPGLCGK	STLVPTCISQPLCPANIGPTI	LNLVYIGCRDVLNKL	180				
DB	121	LAGFAERSRFPGLCGK	STLVPTCISQPLCPANIGPTI	LNLVYIGCRDVLNKL	180				
QY	181	QONGIGVLANSYCP	RPDPFIPESHFLRPVNDSC	FKIPLMLKSDVFL	240				
DB	181	QONGIGVLANSYCP	RPDPFIPESHFLRPVNDSC	FKIPLMLKSDVFL	240				
QY	241	LVHCLAGISRSATIA	IYIMKRDMSLDEAYRFXE	KRPTTSPNFI	300				
DB	241	LVHCLAGISRSATIA	IYIMKRDMSLDEAYRFXE	KRPTTSPNFI	300				
QY	301	QT 302							
DB	301	QT 302							

Best Local Similarity 72.5%; Pred. No. 1.4e-63;
Matches 121; Conservative 27; Mismatches 18; Indels 1; Gaps 1;

QY 134 GLCEGK-STLVPTCISQPCLPVANIPTRIILPNLYGCGQDVANKELIQONGIGYVLNLS 192

Db 1 GLCEGKPAALLPMSLSQPCLPVPSVGLTRILPHLYGSKQDVANKDMQNGISYVLNLS 60

QY 193 YTCPPKDFIPESHFLRVPNVDSFCEKILPWLKSVDFIEKAKASNGCVLVHCLAGISRSA 252

Db 61 NSCPKDFICEBRFMRVPIINDNYCEKILPWLKSTIEFDIKALSSCOVIVHCLAGISRSA 120

QY 253 TTAIAIYIMKRMDSLDEAYRFVKEKRPITSPNPNFLGQLLDYEKKIK 299

Db 121 TTAIAIYIMKTMGMSDDAYRFVXDRRPSISPNFNFLGQLLEVERTLK 167

RESULT 6
US-09-619-380-16
Sequence 16, Application US/09619380
Patent No. 6649391
GENERAL INFORMATION:
APPLICANT: Lucbe, Ralf M.
APPLICANT: Wei, Bo
TITLE OF INVENTION: DSP-11 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.418
CURRENT APPLICATION NUMBER: US/09/619,380
CURRENT FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
US-09-619-380-16

Query Match 41.8%; Score 654.5; DB 4; Length 170;
Best Local Similarity 72.5%; Pred. No. 1.4e-63;
Matches 121; Conservative 27; Mismatches 18; Indels 1; Gaps 1;

QY 134 GLCEGK-STLVPTCISQPCLPVANIPTRIILPNLYGCGQDVANKELIQONGIGYVLNLS 192

Db 1 GLCEGKPAALLPMSLSQPCLPVPSVGLTRILPHLYGSKQDVANKDMQNGISYVLNLS 60

QY 193 YTCPPKDFIPESHFLRVPNVDSFCEKILPWLKSVDFIEKAKASNGCVLVHCLAGISRSA 252

Db 61 NSCPKDFICEBRFMRVPIINDNYCEKILPWLKSTIEFDIKALSSCOVIVHCLAGISRSA 120

QY 253 TTAIAIYIMKRMDSLDEAYRFVKEKRPITSPNPNFLGQLLDYEKKIK 299

Db 121 TTAIAIYIMKTMGMSDDAYRFVXDRRPSISPNFNFLGQLLEVERTLK 167

RESULT 7
US-09-955-732A-6
Sequence 6, Application US/09955732A
Patent No. 6825021
GENERAL INFORMATION:
APPLICANT: Lucbe, Ralf M.
APPLICANT: Wei, Bo
TITLE OF INVENTION: DSP-15 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.433
CURRENT APPLICATION NUMBER: US/09/955,732A
CURRENT FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 155
TYPE: PRT
ORGANISM: Homo sapiens
US-09-955-732A-6

Query Match 39.6%; Score 619; DB 4; Length 155;
Best Local Similarity 73.9%; Pred. No. 9.3e-60;

Matches 113; Conservative 25; Mismatches 15; Indels 0; Gaps 0;

QY 147 ISQPCLPVANIPTRIILPNLYGCGQDVANKELIQONGIGYVLNLSYTCPPKDFIPESHF 206

Db 1 ISQPCLPVPSVGLTRILPHLYGSKQDVANKDMQNGISYVLNLSNSGCPKDFICEBRF 60

QY 207 LRVPNVDSFCEKILPWLKSVDFIEKAKASNGCVLVHCLAGISRSATTAIAIYIMKRMDS 266

Db 61 MRVPINDNYCEKILPWLKSTIEFDIKALSSCOVIVHCLAGISRSATTAIAIYIMKTMGS 120

QY 267 IDEAYRFVKEKRPITSPNPNFLGQLLDYEKKIK 299

Db 121 SDDAYRFVXDRRPSISPNFNFLGQLLEVERTLK 153

RESULT 8
US-09-557-921-2
Sequence 2, Application US/09557921
Patent No. 6551810
GENERAL INFORMATION:
APPLICANT: Lucbe, Ralf M.
APPLICANT: Wei, Bo
TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.416
CURRENT APPLICATION NUMBER: US/09/557,921
CURRENT FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 482
TYPE: PRT
ORGANISM: Homo sapiens
US-09-557-921-2

Query Match 30.0%; Score 469; DB 4; Length 482;
Best Local Similarity 35.9%; Pred. No. 1.4e-42;
Matches 107; Conservative 65; Mismatches 96; Indels 30; Gaps 7;

QY 27 LLIDSRPREVYNTSHILEAININGS-KMKRLQODKYLITIELLO-HSAKHVNDIDCQK 84

Db 173 VIIDCRPMEYKSHIIGAFAHINCAKISRRLQGGITVLDLISCREGKOSFKRIFSK 232

QY 85 VVVYDOSQDVASLSDCFLTVLGLKLEKSFNSVYLAGFAEFGRCPGLCEGK----- 139

Db 223 IIVVDENINERSRWPSPLHIVLESLEKREKEPVVLGGLSFFQNHENLCDNSLOOE 292

QY 140 -----STLVPTCISQPCLP-VANIGPTRILPNLYGCGQDVANKELIQONGIGY 187

Db 293 CREVGGSASASLIPQPI-PTTPDIENAEITPILPFLIGNEDDAQDLDPTMGRNLIGY 350

QY 188 VLANS-----YTCPPKDFIPESHFLRVPNVDSFCEKILPWLKSVDFIEKAKASNGCVLV 242

Db 351 VINVTTLPLVHYEGLP---NYKRLPATDSNNKQNLQYFEAEFEFBEAHQCCGKGLI 406

QY 243 HCLAGISRSATTAIAIYIMKRMDSLDEAYRFVKEKRPITSPNPNFLGQLLDYEKKIK 300

Db 407 HCGAGVRSATIVAIYIMKTRMTWTDAYKFKGRPIISPLNFMGQLLEFEEDLN 464

RESULT 9
US-09-949-016-8486
Sequence 8486, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C0001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768

Query Match 39.6%; Score 619; DB 4; Length 155;
Best Local Similarity 73.9%; Pred. No. 9.3e-60;

;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for windows Version 4.0
;; SEQ ID NO 8486
;; LENGTH: 491
;; TYPE: PRF
;; ORGANISM: Human
US-09-949-016-8486

Query Match 29.8%; Score 466.5; DB 4; Length 491;
Best Local Similarity 34.1%; Pred. No. 2.7e-42;
Matches 110; Conservative 63; Mismatches 105; Indels 45; Gaps 7;

QY 19 LESGTEKVLIDSRPVEVNTSHILEAININCSKLMKRLQODKVLITELIOHSA-KKHV 77
DB 137 LELGNERLLIMCRPOELYESHISAIWVAIPGIMRLQKGNLPVRLFTRGEDRDRF 196
QY 78 DIDC-SQKVVVYDQSSOD-VASISDCEFLTVLLGKLEKSPNSVHLLAGFAEFSRCFPG 135
DB 197 TRCGTDTVLLDESSDMNNTGGESVGLLKKLBKCGCAFYLEGGFSKFOAEFSLH 256
QY 136 CEGKSTLVPTC-ISQPCLFVANIG----- 158
DB 257 CE--TNLDGSCSSSPFLVGLIGLRISDSSSDIESDLDPRDPSATDSDGSPLSNQP 314
QY 159 --PTILPVLVYGCORVNLKELIONGIGVYLNASTYCPKP-DPIPSHFARVVDNSF 215
DB 315 SPFVLLPPLVYGCADSTNLDVLESPGKTYLNTVPLNPLFENAGKFKYQITISDH 374
QY 216 CEKILPWLKSVDFTEKAKANGCVLVHCLAGISSATIAIAYIMKMDMSLDEAYRPFV 275
DB 375 SQNLQFPPEALSPIDEARGKNCGVLVHCLAGISSATVTVAYVLMQKLNLSNDAVDIVK 434
QY 276 EKRPITSPFNFLGQLLDYEKKI 298
DB 435 MKKSNISPFNFMQLDLPFERTL 457

RESULT 10
US-09-371-671B-11
;; Sequence 11, Application US/09371671B
;; Patent No. 6548743
;; GENERAL INFORMATION:
;; APPLICANT: Sheen, Jen
;; APPLICANT: Chiu, Man-ling
;; TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING A
;; FILE REFERENCE: 00786/370002
;; CURRENT APPLICATION NUMBER: US/09/371,671B
;; PRIOR FILING DATE: 1999-08-10
;; PRIOR APPLICATION NUMBER: 60/155,934
;; PRIOR FILING DATE: 1999-01-14
;; PRIOR APPLICATION NUMBER: 60/095,938
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: FastSeq for windows Version 4.0
;; SEQ ID NO 11
;; LENGTH: 314
;; TYPE: PRF
;; ORGANISM: Mus musculus
US-09-371-671B-11

Query Match 27.2%; Score 425; DB 4; Length 314;
Best Local Similarity 34.3%; Pred. No. 5e-36;
Matches 104; Conservative 48; Mismatches 129; Indels 22; Gaps 5;

QY 15 LVALLSSTKVLIDSRPVEVNTSHILEAININCSKLMKRLQODKVLITELIOHSAK 74
DB 13 LRALLRGAACULLDCRSFFAFNAGHAGSVNVRFSIVRRRAKMGLEHIVPNAELR 72
QY 75 HKVDIDSQKVVVYDQSSQDVASISSDCFLTLLGKL--EKSFNSVHLLAGFAEFSRCF 132

DB 73 GRLLAGYHAVVLLDESSASLDGAKRDOGTLLAAGALCREARSTQVFFLQGGYAFASASC 132
QY 133 PGLCEGKSTLVPTCISQP-----CLPVANI-----GPTRIPLPNLYLCCQCDVL 175
DB 133 PELCSKOST--PTGISLPLSTSVDPDSAESGSSCSTPLVDQGVLEILSFYLSAYHAS 190
QY 176 NKEILQONGIGVYNASTYCPKPDPIPSHFLRVVNDSPCEKILPWLKSVDFTEKAKA 235
DB 191 RKMDLMDLGITALLINVSANCPN-HFEGHYQYKSLPVEDNHNKADISSWFNEALDPTIDGKD 249
QY 236 SNGCVLVHCLAGISSATIAIAYIMKMDMSLDEAYRPFVEKRPITSPNENFLGQLDYE 295
DB 250 AGRVFVHCAQAGISRSATICIAIYIMRTNRVCLDEAFEFVQRRSIISPNSFMGQLQFE 309
QY 296 KKI 298
DB 310 SQV 312

RESULT 11
US-08-990-379-6
;; Sequence 6, Application US/08990379
;; Patent No. 5998188
;; GENERAL INFORMATION:
;; APPLICANT: Stork, Philip J
;; APPLICANT: Miska-Press, Anita
;; TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase cDNAs and
;; FILE REFERENCE: 4104-0003220SA
;; CURRENT APPLICATION NUMBER: US/08/990,379
;; PRIOR FILING DATE: 1997-12-15
;; EARLIER APPLICATION NUMBER: PCT/US96/10402
;; EARLIER FILING DATE: 1996-06-14
;; EARLIER APPLICATION NUMBER: 60/000,263
;; EARLIER FILING DATE: 1995-06-16
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 6
;; LENGTH: 367
;; TYPE: PRF
;; ORGANISM: Mus sp.
US-08-990-379-6

Query Match 27.2%; Score 425; DB 2; Length 367;
Best Local Similarity 34.3%; Pred. No. 6.3e-38;
Matches 104; Conservative 48; Mismatches 129; Indels 22; Gaps 5;

QY 15 LVALLSSTKVLIDSRPVEVNTSHILEAININCSKLMKRLQODKVLITELIOHSAK 74
DB 13 LRALLRGAACULLDCRSFFAFNAGHAGSVNVRFSIVRRRAKMGLEHIVPNAELR 72
QY 75 HKVDIDSQKVVVYDQSSQDVASISSDCFLTLLGKL--EKSFNSVHLLAGFAEFSRCF 132
DB 73 GRLLAGYHAVVLLDESSASLDGAKRDOGTLLAAGALCREARSTQVFFLQGGYAFASASC 132
QY 133 PGLCEGKSTLVPTCISQP-----CLPVANI-----GPTRIPLPNLYLCCQCDVL 175
DB 133 PELCSKOST--PTGISLPLSTSVDPDSAESGSSCSTPLVDQGVLEILSFYLSAYHAS 190
QY 176 NKEILQONGIGVYNASTYCPKPDPIPSHFLRVVNDSPCEKILPWLKSVDFTEKAKA 235
DB 191 RKMDLMDLGITALLINVSANCPN-HFEGHYQYKSLPVEDNHNKADISSWFNEALDPTIDGKD 249
QY 236 SNGCVLVHCLAGISSATIAIAYIMKMDMSLDEAYRPFVEKRPITSPNENFLGQLDYE 295
DB 250 AGRVFVHCAQAGISRSATICIAIYIMRTNRVCLDEAFEFVQRRSIISPNSFMGQLQFE 309
QY 296 KKI 298
DB 310 SQV 312

```

12 RESULT 12
13 US-08-530-290-23
14 : Sequence 23, Application US/08530290
15 : Patent No. 5958721
16 : GENERAL INFORMATION:
17 : APPLICANT: Marshall, Christopher John
18 : APPLICANT: Ashworth, Alan
19 : APPLICANT: Hughes, David Anthony
20 : TITLE OF INVENTION: Methods for Screening of Substances for
21 : TITLE OF INVENTION: Therapeutic Activity and Yeast for Use Therein
22 : NUMBER OF SEQUENCES: 24
23 : CORRESPONDENCE ADDRESS:
24 : ADDRESSEE: Townsend and Townsend and Crew LLP
25 : STREET: Two Embarcadero Center, Eighth Floor
26 : CITY: San Francisco
27 : STATE: California
28 : COUNTRY: USA
29 : ZIP: 94111-3834
30 : COMPUTER READABLE FORM:
31 : MEDIUM TYPE: Floppy disk
32 : COMPUTER: IBM PC compatible
33 : OPERATING SYSTEM: PC-DOS/MS-DOS
34 : SOFTWARE: Patent Release #1.0, Version #1.30
35 : CURRENT APPLICATION DATA:
36 : APPLICATION NUMBER: US/08/530,290
37 : FILING DATE: 14-DEC-1995
38 : CLASSIFICATION: 435
39 : PRIOR APPLICATION DATA:
40 : APPLICATION NUMBER: WO PCT/GB94/00694
41 : FILING DATE: 31-MAR-1994
42 : PRIOR APPLICATION DATA:
43 : APPLICATION NUMBER: GB 9402573.1
44 : FILING DATE: 10-FEB-1994
45 : PRIOR APPLICATION DATA:
46 : APPLICATION NUMBER: GB 9307250.2
47 : FILING DATE: 07-APR-1993
48 : ATTORNEY/AGENT INFORMATION:
49 : NAME: Baetian, Kevin L.
50 : REGISTRATION NUMBER: 34, 774
51 : REFERENCE/DOCKET NUMBER: 084611-000000US
52 : TELECOMMUNICATION INFORMATION:
53 : TELEPHONE: (415) 576-0200
54 : TELEFAX: (415) 576-0300
55 : INFORMATION FOR SEQ ID NO: 23:
56 : SEQUENCE CHARACTERISTICS:
57 : LENGTH: 394 amino acids
58 : TYPE: amino acid
59 : STRANDEDNESS:
60 : TOPOLOGY: linear
61 : MOLECULE TYPE: peptide
62 : US-08-530-290-23
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[illegible]

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? CURRENT APPLICATION NUMBER: US/09/702,705
? CURRENT FILING DATE: 2000-10-30
? NUMBER OF SEQ ID NOS: 1833
? SOFTWARE: FastSeq Version 3.0
? SEQ ID NO 827
? LENGTH: 394
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-702-705-827

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Query Match	27.2%;	Score 425;	DB 4;	Length 394;
Best Local Similarity	33.4%;	Pred. No. 7e-38;		
Matches 100;	Conservative 64;	Mismatches 113;	Indels 22;	Gaps 9

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Qy 77 VVIDCQKVVYVYDQSDVAISSLDFCLTVLIGLKEKF--NSVHLAAGFAEFSRCPFG 134
Db 39 LPBG-KDCLLDORPFLAHSAQITIGSVAVRCNTIVRR-AKGSVLEQLIPAEVVRAR 96

Qy 19 LBSGTKEVLLISRPVEVNTSHILEAININSKIMKRRLOODKYLITELL--OHSAKHK 76
Db 39 LPBG-KDCLLDORPFLAHSAQITIGSVAVRCNTIVRR-AKGSVLEQLIPAEVVRAR 96

Qy 97 LBSGLVSAIVYDERBPRAESLRBDSVTSLVQALRRNAERTDCLLKGVERFSSSEYPR 156
Db 97 LBSGLVSAIVYDERBPRAESLRBDSVTSLVQALRRNAERTDCLLKGVERFSSSEYPR 156

Qy 135 LCEGKSTL-----VETCISOP-----C-LPVANI-GPRRTILPNLYLGGQBDVLMKEL 179
Db 157 FCGKTKALAIIPRPVPSRTEFLDGCSCCGPRLHDQGPVEILPFLYLSAHTAARDM 216

Qy 180 IQONGIGVYIANSYTCPKPDPFLPESHPLRVPNVDSFCEKILPWLDRKVSDFTEKKAANGC 239
Db 217 LDALGITALLNVSDDCPN-HFEGAHYQYKCIPEVDNHHKADISSMPEALEYIDAVKDCGR 275

Qy 240 VLVHICLAGISRSATTLAIYIMKRMDSIDEARPTKEKRPITISPNFNLOGLDYEKKI 298
Db 276 VLVHICAGISRSATTCILAYIMKKRVKRLAEARFQKORRSITISPNFSMGOLLOFESOV 334

```

RESULT 15
US-09-736-457-805

```

GENERAL INFORMATION:
APPLICANT: Mang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Iodee, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Dartrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Pan, Liqun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 805
LENGTH: 394
TYPE: PRT
ORGANISM: Homo sapiens
IS-09-736-457-805

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Query Match	27.2%;	Score 425;	DB 4;	Length 394;
Best Local Similarity	33.1%;	Pred. No. 7e-38;		
Matches 99;	Conservative 62;	Mismatches 116;	Indels 22;	Gaps 8;

QY 19 LBSGTEKVLVILSRPVEVNTSHILEAININOSKLMKRRLQQDKYLIEL--QHSAKH 76
Db 39 LPBG-KCILLDCRPPLASHAGYILIGSVNRCNTIVRR--AKGSVDLEQIIPAEEVRR 96
QY 77 VPIDSQKVNVYDSSQDVASLSDPCFLTVLLGLKEFSF--NSVHLLAGGAPEFSRCPFG 134

Db 97 LRGLSAVIYVDESRPAESLRBDSTVSLVWQLRRNAERTDCLLKGTERFSSBPE 156

Qy 135 LRGKSTL-----VPTCLSDP---CLPVA-----NIGPRLLIPNLYLGCQDVLANKEL 179

Db 157 FCSKTRALAIIPPPSPATEBLDLDSCSCGPTLHDGEPYELIPFLYLSAAHARRDM 216

Qy 180 IQONGGYVLNASTYCPKRPDIRESHFLRYAVVNDSPFCKLLPMLDKSVDPTRKAKSNGC 239

Db 217 LDALGITALLNASSDCPN-HFEGHYQXCIPIVEENHKRADLSWMEMAEIYIDAVKORRG 275

Qy 240 VLTVHCLAGISRGATTAIVYIMKRDMSLDEAYRFLVKEKRPITISPNFPLQLLDYEKKI 298

Db 276 VLTVHCGAGISRGATTCIYILMMKRVRLVEEFLVEYKCRKSTISDPSFMQLQLQFSQV 334

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Search completed: February 9, 2005, 12:13:09
Job time : 20.363 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2005, 12:09:54 ; Search time 57.152 Seconds
(without alignments)
1721.062 Million cell updates/sec

Title: US-10-029-345a-109_COPY_1_302
Perfect score: 1564
Sequence: 1 MAHEMIGQIVTERLVALL.....PNNFLGLLDYEKKIKNGT 302

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1552	99.2	662	15	US-10-072-012-258
2	1552	99.2	665	9	US-09-816-494-2
3	1552	99.2	665	9	US-09-964-277-2
4	1552	99.2	665	15	US-10-377-072-26
5	1552	99.2	665	15	US-10-072-012-660
6	1552	99.2	665	15	US-10-168-506-14
7	1552	99.2	665	15	US-10-343-357-7
8	1552	99.2	665	15	US-10-257-026-2
9	1552	99.2	665	16	US-10-648-593-240
10	1552	99.2	665	16	US-10-648-593-247
11	1552	99.2	665	16	US-10-377-072-26
12	1552	99.2	690	15	US-10-072-012-679
13	1552	99.2	690	15	US-10-072-012-703

14	1552	99.2	690	15	US-10-425-114-54204	Sequence 54204, A
15	1545	98.8	665	15	US-10-094-749-2312	Sequence 2312, Ap
16	1545	98.8	665	15	US-10-072-012-681	Sequence 681, App
17	1544	98.7	672	15	US-10-296-115-1259	Sequence 1259, Ap
18	1517	97.0	660	15	US-10-072-012-682	Sequence 682, App
19	1514	96.8	677	15	US-10-072-012-683	Sequence 683, App
20	1504.5	96.2	680	15	US-10-072-012-256	Sequence 256, App
21	988	63.2	625	15	US-10-072-012-699	Sequence 699, App
22	985	63.0	663	15	US-10-072-012-700	Sequence 700, App
23	837	53.5	616	15	US-10-072-012-266	Sequence 266, App
24	807	51.6	155	9	US-09-964-277-7	Sequence 7, Appl
25	654.5	41.8	169	14	US-10-346-356-15	Sequence 15, Appl
26	654.5	41.8	170	9	US-09-775-925-26	Sequence 26, Appl
27	654.5	41.8	170	9	US-09-847-519A-11	Sequence 11, Appl
28	654.5	41.8	170	14	US-10-314-058-14	Sequence 14, Appl
29	654.5	41.8	170	14	US-10-405-808-16	Sequence 16, Appl
30	654.5	41.8	170	15	US-10-655-073-16	Sequence 16, Appl
31	646	41.3	517	9	US-09-964-277-21	Sequence 21, Appl
32	631.5	40.4	461	15	US-10-072-012-701	Sequence 701, App
33	620	39.6	501	15	US-10-072-012-702	Sequence 702, App
34	619	39.6	155	9	US-09-964-277-6	Sequence 6, Appl
35	619	39.6	155	9	US-09-955-732-6	Sequence 6, Appl
36	566	36.2	140	17	US-10-803-738-12	Sequence 12, Appl
37	469	30.0	444	9	US-09-964-899-47	Sequence 47, Appl
38	469	30.0	482	14	US-10-346-356-2	Sequence 2, Appl
39	469	30.0	482	15	US-10-058-270A-130	Sequence 130, App
40	469	30.0	482	16	US-10-648-593-164	Sequence 164, App
41	462.5	29.6	381	14	US-10-184-832-2	Sequence 2, Appl
42	440.5	28.2	419	16	US-10-472-380-2	Sequence 25, Appl
43	426	27.2	394	14	US-10-060-065-25	Sequence 46, Appl
44	426	27.2	394	14	US-10-059-585-46	Sequence 805, App
45	425	27.2	394	9	US-09-736-457-805	

ALIGNMENTS

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RESULT 1
US-10-072-012-258
; Sequence 258, Application US/10072012
; Publication No. US2004003493A1
; GENERAL INFORMATION:
; APPLICANT: Tehernev, Velizar
; APPLICANT: Spyrek, Kimberly
; APPLICANT: Zernusen, Bryan
; APPLICANT: Patnrajjan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangoli, Baha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Groesse, William M.
; APPLICANT: Alabrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
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/ PRIOR APPLICATION NUMBER: 60/265,517
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,412
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,395
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/266,406
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 60/266,767
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: 60/267,057
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/266,975
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/267,459
/ PRIOR FILING DATE: 2001-02-08
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 258
/ LENGTH: 662
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-072-012-258
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Query Match          99.2%; Score 1552; DB 15; Length 662;
Best Local Similarity 99.3%; Pred. No. 2,1e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MAHEMIGTOIVTERLVALLBSGTEKVLIDSRPFVEYNTSHLEAININCSKLMKRRLOQ 60
DB 1 MAHEMIGTOIVTERLVALLBSGTEKVLIDSRPFVEYNTSHLEAININCSKLMKRRLOQ 60
QY 61 DKVLITELIHSKAKHVDIDCSQKVVVYDQSSQDVASLSDCFLTVLLGKLEKSFNSVHL 120
DB 61 DKVLITELIHSKAKHVDIDCSQKVVVYDQSSQDVASLSDCFLTVLLGKLEKSFNSVHL 120
QY 121 LAGFAFBSRCFPGLCGKSTLVPTCISQPCLPVANIIGPTRIIPNLVYGQORDVANKELI 180
DB 121 LAGFAFBSRCFPGLCGKSTLVPTCISQPCLPVANIIGPTRIIPNLVYGQORDVANKELI 180
QY 181 QONGIGYVLNASYTCPEKDPFIPESHFLRVPNVDSFCEKILPMLDKSVDFIEKAKASNGCV 240
DB 181 QONGIGYVLNASYTCPEKDPFIPESHFLRVPNVDSFCEKILPMLDKSVDFIEKAKASNGCV 240
QY 241 LVHCLAGISRSATTAIAYIMKRMDSLDEAYRFVYKERTISPNNFLGQLLDYEKKIKN 300
DB 241 LVHCLAGISRSATTAIAYIMKRMDSLDEAYRFVYKERTISPNNFLGQLLDYEKKIKN 300
QY 301 QT 302
DB 301 QT 302

RESULT 2
US-09-816-494-2
/ Sequence 2, Application US/09816494
/ Patent No. US20020034807A1
/ GENERAL INFORMATION:
/ APPLICANT: Meyers, Rachel A.
/ TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
/ FILE REFERENCE: 10448-030002
/ CURRENT APPLICATION NUMBER: US/09/816,494
/ PRIOR FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: US 60/191,858
/ PRIOR FILING DATE: 2000-03-24
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 665
/ TYPE: PRT
/ ORGANISM: Homo sapiens
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US-09-816-494-2

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Query Match          99.2%; Score 1552; DB 9; Length 665;
Best Local Similarity 99.3%; Pred. No. 2,2e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MAHEMIGTOIVTERLVALLBSGTEKVLIDSRPFVEYNTSHLEAININCSKLMKRRLOQ 60
DB 1 MAHEMIGTOIVTERLVALLBSGTEKVLIDSRPFVEYNTSHLEAININCSKLMKRRLOQ 60
QY 61 DKVLITELIHSKAKHVDIDCSQKVVVYDQSSQDVASLSDCFLTVLLGKLEKSFNSVHL 120
DB 61 DKVLITELIHSKAKHVDIDCSQKVVVYDQSSQDVASLSDCFLTVLLGKLEKSFNSVHL 120
QY 121 LAGFAFBSRCFPGLCGKSTLVPTCISQPCLPVANIIGPTRIIPNLVYGQORDVANKELI 180
DB 121 LAGFAFBSRCFPGLCGKSTLVPTCISQPCLPVANIIGPTRIIPNLVYGQORDVANKELI 180
QY 181 QONGIGYVLNASYTCPEKDPFIPESHFLRVPNVDSFCEKILPMLDKSVDFIEKAKASNGCV 240
DB 181 QONGIGYVLNASYTCPEKDPFIPESHFLRVPNVDSFCEKILPMLDKSVDFIEKAKASNGCV 240
QY 241 LVHCLAGISRSATTAIAYIMKRMDSLDEAYRFVYKERTISPNNFLGQLLDYEKKIKN 300
DB 241 LVHCLAGISRSATTAIAYIMKRMDSLDEAYRFVYKERTISPNNFLGQLLDYEKKIKN 300
QY 301 QT 302
DB 301 QT 302

RESULT 3
US-09-964-277-2
/ Sequence 2, Application US/09964277
/ Patent No. US20020137170A1
/ GENERAL INFORMATION:
/ APPLICANT: Luche, Ralf M.
/ TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
/ FILE REFERENCE: 200125,434
/ CURRENT APPLICATION NUMBER: US/09/964,277
/ PRIOR FILING DATE: 2001-09-25
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 665
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-964-277-2
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```
Query Match          99.2%; Score 1552; DB 9; Length 665;
Best Local Similarity 99.3%; Pred. No. 2,2e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 MAHEMIGTOIVTERLVALLBSGTEKVLIDSRPFVEYNTSHLEAININCSKLMKRRLOQ 60
DB 1 MAHEMIGTOIVTERLVALLBSGTEKVLIDSRPFVEYNTSHLEAININCSKLMKRRLOQ 60
QY 61 DKVLITELIHSKAKHVDIDCSQKVVVYDQSSQDVASLSDCFLTVLLGKLEKSFNSVHL 120
DB 61 DKVLITELIHSKAKHVDIDCSQKVVVYDQSSQDVASLSDCFLTVLLGKLEKSFNSVHL 120
QY 121 LAGFAFBSRCFPGLCGKSTLVPTCISQPCLPVANIIGPTRIIPNLVYGQORDVANKELI 180
DB 121 LAGFAFBSRCFPGLCGKSTLVPTCISQPCLPVANIIGPTRIIPNLVYGQORDVANKELI 180
QY 181 QONGIGYVLNASYTCPEKDPFIPESHFLRVPNVDSFCEKILPMLDKSVDFIEKAKASNGCV 240
DB 181 QONGIGYVLNASYTCPEKDPFIPESHFLRVPNVDSFCEKILPMLDKSVDFIEKAKASNGCV 240
QY 241 LVHCLAGISRSATTAIAYIMKRMDSLDEAYRFVYKERTISPNNFLGQLLDYEKKIKN 300
DB 241 LVHCLAGISRSATTAIAYIMKRMDSLDEAYRFVYKERTISPNNFLGQLLDYEKKIKN 300
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QY 301 QT 302
Db 301 QT 302

RESULT 4
US-10-377-072-26
Sequence 26, Application US/10377072
Publication No. US2004009501A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals Inc.
APPLICANT: Curtis, Rony A.J.
APPLICANT: Logan, Thomas Joseph
APPLICANT: Glucksmann, Maria A.
APPLICANT: Meyers, Rachel E.
APPLICANT: Williamson, Mark J.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Tsai, Peng-Ying
TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117
TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
FILE REFERENCE: MP103-0180KNIM
CURRENT APPLICATION NUMBER: US/10/377, 072
PRIOR FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US 09/895, 860
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215, 370
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/723, 806
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/187, 455
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/843, 297
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199, 801
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: US 09/861, 801
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205, 508
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/816, 494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/815, 419
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 665
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-377-072-26

Query Match 99.2%; Score 1552; DB 15; Length 665;
Best Local Similarity 99.3%; Pred. No. 2, 2e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAHEMGTOTVTRVALLESGETEKLLIDSRFEVNTSHLEAININCKLMKRRLQ 60
Db 1 MAHEMGTOTVTRVALLESGETEKLLIDSRFEVNTSHLEAININCKLMKRRLQ 60

QY 61 DKVLITELIQHSKHKVDIDSCQKVVVVYQSSQDVASLSSDCEFLTVLLKLEKSFNSVH 120
Db 61 DKVLITELIQHSKHKVDIDSCQKVVVVYQSSQDVASLSSDCEFLTVLLKLEKSFNSVH 120

QY 121 LAGGFAPRCRPGCLCEGSTVPTCTISQPCPLPVANIGPRILPNLYLCOQDVINKEL 180
Db 121 LAGGFAPRCRPGCLCEGSTVPTCTISQPCPLPVANIGPRILPNLYLCOQDVINKEL 180

QY 181 QONGIGVYVNASATCPKPDPIPESHFLRPVNDSPCEKILPMLDKSVDFIEKAKASNGCV 240
Db 181 QONGIGVYVNASATCPKPDPIPESHFLRPVNDSPCEKILPMLDKSVDFIEKAKASNGCV 240

Db 181 QONGIGVYVNASATCPKPDPIPESHFLRPVNDSPCEKILPMLDKSVDFIEKAKASNGCV 240
QY 241 LVHCLAGTSRSATIAIAYMKRMDSLDEAYRFVKEKRPRTISPNEFLGQLLDYEKKIN 300
Db 241 LVHCLAGTSRSATIAIAYMKRMDSLDEAYRFVKEKRPRTISPNEFLGQLLDYEKKIN 300

QY 301 QT 302
Db 301 QT 302

RESULT 5
US-10-072-012-680
Sequence 680, Application US/10072012
Publication No. US2004003493A1
GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zehnusen, Bryan
APPLICANT: Patnursajan, Meera
APPLICANT: Shinkets, Richard
APPLICANT: Li, Li
APPLICANT: Gangolli, Esba
APPLICANT: Padigaru, Muralidhara
APPLICANT: Anderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie
APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Coleman, Steven D.
APPLICANT: Molenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosee, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072, 012
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265, 102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265, 514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265, 517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265, 412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265, 395
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266, 406
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266, 767
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267, 057
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266, 975
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267, 459
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: Patencin Ver. 2.1
SEQ ID NO 680
LENGTH: 665
TYPE: PRT
ORGANISM: Homo sapiens
US-10-072-012-680

Query Match 99.2%; Score 1552; DB 15; Length 665;

Best Local Similarity 99.3%; Pred. No. 2.2e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MAHEMIGTQVTERLVALLSGETEKLIDSRPVEVNTSHILEAININCSKLMKRLQ 60
DB 1 MAHEMIGTQVTERLVALLSGETEKLIDSRPVEVNTSHILEAININCSKLMKRLQ 60
QY 61 DKVLITELIHSAXKHVDIDCSQKVYVYDSSQDVASLSDDCFITVLGLGKLEKSFNSVHL 120
DB 61 DKVLITELIHSAXKHVDIDCSQKVYVYDSSQDVASLSDDCFITVLGLGKLEKSFNSVHL 120
QY 121 LAGFAFRSFCFPGLCGKSTLVPTCISQPCLPVANIGPTRILPNIYLGCQRDVANKELI 180
DB 121 LAGFAFRSFCFPGLCGKSTLVPTCISQPCLPVANIGPTRILPNIYLGCQRDVANKELI 180
QY 181 QONGIGVYVNASYTCPPKDPFIPESHFLRPVNDSPFCKILPWLDKSVDFIEKAKANGCV 240
DB 181 QONGIGVYVNASYTCPPKDPFIPESHFLRPVNDSPFCKILPWLDKSVDFIEKAKANGCV 240
QY 241 LVHCLAGISRSATIAIAYIMKRMDSLDEAYRFVKEKRPISPNFPLGQLDYEKKIKN 300
DB 241 LVHCLAGISRSATIAIAYIMKRMDSLDEAYRFVKEKRPISPNFPLGQLDYEKKIKN 300
QY 301 QT 302
DB 301 QT 302
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RESULT 6

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US-10-168-506-14
; Sequence 14, Application US/10168506
; Publication No. US20040053229A1
; GENERAL INFORMATION:
; APPLICANT: PLOMMAN, GREGORY D.
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHITE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; APPLICANT: HILL, RON
; APPLICANT: FLANNAGAN, PETER
; TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
; FILE REFERENCE: 038602/1351
; CURRENT APPLICATION NUMBER: US/10/168,506
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: PCT/US00/34736
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-506-14
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Query Match 99.2%; Score 1552; DB 15; Length 665;
Best Local Similarity 99.3%; Pred. No. 2.2e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MAHEMIGTQVTERLVALLSGETEKLIDSRPVEVNTSHILEAININCSKLMKRLQ 60
DB 1 MAHEMIGTQVTERLVALLSGETEKLIDSRPVEVNTSHILEAININCSKLMKRLQ 60
QY 61 DKVLITELIHSAXKHVDIDCSQKVYVYDSSQDVASLSDDCFITVLGLGKLEKSFNSVHL 120
DB 61 DKVLITELIHSAXKHVDIDCSQKVYVYDSSQDVASLSDDCFITVLGLGKLEKSFNSVHL 120
QY 121 LAGFAFRSFCFPGLCGKSTLVPTCISQPCLPVANIGPTRILPNIYLGCQRDVANKELI 180
DB 121 LAGFAFRSFCFPGLCGKSTLVPTCISQPCLPVANIGPTRILPNIYLGCQRDVANKELI 180
QY 181 QONGIGVYVNASYTCPPKDPFIPESHFLRPVNDSPFCKILPWLDKSVDFIEKAKANGCV 240
DB 181 QONGIGVYVNASYTCPPKDPFIPESHFLRPVNDSPFCKILPWLDKSVDFIEKAKANGCV 240
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QY 241 LVHCLAGISRSATIAIAYIMKRMDSLDEAYRFVKEKRPISPNFPLGQLDYEKKIKN 300
DB 241 LVHCLAGISRSATIAIAYIMKRMDSLDEAYRFVKEKRPISPNFPLGQLDYEKKIKN 300
QY 301 QT 302
DB 301 QT 302
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RESULT 7

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US-10-343-357-7
; Sequence 7, Application US/10343357
; Publication No. US20040058341A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom
; APPLICANT: ELIOTT, Vicki S.; RAMKUMAR, Jayalaxmi
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: WANG, Yumei E.; STEWART, Elizabeth A.
; APPLICANT: GANDHI, Ameena R.; ARVIZU, Chandra S.
; APPLICANT: LEE, Ernestine A.; HARALIA, April J.A.
; APPLICANT: LU, Dying Aina M.; TRIBOUTY, Catherine M.
; APPLICANT: GRIFFIN, Jennifer A.; BAUGHN, Mariah R.
; APPLICANT: YUE, Henry; WARREN, Bridget A.
; APPLICANT: NGUYEN, Daniel B.; CHAMLA, Narinder K.
; APPLICANT: KEARNEY, Liam
; TITLE OF INVENTION: PROTEIN PHOSPHATASES
; FILE REFERENCE: PI-0173 PCT
; CURRENT APPLICATION NUMBER: US/10/343,357
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: PCT/US01/23716
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 60/221,679
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/223,272
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/224,309
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 60/226,728
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/229,254
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: US 60/231,366
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040058341A1 7480570CD1
US-10-343-357-7
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Query Match 99.2%; Score 1552; DB 15; Length 665;
Best Local Similarity 99.3%; Pred. No. 2.2e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MAHEMIGTQVTERLVALLSGETEKLIDSRPVEVNTSHILEAININCSKLMKRLQ 60
DB 1 MAHEMIGTQVTERLVALLSGETEKLIDSRPVEVNTSHILEAININCSKLMKRLQ 60
QY 61 DKVLITELIHSAXKHVDIDCSQKVYVYDSSQDVASLSDDCFITVLGLGKLEKSFNSVHL 120
DB 61 DKVLITELIHSAXKHVDIDCSQKVYVYDSSQDVASLSDDCFITVLGLGKLEKSFNSVHL 120
QY 121 LAGFAFRSFCFPGLCGKSTLVPTCISQPCLPVANIGPTRILPNIYLGCQRDVANKELI 180
DB 121 LAGFAFRSFCFPGLCGKSTLVPTCISQPCLPVANIGPTRILPNIYLGCQRDVANKELI 180
QY 181 QONGIGVYVNASYTCPPKDPFIPESHFLRPVNDSPFCKILPWLDKSVDFIEKAKANGCV 240
DB 181 QONGIGVYVNASYTCPPKDPFIPESHFLRPVNDSPFCKILPWLDKSVDFIEKAKANGCV 240
```

```
Db      181 QONGIGYVLAASNTCPKDPFIPESHFLRVVNDSPCEKILPWLDSVDFIERAKASNGCV 240
Qy      241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPPTISPNFPGQLLDYEKKIN 300
Db      241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPPTISPNFPGQLLDYEKKIN 300
Qy      301 QT 302
        ||
Db      301 QT 302

RESULT 8
US-10-257-026-2
; Sequence 2, Application US/10257026
; Publication No. US20040086859A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: New dual specificity phosphatase
; FILE REFERENCE: DUSP10KDM5
; CURRENT APPLICATION NUMBER: US/10/257,026
; CURRENT FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-257-026-2

Query Match      99.2%; Score 1552; DB 15; Length 665;
Best Local Similarity 99.3%; Pred. No. 2.2e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MAHEMIGTQIVTERLVALLSEGTSEKVLIDSRPFVYNTSHLEAININCSKLMKRRLQ 60
        |||
Db      1 MAHEMIGTQIVTERLVALLSEGTSEKVLIDSRPFVYNTSHLEAININCSKLMKRRLQ 60

Qy      61 DKVLITELIQHSAKHKVIDCSQKVVYDQSSQDVASLSDCFITVLGKLEKSFNSVHL 120
        |||
Db      61 DKVLITELIQHSAKHKVIDCSQKVVYDQSSQDVASLSDCFITVLGKLEKSFNSVHL 120

Qy      121 LAGFAEFSRCPGGLCEGKSTLVPTCISQPCLPVANIGPTRILPMLYLGCQRDVANKELI 180
        |||
Db      121 LAGFAEFSRCPGGLCEGKSTLVPTCISQPCLPVANIGPTRILPMLYLGCQRDVANKELI 180

Qy      121 LAGFAEFSRCPGGLCEGKSTLVPTCISQPCLPVANIGPTRILPMLYLGCQRDVANKELI 180
        |||
Db      121 LAGFAEFSRCPGGLCEGKSTLVPTCISQPCLPVANIGPTRILPMLYLGCQRDVANKELI 180

Qy      181 QONGIGYVLAASNTCPKDPFIPESHFLRVVNDSPCEKILPWLDSVDFIERAKASNGCV 240
        |||
Db      181 QONGIGYVLAASNTCPKDPFIPESHFLRVVNDSPCEKILPWLDSVDFIERAKASNGCV 240

Qy      241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPPTISPNFPGQLLDYEKKIN 300
        |||
Db      241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPPTISPNFPGQLLDYEKKIN 300

Qy      301 QT 302
        ||
Db      301 QT 302

RESULT 9
US-10-648-593-240
; Sequence 240, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
```

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; SOFTWARE: Patentin version 3.2
; SEQ ID NO 240
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-593-240

Query Match      99.2%; Score 1552; DB 16; Length 665;
Best Local Similarity 99.3%; Pred. No. 2.2e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MAHEMIGTQIVTERLVALLSEGTSEKVLIDSRPFVYNTSHLEAININCSKLMKRRLQ 60
        |||
Db      1 MAHEMIGTQIVTERLVALLSEGTSEKVLIDSRPFVYNTSHLEAININCSKLMKRRLQ 60

Qy      61 DKVLITELIQHSAKHKVIDCSQKVVYDQSSQDVASLSDCFITVLGKLEKSFNSVHL 120
        |||
Db      61 DKVLITELIQHSAKHKVIDCSQKVVYDQSSQDVASLSDCFITVLGKLEKSFNSVHL 120

Qy      121 LAGFAEFSRCPGGLCEGKSTLVPTCISQPCLPVANIGPTRILPMLYLGCQRDVANKELI 180
        |||
Db      121 LAGFAEFSRCPGGLCEGKSTLVPTCISQPCLPVANIGPTRILPMLYLGCQRDVANKELI 180

Qy      121 LAGFAEFSRCPGGLCEGKSTLVPTCISQPCLPVANIGPTRILPMLYLGCQRDVANKELI 180
        |||
Db      121 LAGFAEFSRCPGGLCEGKSTLVPTCISQPCLPVANIGPTRILPMLYLGCQRDVANKELI 180

Qy      181 QONGIGYVLAASNTCPKDPFIPESHFLRVVNDSPCEKILPWLDSVDFIERAKASNGCV 240
        |||
Db      181 QONGIGYVLAASNTCPKDPFIPESHFLRVVNDSPCEKILPWLDSVDFIERAKASNGCV 240

Qy      241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPPTISPNFPGQLLDYEKKIN 300
        |||
Db      241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPPTISPNFPGQLLDYEKKIN 300

Qy      301 QT 302
        ||
Db      301 QT 302

RESULT 10
US-10-648-593-247
; Sequence 247, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 247
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-593-247

Query Match      99.2%; Score 1552; DB 16; Length 665;
Best Local Similarity 99.3%; Pred. No. 2.2e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 MAHEMIGTQIVTERLVALLSEGTSEKVLIDSRPFVYNTSHLEAININCSKLMKRRLQ 60
        |||
Db      1 MAHEMIGTQIVTERLVALLSEGTSEKVLIDSRPFVYNTSHLEAININCSKLMKRRLQ 60

Qy      61 DKVLITELIQHSAKHKVIDCSQKVVYDQSSQDVASLSDCFITVLGKLEKSFNSVHL 120
        |||
Db      61 DKVLITELIQHSAKHKVIDCSQKVVYDQSSQDVASLSDCFITVLGKLEKSFNSVHL 120

Qy      121 LAGFAEFSRCPGGLCEGKSTLVPTCISQPCLPVANIGPTRILPMLYLGCQRDVANKELI 180
        |||
Db      121 LAGFAEFSRCPGGLCEGKSTLVPTCISQPCLPVANIGPTRILPMLYLGCQRDVANKELI 180

Qy      121 LAGFAEFSRCPGGLCEGKSTLVPTCISQPCLPVANIGPTRILPMLYLGCQRDVANKELI 180
        |||
Db      121 LAGFAEFSRCPGGLCEGKSTLVPTCISQPCLPVANIGPTRILPMLYLGCQRDVANKELI 180
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61 DKVLITELIQHSAGKVDIDCSQKVVYDQSSQDVASLSSDCFLTVLGKLEKSFNSVHL 120

EXPIRATION DATE: 2001-02-08
; Remaining Prior Application da

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/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 679
/ LENGTH: 690
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-072-012-679

Query Match      99.2% Score 1552; DB 15; Length 690;
Best Local Similarity 99.3%; Pred. No. 2.3e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAHEMIGTQVTERLVALLSEGTETKVLIDSRPFVEYNTSHLEAININCSKLMKRRLOQ 60
DB 26 MAHEMIGTQVTERLVALLSEGTETKVLIDSRPFVEYNTSHLEAININCSKLMKRRLOQ 85
QY 61 DKVLTTELIOHSAKAKVIDCSQKVVYVDQSSQDVASLSSDCLFYLLGKLEKSPSVYHL 120
DB 86 DKVLTTELIOHSAKAKVIDCSQKVVYVDQSSQDVASLSSDCLFYLLGKLEKSPSVYHL 145
QY 121 LAGGFAEFSRCPFGCEGKSTLVPTCISQPCLPVANIGTRILPNLYLGGQDVLNKEIL 180
DB 146 LAGGFAEFSRCPFGCEGKSTLVPTCISQPCLPVANIGTRILPNLYLGGQDVLNKEIL 205
QY 181 QONGIGYVLMASVTCPPKDPFIPESHFLRVVNDSCFCEKILPWLKSVDFIEKAKSNGCV 240
DB 206 QONGIGYVLMASVTCPPKDPFIPESHFLRVVNDSCFCEKILPWLKSVDFIEKAKSNGCV 265
QY 241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPITSPNFFLGQLLDYEKKIKN 300
DB 266 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPITSPNFFLGQLLDYEKKIKN 325
QY 301 QT 302
DB 326 QT 327

RESULT 13
US-10-072-012-703
/ Sequence 703, Application US/10072012
/ Publication No. US20040033493A1
/ GENERAL INFORMATION:
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Zernhusen, Bryan
/ APPLICANT: Patuturajan, Weera
/ APPLICANT: Shimkets, Richard
/ APPLICANT: Li, Li
/ APPLICANT: Gangoli, Esha
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Anderson, David W.
/ APPLICANT: Raasteili, Luca
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Taupler Jr, Raymond J.
/ APPLICANT: Gusev, Vladimiro Y.
/ APPLICANT: Coleman, Steven D.
/ APPLICANT: Wolenc, Adam R.
/ APPLICANT: Pena, Carol E. A
/ APPLICANT: Furtak, Katarzyna
/ APPLICANT: Grosee, William M.
/ APPLICANT: Alsobrook II, John P.
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Rieger, Daniel K.
/ APPLICANT: Burgess, Catherine E.
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-258
/ CURRENT APPLICATION NUMBER: US/10/072,012
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: 60/265,102
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/265,514
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,517
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/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,412
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,395
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/266,406
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 60/266,767
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: 60/267,057
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/266,975
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/267,459
/ Remaining prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 703
/ LENGTH: 690
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-072-012-703

Query Match      99.2% Score 1552; DB 15; Length 690;
Best Local Similarity 99.3%; Pred. No. 2.3e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAHEMIGTQVTERLVALLSEGTETKVLIDSRPFVEYNTSHLEAININCSKLMKRRLOQ 60
DB 26 MAHEMIGTQVTERLVALLSEGTETKVLIDSRPFVEYNTSHLEAININCSKLMKRRLOQ 85
QY 61 DKVLTTELIOHSAKAKVIDCSQKVVYVDQSSQDVASLSSDCLFYLLGKLEKSPSVYHL 120
DB 86 DKVLTTELIOHSAKAKVIDCSQKVVYVDQSSQDVASLSSDCLFYLLGKLEKSPSVYHL 145
QY 121 LAGGFAEFSRCPFGCEGKSTLVPTCISQPCLPVANIGTRILPNLYLGGQDVLNKEIL 180
DB 146 LAGGFAEFSRCPFGCEGKSTLVPTCISQPCLPVANIGTRILPNLYLGGQDVLNKEIL 205
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DB 266 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPITSPNFFLGQLLDYEKKIKN 325
QY 301 QT 302
DB 326 QT 327

RESULT 14
US-10-425-114-54204
/ Sequence 54204, Application US/10425114
/ Publication No. US20040034688A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jindong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E.
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(5313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ PRIOR FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 54204
/ LENGTH: 690
/ TYPE: PRT
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Clone ID: LIB4119-028-H6_Full.pep
US-10-425-114-54204

Query Match 99.2%; Score 1552; DB 15; Length 690;
Best Local Similarity 99.3%; Pred. No. 2,3e-143;
Matches 300; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAHEMIGTQIVTERLVALLESSTGTEKVLIDSRPFVEYNTSHLEAININCSKLMKRRLOQ 60
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QY 61 DKVLITELIQHSAKHKVDIDCSQKVVYDQSSQDVASLSDCFLVTLGKLEKSFNSVHL 120
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QY 121 LAGGFAEFSRCFPGLCBGKSTLVPTCISQPCLVANIGPTRILPMLYLGCQRDVNLKELI 180
DB 146 LAGGFAEFSRCFPGLCBGKSTLVPTCISQPCLVANIGPTRILPMLYLGCQRDVNLKELI 205
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DB 206 QONGIGYVLMASNTCPKDPFIPESHFLRPVNDSECEKILPMLDKSVDFIEKAKASNGCV 265
QY 241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPPTISPENFPGQLDYEKKIKN 300
DB 266 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPPTISPENFPGQLDYEKKIKN 325
QY 301 QT 302
DB 326 QT 327

RESULT 15

US-10-094-749-2312.
Sequence 2312, Application US/10094749
Publication No. US20030219741A1

GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHITO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOMYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
PRIOR FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2312
LENGTH: 665
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-2312

Query Match 98.8%; Score 1545; DB 15; Length 665;
Best Local Similarity 99.0%; Pred. No. 1e-142;
Matches 299; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 121 LAGGFAEFSRCFPGLCBGKSTLVPTCISQPCLVANIGPTRILPMLYLGCQRDVNLKELI 180
DB 121 LAGGFAEFSRCFPGLCBGKSTLVPTCISQPCLVANIGPTRILPMLYLGCQRDVNLKELI 180
QY 181 QONGIGYVLMASNTCPKDPFIPESHFLRPVNDSECEKILPMLDKSVDFIEKAKASNGCV 240
DB 181 QONGIGYVLMASNTCPKDPFIPESHFLRPVNDSECEKILPMLDKSVDFIEKAKASNGCV 240
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DB 241 LVHCLAGISRSATIAIAYIMKMDMSLDEAYRFVKEKRPPTISPENFPGQLDYEKKIKN 300
QY 301 QT 302
DB 301 QT 302

Search completed: February 9, 2005, 12:28:42
Job time : 58.152 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: February 14, 2005, 09:42:14 ; Search time 133.355 Seconds
(without alignments)
3705.573 Million cell updates/sec

Title: US-10-029-345a-109_COPY_1_302
Perfect score: 1564
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 1202784 seqs, 818138359 residues
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1552	99.2	1998	4	US-09-816-494-3
2	1552	99.2	3544	4	US-09-816-494-1
3	989	63.2	2351	4	US-09-949-016-3250
4	988	63.2	2377	4	US-09-920-668-3
5	475	30.4	333	4	US-09-513-999C-2877
6	469	30.0	1830	4	US-09-557-921-1
7	467.5	29.9	2109	4	US-09-016-434-1135
8	467.5	29.9	2109	4	US-09-023-655-946
9	466.5	29.8	2475	4	US-09-949-016-2615
10	464.5	29.7	13782	4	US-09-949-016-14992
11	426	27.2	2240	4	US-09-016-434-1100
12	425	27.2	944	4	US-09-371-671B-10

13	425	27.2	1238	2	US-08-530-230-11	Sequence 11, Appl
14	425	27.2	1238	4	US-09-702-705-803	Sequence 803, App
15	425	27.2	1238	4	US-09-736-457-803	Sequence 803, App
16	425	27.2	1238	4	US-09-614-124B-803	Sequence 803, App
17	425	27.2	1238	4	US-09-671-325-803	Sequence 803, App
18	425	27.2	1238	4	US-09-589-184-803	Sequence 803, App
19	425	27.2	1238	4	US-09-658-824-803	Sequence 825, App
20	425	27.2	1238	4	US-09-702-705-825	Sequence 825, App
21	425	27.2	1238	4	US-09-736-457-825	Sequence 825, App
22	425	27.2	1238	4	US-09-614-124B-825	Sequence 825, App
23	425	27.2	1238	4	US-09-671-325-825	Sequence 825, App
24	425	27.2	1238	4	US-09-589-184-825	Sequence 825, App
25	425	27.2	1238	4	US-09-658-824-825	Sequence 826, App
26	425	27.2	1238	4	US-09-702-705-826	Sequence 826, App
27	425	27.2	1238	4	US-09-736-457-826	Sequence 826, App
28	425	27.2	1238	4	US-09-614-124B-826	Sequence 826, App
29	425	27.2	1238	4	US-09-671-325-826	Sequence 826, App
30	425	27.2	1238	4	US-09-589-184-826	Sequence 826, App
31	425	27.2	1238	4	US-09-658-824-826	Sequence 826, App
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33	423.5	27.1	1993	2	US-08-990-379-2	Sequence 2, Appl
34	415	26.5	2000	4	US-09-016-434-1291	Sequence 1291, Ap
35	415	26.5	2000	4	US-09-919-437-10	Sequence 10, Appl
36	415	26.5	2015	4	US-09-949-016-4369	Sequence 4969, Ap
37	408	26.1	2283	4	US-09-949-016-4617	Sequence 4617, Ap
38	408	26.1	2303	4	US-09-922-146-3	Sequence 3, Appl
39	382	24.4	1987	2	US-08-990-379-1	Sequence 1, Appl
40	380	24.3	279	4	US-09-016-434-91	Sequence 91, Appl
41	357	22.8	1619	4	US-09-702-705-801	Sequence 801, App
42	357	22.8	1619	4	US-09-736-457-801	Sequence 801, App
43	357	22.8	1619	4	US-09-614-124B-801	Sequence 801, App
44	357	22.8	1619	4	US-09-671-325-801	Sequence 801, App
45	357	22.8	1619	4	US-09-589-184-801	Sequence 801, App

ALIGNMENTS

RESULT 1
US-09-816-494-3
Sequence 3, Application US/09816494
Patent No. 6664089
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
FILE REFERENCE: 10448-030002
CURRENT APPLICATION NUMBER: US/09/816, 494
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191, 858
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens
US-09-816-494-3

Alignment Scores:
Pred. No.: 2.74e-200
Score: 1552.00
Length: 1998
Matches: 300
Percent Similarity: 99.67%
Conservative: 1
Best Local Similarity: 99.34%
Mismatches: 1
Query Match: 99.23%
Indels: 0
Gaps: 0

US-10-029-345a-109_COPY_1_302 (1-302) x US-09-816-494-3 (1-1998)

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QY 21 SerGlyThrGluValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40

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Db      61 AGTGAACGGAAGAAAGTGGCTAATTGATAGCCGGCAGCTTTGGAAATACATAATATCC 120
Qy      41 HsHlleuGlulAlleasnIleasnCySerIyleuMetIyleuArgIleuGln 60
Db      121 CAGATTTTGGAAAGCCATTAATATCAACTGCTCCAACTTAATGAAAGGTTGGCAACAG 180
Qy      61 AspIyleuValIleuIlethrgIleuIleGlnHsIleSerAlaIleHisIleValAspIleAsp 80
Db      181 GACAAAGTGTAAATTCAGAGCTCATCCAGCATTCAGCAAAACATTAAGCTTGAATTGAT 240
Qy      81 CySerGlnIlyValIleValIleValIleValIleValIleValIleValIleValIleVal 100
Db      241 TGCAGTCAGAAAGGTTGATGATTAACATCAAGCTCCCAAGAGTTGCTCTCTCTTCA 300
Qy      101 AspCySerPheIleuThrValIleuGlnIlyIyleuGlnIlySerPheAsnSerValHisIleu 120
Db      301 GACTGTTTCTCAGCTGACTTCTGGGTAAACTGGAGAAAGCTTCAACTCTGTTCACTCG 360
Qy      121 LeuAlaGlyIlePheAlaGlnPheSerArgCySerPheProGlyIleuCySerGlnIlyIleSer 140
Db      361 CTTCGAGGTGGGTTGCTGATGTTCTCTGTTGTTCCCTGGCTCTGTAAAGAAATATCC 420
Qy      141 ThrIleuValProThrCySerIleSerGlnProCySerIleuProValAlaAsnIleGlyProThr 160
Db      421 ACTCTAGTCCCTACCTGCAATTTCTCAGCCTTGCTTACTGTTGCCAAACATGGGCCAACCC 480
Qy      161 ArgIleIleuProAsnIleuIyleuGlnIlySerGlnIlyArgAspValIleuAsnIleGlnIle 180
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Qy      181 GlnGlnAsnGlyIleGlyIleValIleuAsnAlaSerIleThrCySerProIlySerPheAsp 200
Db      541 CAGCAAGATGGAGTTGGTATGATGTTAATGCCAGCAATACCTGTCCAAAGCTGACTTT 600
Qy      201 IleProGlnIleHisPheIleuArgValProValIleuAspSerPheCySerGlnIlyIleu 220
Db      601 ATCCCCGAGTCAATTTCTGCGCTGCTGCTGAGTGAACAGCTTTGTGAGAAATTTTGG 660
Qy      221 ProTyrIleuAspIlySerValIleAspPheIleGlnIlyValIleValIleSerAsnIlyCySer 240
Db      661 CCGGTGTGGACAAATCAGTAATTCATTAATGAAAGCAAAAGCCCTCCAAATGGAATGTT 720
Qy      241 LeuValHisCySerIleuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIleAlaIleMet 260
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Qy      261 LysArgMetAspMetSerIleuAspGlnAlaIleValIleValIleValIleValIleValIle 280
Db      781 AAGAGGATGCAATGCTTTAGATGATGAGCTTACAGATTTGTGAAAGAAAGAAAGAAAGCTTACT 840
Qy      281 IleSerProAsnPheAsnPheIleuGlnIlyIleuIleuAspIleuIlyIleValIleValIle 300
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Qy      301 GlnThr 302
Db      901 CAGACT 906

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RESULT 2

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US-09-816-494-1
; Sequence 1, Application US/09816494
; Patent No. 6664089
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; FILE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; NUMBER OF SEQ ID NOS: 10

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3544
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (589)...(2583)
US-09-816-494-1

Alignment Scores:
Pred. No.: 7.39e-200 Length: 3544
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 4 Gaps: 0

US-10-029-345A-109_COPY_1_302 (1-302) x US-09-816-494-1 (1-3544)
Qy      1 MetAlaHisGlnMetIleGlyThrGlnIleValIleThrGlnArgIleuValAlaIleuGln 20
Db      589 ATGGCCATGAGATGATTGGAATCAATATGTTACTAGAGAGTTGGTCTGCTGCTGAA 648
Qy      21 SerGlyThrGlnIlyValIleuIleAspSerArgProPheValGlnIlyIleValIleValIle 40
Db      649 AGTGAACGGAAGAAAGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708
Qy      41 HsIleuGlnAlaIleAsnIleAsnCySerIyleuMetIyleuArgIleuGln 60
Db      709 CACATTTTGGAAAGCCATTAATATCACTGCTCCAAAGCTTAAAGCAAGGTTGCCAACAG 768
Qy      61 AspIyleuValIleuIlethrgIleuIleGlnHsIleSerAlaIleHisIleValAspIleAsp 80
Db      769 GACAAAGTGTAAATTCAGAGCTCATCCAGCATTCAGCAAAACATTAAGTTGACATTTGAT 828
Qy      81 CySerGlnIlyValIleValIleValIleValIleValIleValIleValIleValIleVal 100
Db      829 TGCAGTCAGAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 888
Qy      101 AspCySerPheIleuThrValIleuGlnIlyIyleuGlnIlySerPheAsnSerValHisIleu 120
Db      889 GACTGTTTCTCAGCTGATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 948
Qy      121 LeuAlaGlyIlePheAlaGlnPheSerArgCySerPheProGlyIleuCySerGlnIlyIleSer 140
Db      949 CTTCGAGGTGGGTTGCTGATGTTCTCTGTTGTTCCCTGGCTCTGTAAAGAAATATCC 1008
Qy      141 ThrIleuValProThrCySerIleSerGlnProCySerIleuProValAlaAsnIleGlyProThr 160
Db      1009 ACTCTAGTCCCTACCTGCAATTTCTCAGCCTTGCTTACTGTTGCCAAACATTTGGGCCAACCC 1068
Qy      161 ArgIleIleuProAsnIleuIyleuGlnIlySerGlnIlyArgAspValIleuAsnIleGlnIle 180
Db      1069 CGAATTTCTCCCAATCTTTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1128
Qy      181 GlnGlnAsnGlyIleGlyIleValIleuAsnAlaSerIleThrCySerProIlySerPheAsp 200
Db      1129 CAGCAAGATGGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1188
Qy      201 IleProGlnIleHisPheIleuArgValProValIleuAspSerPheCySerGlnIlyIleu 220
Db      1189 ATCCCGAGTCTCATTTCTGCGGTGCTGCTGATGATGACAGCTTTTGTGAAAGATTTTG 1248
Qy      221 ProTyrIleuAspIlySerValIleAspPheIleGlnIlyAlaIleValIleValIleValIle 240
Db      1249 CCGGTGTGGACAAATCAGTAATTCATTAATGAAAGCAAAAGCTCCCAATGATGATGTT 1308
Qy      241 LeuValHisCySerIleuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIleAlaIleMet 260
Db      1309 CTAGTCACTGTTTAGTGGAGATCTCCGCTCCGCCAATCGCTATGCTTACATCATG 1368
Qy      261 LysArgMetAspMetSerIleuAspGlnAlaIleValIleValIleValIleValIleValIle 280

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Db      1369  AAGAGATGACATGCTTTAAGATGAAGCTTACAGATTTGTGTGAAGAAAAAAGACCTACT 1428
Qy      281  IIESePrioASnPhesAnDheLeuGIyGInLeuLeuAePryGIuLybLyIleYsaAn 300
Db      1429  ATATCTCCAAACTTCAATTTTCTGGGCGCAACTCCTGCACTATGAGAAGAAAGATTAAAGAC 1488
Qy      301  GInThr 302
Db      1489  CAGACT 1494

RESULT 3
US-09-949-016-3250
; Sequence 3250, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO010307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3250
; LENGTH: 2351
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3250

Alignment Scores:
Pred. No.:      1,59e-123      Length:      2351
Score:          989.00         Matches:      190
Percent Similarity: 81.40%     Conservative: 55
Best Local Similarity: 63.12%  Mismatches:    54
Query Match:     63.24%       Indels:       2
DB:              4            Gaps:         2

US-10-029-345A-109_COPY_1_302 (1-302) x US-09-949-016-3250 (1-2351)
Qy      1      MetalAHAGluMeTIEgLyThrGInIleVal---ThrGluAryhValAlaleuLeu 19
Db      109  ATGGCTGGGGAGCCGGGTCCCGAGAAAGGTGATGATCCAAAGAAAGTGGCCCGCTGG 168
Qy      20  GInSeRgLyThrGInuLybValLeuLeuIleAePSeRgProPhVaIaGluTyRaeAnthr 39
Db      169  CGGGCGGGCGCTGGGGGGGGCGCGCTGTCATCGACGACCGCTCTTCTGTGAATCAACAGC 228
Qy      40  SerHisIleLeuGInAlaIleAsnIleAsnCySeRLeuWeLySaIryArgLeuGIn 59
Db      229  TGGCATGTGCTCAGCTCCGTCACAACTCTGCTCTCCAAAGCTGGTGAAGCGCGCTGCAG 288
Qy      60  GInAePrybValLeuIleThrGInuLeuIleGInHisSerAlaIlybIbValaAple 79
Db      289  CAGGGCAAGGTGACCACTTGGGAGCTCATCCAGCCGGCTGCACGCGCAGAGGTGAGGCT 348
Qy      80  AePcySeRgInuLybValValaIyTyRAePginSeSerGInAePryAlaIeSerLeuSer 99
Db      349  ACGGAGCCACAGAGAGCTGTGTGTCATGACAGAGACCGGGAGCCGACGCTGTGGCC 408
Qy      100  SeRAePcybPhLeuThrValLeuLeuGlyLybLeuGInuLySeRPhesAnSeRValHis 119
Db      409  GCAGACAGCTTCTCTCCATCTGCTGACAGCAAGCTGACGCGCTGTCAGACAGCGTGGCC 468
Qy      120  LeuLeuAlaGIyLybPhenAlaGInPheseraGcybPhProGIyLeuCybGIuLyb 139
Db      469  ATCTTCATCTGGGGGGCTTGGCGACCTTCTCTCTGCTTCCCGGGCTTCGCGAGGGCAAG 528

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QY 140 ---serthrlauValProthmCysIleSeG1ProCyseLeuProValAlaenIleGly 156
 Db 529 CCGTCGCCCTGCTACCAAGACCTCTCCAGCCCTGCTGCTGCGCCAGCTGGG 588
 QY 159 ProthrlaG1leLeuProAenLeuTyrLeuGlyCyseGlnAgsaPValleuAenLySglu 178
 Db 589 CTGACCGGCANCTCGCTCACTTACCTGGGGCTCGAGAAGAGCGTCTTAACAGAT 648
 QY 179 leuIleGlnInaenGlyIleGlyTyrValleuAenAlaSerTyrThrCyseProLySPro 198
 Db 649 CTGATGACGCAAAATGAAATAGCTACGCTCTCAACCCAGCAACTCTCCGCCAGCT 708
 QY 199 AspheIleProG1uSeSerthrlaPheLeuAgsValProValAenApsSerPheCyseGluLyS 218
 Db 709 GACTTCATCTGCGAGAGCCGCTTATCGAGGGTCCCACTAACGCAACTCTGTGA AAAA 768
 QY 219 IleLeuProTrrpleuAenAlySseValaPheIleGluLySAlaLySAlaSerAenGly 238
 Db 769 CTGCTGCCCTGGCTGAGCAAGTCATGACGAGTTCATGAAGCCAAAGCTCTCCAGCTGC 828
 QY 239 CyseValleuValHisCyseLeuAlaGlyIleSerAgsSerAlaThrIleAlaIleAlaTyr 258
 Db 829 CAATCTATCGTCCACTGCTGCGTGGCATCTCCGCTCTCCACATCGGCATCGCTAC 888
 QY 259 IleLeuTyrAgsMetApsMetSerLeuApsGluAlaTyrAgsPheValLySg1uLySArg 278
 Db 889 ATCATGAAGACCATGGGCAATGCTCTCGAGAGAGCCCTACAGGTTCTGTAAGAGAGGCGC 948
 QY 279 ProthrlaSerProAenPheAenPheLeuGlyGlnleuLeuApsTyrGluLySlyle 298
 Db 949 CCGTCATCTCGCCCACTTCACTCTCTGGGCGAGTGTGGAGTACGAGCGCAGCGCTG 1008
 QY 299 Lys 299
 Db 1009 AAG 1011
 RESULT 4
 US-09-920-668-3
 : Sequence 3, Application US/09920668
 : Patent No. 6482644
 : GENERAL INFORMATION:
 : APPLICANT: Lex M. Cowser
 : APPLICANT: Brett P. Monia
 : TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 8 EXPRESSION
 : FILE REFERENCE: RRS-0246
 : CURRENT APPLICATION NUMBER: US/09/920,668
 : CURRENT FILING DATE: 2001-08-01
 : NUMBER OF SEQ ID NOS: 49
 : SEQ ID NO 3
 : LENGTH: 2377
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURES:
 : NAME/KEY: CDS
 : LOCATION: (135)...(2012)
 US-09-920-668-3
 Alignment Scores:
 Pred. No.: 2,21e-123 Length: 2377
 Score: 988.00 Matches: 190
 Percent Similarity: 81.40% Conservative: 55
 Best Local Similarity: 63.12% Mismatches: 54
 Query Match: 63.17% Indels: 2
 DB: 4 Gaps: 2
 US-10-029-345A-109_COPY_1_302 (1-302) x US-09-920-668-3 (1-2377)
 QY 1 MetLlaIsgIuectIleGlyThrGlnIleVal---ThcJugrGluValAlaLeuLeu 19
 Db 135 ATGGCTGGGAGACCGGCTCCGAGAGAGGTATGATGATGCCAAGAGCTGGCCACCTGG 194
 QY 20 GluSer1yThrGluLySValleuLeuIleApsSerAgsProPheValGluTyrAenThr 39

Dd		195	CGGGGCGGGCCCTGGGGGGGCCGGCTGCATTCAGACGCCGCTCCTTGGTAGATCAACAGC	254
Oy		40	SerHisIleLeuGluValIalleasnIIeaSnCySerLysLeuMetLysArgLeuGln	59
Dd		255	TGGCATGTCTCAGCTCCGTCACAACATCTGCTCTCCAGCTGGTAGAAGGGCGGCTGCAG	314
Oy		60	GlnAspLysValLeuIleThrGluLeuIleGlnHisSerAlaYshIstLysValAspIle	79
Dd		315	CAGGGGAAGSTGACCATTGGAGACTATCCAGCCGGCTGCAGCACAGGAGGGGCT	374
Oy		80	AapCySerGlnLysValValValTYraSpGlnSerSerGlnAspValAlaSerLeuSer	99
Dd		375	ACGGAGCCACAGAGACGTGGTGCTATGACACAGACCGGGAGCGCAGCGTGCGGCC	434
Oy		100	SeraAPCyPheLeuThrValLeuLeuGlyLysLeuGluLysSerThesnsnervAlaHis	119
Dd		435	GGAGAGAGCTTCCTCTCCATCTCGTAGACAGACGTGAAGGGCTGCTTCACAGCGTGCCC	494
Oy		120	LeuLeuAlaGlyGlyPheAlaGluPheSerArgCySPheProGlyLysCySglnGlyLys	139
Dd		495	ATCTTCACGTGGGGGGCTTGCCACCTTCTCTCTGCTTTCCGGGCTCTGGAGGGCAAG	554
Oy		140	---SerThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGly	158
Dd		555	CCTGCGCCCTGCTCCACCAAGAAGCTCTCCAGCCCTGCTGCTCTGTCGCCAGCGGGCC	614
Oy		159	ProThrArgIleLeuProAsnLeuTyrlsueGlyCySGlnArgAspValLeuAsnLysGlu	178
Dd		615	CTGACCCCGATCTCTCTCACCCTTAACCTGGGCTGGCAGAAAGACGTCTTAACAAGGAT	674
Oy		179	LeuIleGlnGlnAsnGlyTllegLYrValLeuAsnAlaSerTYrThrCysProLysPro	198
Dd		675	CTGAAGAAGCAAAATGATAATAGCTACGCTCCAACGCGCAGACACTCCGCCCCAAGCT	734
Oy		199	AspPheIleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGlnLys	218
Dd		735	GACTTCATCTCGAAGACCGCGCTTCAAGGGGTCCTCAACAGACAACACTGTAAGAAA	794
Oy		219	IleLeuProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsnGly	238
Dd		795	CTGCTGCCCTGGCTGGAACAAGTCCATCGATTCACTAAAGCCAAAGCTCTCCAGCTGC	854
Oy		239	CysValLeuValHisCysLeuAlaIleLysSerArgSerAlaThrIleAlaIleAlaTYr	258
Dd		855	CAGGATCATGTCACACTGTCTGCTGGCATCTCCGCTCTGCACACATGGCCATCCCTAAC	914
Oy		259	IleMetLysArgMetAspMetSerLeuAspGluAlaTYrArgPheValLysGlnLysArg	278
Dd		915	ATCATGAAGACCATGGGATGTCCTCGACACAGCGCTACAGTTCTGAAGACACGGCC	974
Oy		279	ProThrIleSerProAsnPheAsnPhelLeuGlyGlnLeuLeuAspTYrGluLysLysIle	298
Dd		975	CGGTCCATCTCGCCCACTTCAAATTCTTGGGCGAGCTGAGTAGACGAGCGACGCTG	1034
Oy		299	Lys 299	
Dd		1035	AAG 1037	
 RESULT 5 US-09-513-999C-2877 Sequence 2877, Application US/09513999C Patent No. 6783961 GENERAL INFORMATION: APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Duclert, A. TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. FILE REFERENCE: 59, US2, REG CURRENT APPLICATION NUMBER: US/09/513, 999C CURRENT FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/122,487				

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/ PRIOR FILING DATE: 1999-02-26
/ NUMBER OF SEQ ID NOS: 36681
/ SOFTWARE: Patent.pm
/ SEQ ID NO 2877
/ LENGTH: 333
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 127..333
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 17
/ OTHER INFORMATION: h=a or c or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 18
/ OTHER INFORMATION: y=c or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 19
/ OTHER INFORMATION: k=g or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 36
/ OTHER INFORMATION: n=a, g, c or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 58
/ OTHER INFORMATION: r=a or g
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 237
/ OTHER INFORMATION: w=a or t
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: 37
/ OTHER INFORMATION: Xaa=His or Gln
/ US-09-513-999C-2877

Alignment Scores:
Pred. No.: 5e-55      Length: 333
Score: 475.00      Matches: 106
Percent Similarity: 93.81%      Conservative: 0
Best Local Similarity: 93.81%      Mismatches: 5
Query Match: 30.37%      Indels: 3
DB: 4      Gaps: 0

US-10-029-345A-109_COPY_1_302 (1-302) x US-09-513-999C-2877 (1-333)

QY      12  ThGluArgLeuValAlaLeuLeuGlnSerGlyThr-GluIysValLeuLeuIleAspSe 31
Db      1  ACTGAGAGGTTGGTGGHYK--CTGGAAAGTGGACGGGAAAAAGTGGCTGAATTGTATAR 58
QY      31  rAGSPProPheValGluTyr-AsenThrSerHisIleLeuGlnAlaIleAsnIleAsnCys 51
Db      59  CCGGCGATTGTTGGAAATACCAATACATCCACACATTTTGAAGCCATTAAATACACTGCT 118
QY      51  erIysLeuMetIysaTargLeuGlnGlnIAspIysValLeuIleThrGlnLeuIleGln 71
Db      119 CCAAGCTTATGAAGCGCAAGTGGCAACAGGAAAGTGTAAATTACAGAGCTATCCAGC 178
QY      71  iAserAlaIysHisIysValAlaIleAspIleAspCysSerGlnIysValIValItyrAspGln 91
Db      179  ATTCAACGAAACATTAAGTTCACATTCATTGACATGACAGAAAGTGTATGATTACATCAWA 238
QY      91  erSerGlnAspValAlaSerLeuSerSerAspCysPheLeuThrValLeuLeuGlyLysI 111
Db      239  GCTCCCAAGATGTGGCTCTCTCTCTTTAAGACTGTCTTTTTCACCTGTACTTGGGTAAAC 298
QY      111  enGlnIysSerPheIAsnSerValHisLeuLeuAla 122
Db      299  TGGAGAAAGAGCTTCAACTCTGTTCACTGCTTTGCA 333

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RESULT 6
US-09-557-921-1
; Sequence 1, Application US/09557921
; Patient No. 6551810
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; TITLE OF INVENTION: DSP-10 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.416
; CURRENT APPLICATION NUMBER: US/09/557, 921
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1830
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-921-1

Alignment Scores:
Pred. No.: 6,296-53 Length: 1830
Score: 469.00 Matches: 107
Percent Similarity: 57.72% Conservative: 65
Best Local Similarity: 35.91% Mismatches: 96
Query Match: 29.99% Indels: 30
DB: 4 Gaps: 7

US-10-029-345A-109_COPY_1_302 (1-302) x US-09-557-921-1 (1-1830)
Qy 27 LeuLeuIleAspSerArgProPheValGluTyraenThrSerHisIleLeuGluAlaIle 46
Db 603 GTCAATCATGATGAGAGCCCTTCATGAGTCAACAGAGTCAATCAAGAGAGCTGTC 662
Qy 47 AsnIleAsnCySer--LysIleuNeuIySarGatGleuGlnGlnAspIyValIle 65
Db 663 CACATTAATCTGCGCGATGATGATGATGATGATGATGATGATGATGATGATGATG 722
Qy 66 ThrGluuIleGln--HisSerAlaIyHisIySarValAspIleAspCySerGlnIy 84
Db 723 CTGAGCTGATTTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 782
Qy 85 ValValIleTyraenGlnSerSerGlnAspValAlaSerLeuSerSerAspCySphLeu 104
Db 783 ATTATAGTTTATGATGAGATTCATGATGATGATGATGATGATGATGATGATGATG 842
Qy 105 ThrValLeuLeuGlyIyLysLeuGluIyLysSerPheAsnSerValHisLeuLeuAlaGly 124
Db 843 CACATAGTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 902
Qy 125 PheAlaGluPheSerArgCySphProGlyLeuCyGluGlyLys----- 139
Db 903 CTTAGTATGTTTAAACAGAACATGAAAACTCTGTGACACTCCCTCCAGTCCAGAG 962
Qy 140 -----SerThrLeuValProThrCySphIleSer 148
Db 963 TGGCGGAGGTGGGGGGGCGGCGCATCCGCGGCTGAGAGTCTGATCCTCAGCCCATC 1019
Qy 149 GlnProCyLeuPro--ValAlaAsnIleGlyProThrArgIleLeuProAsnLeuTy 167
Db 1020 ---CCCACACCCCTGAGATGAGAAAGGTGAGTCAACCCCATCTTCCCTCTGTTTC 1076
Qy 168 LeuGlyCyGlnArgAspValLeuAsnIyGluLeuIleGlnGlnAsnGlyIleGlyTy 187
Db 1077 CTGGCAATGAGCAATGCTGACAGCTGACACATGACAGGAGGAGGAGGAGGAGGAG 1136
Qy 188 ValLeuAsnAlaSer-----TyrThrCySphProIyProAspPheIlePro 202
Db 1137 GTCAATCAACGTACCACTCATCTTCCCTCTGATGATGATGATGATGATGATGATG 1190
Qy 203 GluSerHisPheLeuArgValProValAsnAspSerPheCyGluIyIleLeuProTr 222
Db 1191 -----AACTACAAAGCGGCTGCGCAGCACTGACAGCAACAGCAACAGCAACAG 1244

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Qy 223 LeuAspIySerValAspPheIleGluIyAlaIyAlaSerAsnGlyCySphValLeuVal 242
Db 1245 TTGAGAGGCTTTTGAATTCATTCATGAGAGCTACCAAGTGTGGAGGGCTTTCATC 1304
Qy 243 HisCySphLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIyIleMetIySar 262
Db 1305 CACTGCCAGCGCTGGGGGTCTCCCGCTCCGCCACATCTGATCGCTTACTGATGAGCAC 1364
Qy 263 MetAspMetSerLeuAspGluAlaTyrThrGpPheValIySgIyValArgProThrIleSer 282
Db 1365 ACTGGATGACCATCTACTGATGATCTTAATAATTTGCAAGGCAACGACCAATTATCTCC 1424
Qy 283 ProPheAsnPheAspLeuGlyIleLeuAspIyArgIyIyValIleIySgIleIySgIle 300
Db 1425 CCAATCTTAATCTCATGCGGCGAGTGTGATGAGTTCAGAGAAAGCACTTAACAC 1478

RESULT 7
US-09-016-434-1135
; Sequence 1135, Application US/09016434
; Patient No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016, 434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37, 071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1135:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2109 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1418933
; US-09-016-434-1135

Alignment Scores:
Pred. No.: 1,296-52 Length: 2109
Score: 467.50 Matches: 110
Percent Similarity: 53.56% Conservative: 63
Best Local Similarity: 34.06% Mismatches: 105
Query Match: 29.89% Indels: 45
DB: 4 Gaps: 7

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Db      670 GAGAAATACGGCGCGGAGTCTGTCGCGCTGCTCTCAAGAGCTCAAGAGCAGAGGCG 729
      116 AenSerValHisLeuLeuValaglygylpheAlaGluPheSerArgCybProGlyLeu 135
Db      730 TCCCGGCGCTTCTCACTCGAAGGTGGCTTCAGAGTTCACAGCCAGATTCCTCCGCAAT 789
      136 CysGluGlyLySerThrLeuValProThrCys---LleSerGlnProCysLeuProVal 154
      790 TCGAGC-----ACCAATCTAGACGGCTGCTGTAGACAGACGCTCGCGCTTGCACAGT 843
      155 AlaAenIleGly----- 158
Db      844 CTGGGCGCTCGGGGCGCTGGCGATCAGCTCTGACTTCTTCCGAGCATGAGTCTGACTT 903
      158 ----- 158
Db      904 GACCGAGACCCCAATAGTCAACAGACTCGGATGTAGTCCGCTGTCCAAAGCCAGCCT 963
      159 -----ProThrArgIleLeuProAenLeuTyrlLeuGlyCysGlnArgAspValLeuAen 176
      964 TCCCTCCAGTGGAGATCTTGCCTTCTCTACTTGGCTGTCCAAAGTCTCCACCAAC 1023
      177 LySGluLeuIleGlnGlnAenGlyIleGlyTyrlValLeuAenAlaSerTyrlThrCysPro 196
      1024 TTGAGACGTGTGGAGAAATTCGGCATCAAGTACATCTTGAAAGCTCAACCCCAATTGGCG 1083
      197 LySPro---AspPheIleProGluSerHisPheLeuArgValProValAenAspSerPhe 215
      1084 AATCTCTTTGAGAACGACGAGAGTTTAATACAAACCAATCCCACTCGATCACTCG 1143
      216 CysGluLySleIleuProTrIleuPheAspLySerValAspPheIleGluLySleVal 235
      1144 ACCCAAAACCTGCTCCAGTTCCTCCCTGAGCCATTCTTCTTCAATAGTAAAGCCGGGCG 1203
      236 SerAenGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAla 255
      1204 AAGAACTGTGTCTTGTGGATCATCTTGGCTGAGGATTAAGCCGCTCAGACTGTGACT 1263
      256 IleAlaTyrlIleMetLyArgMetAspMetSerLeuAspGluAlaTyrlArgPheValLyS 275
      1264 GTGGCTTACTTATGCAAGAGCTCAATCTGTCAATCAAGATGCCATATGATTCGCAAA 1323
      276 GluLyArgProThrIleSerProAenPheAenPheLeuGlyGlnLeuLeuAspTyrlGlu 295
      1324 ATGAAATAATCCAAATATCCCTTCACTTCACTTCAAGTCAAGTGTGAGCTTGCAG 1383
      296 LySlySle 298
      1384 AGGAGCGCTG 1392

```

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; ORGANISM: Human
US-09-949-016-2615

Alignment Scores:
Pred. No.: 2,336-52
Score: 466.50
Percent Similarity: 53.56%
Best Local Similarity: 34.06%
Query Match: 29.83%
DB: 4
Gaps: 7

US-10-029-345A-109_COPY_1_302 (1-302) x US-09-949-016-2615 (1-2475)

      19 LeuGluSerGlyThrGluLySleValLeuLeuIleAspSerArgProPheValGluTyrlAen 38
      519 CTGAGCTGGGAGACGAGGCGCTGCTCTGATGAGTCTCCGCGCAGAGACTATACGAG 578
      39 ThrSerHisIleLeuGluAlaIleAenIleAenCysSerLySleuMetLyArgArgLeu 58
      579 TCGTCGACATCGAGTCCGCGCATCAACGTGGCATCCCGGATCATGTCTGGCGCGCTG 638
      59 GlnGlnAspLySleValLeuIleThrGluLeuIleGlnHisSerAla---LySHisVal 77
      639 CAGAAAGGTAACTCCGCTGCGCGCTCTTACGCGCGGAGAGACCGGAGACCGCTTC 698
      78 AspIleAspCys---SerGlnLySleValValTyrlAspGlnSerSerGlnAsp---Val 95
      699 ACCCGCGCTGTGGACCAACGACAGTGTGCTCTTCAAGACAGACAGCAGCACTGGAAC 758
      96 AlaSerLeuSerSerAspCysPheLeuThrValLeuLeuGlyLySleGluLySlePhe 115
      759 GAGAAATACGGGAGGAGAGTGGTCTCGGCTGCTGTCAAGAGTCAAGAGTCAAGAGCGAG 818
      116 AenSerValHisLeuLeuValaglygylpheAlaGluPheSerArgCybProGlyLeu 135
      819 TCCCGGCGCTTCTTACTGTGAAGGTGGCTTCAATAGTTCAAAGCCAGATTCCTCCGCAAT 878
      136 CysGluGlyLySerThrLeuValProThrCys---LleSerGlnProCysLeuProVal 154
      879 TCGAGC-----ACCAATCTAGACGGCTGCTGTAGACAGACGCTCGCGCTTGCAGT 932
      155 AlaAenIleGly----- 158
      933 CTGGGCGCTCGGGGCGCTGGCATCAGCTCTGACTTCTCTCGGACATGAGTCTGACTT 992
      158 ----- 158
      993 GACCGAGACCCCAATAGTCAACAGACTCGATGTAGTCCGCTGTCCAAAGCCAGCCT 1052
      159 -----ProThrArgIleLeuProAenLeuTyrlLeuGlyCysGlnArgAspValLeuAen 176
      1053 TCCCTCCAGTGGAGATCTTGCCTTCTCTTACTTGGGCTGTGCCAAAGCTCCACCAAC 1112
      177 LySGluLeuIleGlnGlnAenGlyIleGlyTyrlValLeuAenAlaSerTyrlThrCysPro 196
      1113 TTGAGACGTGTGGAGAAATTCGGCATCAAGTACATCTTGAAAGCTCAACCCCAATTGGCG 1172
      197 LySPro---AspPheIleProGluSerHisPheLeuArgValProValAenAspSerPhe 215
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      216 CysGluLySleIleuProTrIleuPheAspLySerValAspPheIleGluLySleVal 235
      1233 ACCCAAAACCTGCTCCAGTTCCTCCCTTCAATTCCTTCTTATGATGAAAGCCGGGCG 1292
      236 SerAenGlyCysValLeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAla 255
      1293 AAGAACTGTGTCTTGTGATCATCTTGGCTGAGGATTAAGCCGCTCAGTCTGACT 1352
      256 IleAlaTyrlIleMetLyArgMetAspMetSerLeuAspGluAlaTyrlArgPheValLyS 275
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Qy	276	GLULYSALGPRCTHILLESERPROKSNHKEANPELENGIYGINLEULEASPTXGJ	295
	1413	ATGAAAAAATCCACATATATCCCTTACTTCACTTCAAGGTCACTGCTGGAATTGGAG	1472
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RESULT 10
US-09-949-016-14992
; Sequence 14992, Application US/09949016

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; PATENT NO. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14992
; LENGTH: 13782
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-14992

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Db	8939	CTGCTACCCAAAGACCTCTCCACAGCCCTGCTGCTGTGCCAGGAGTGAGGACTGACCGC	8999
QY	162	IleLeuProAsnLeuTYrLeuGluCYGluInrGAspValLeuAsnIlyGlu-----	178
Db	8999	ATCTGCTCTCACTCTCACTGGGCTGGCAGAGGACGTCCTAAACAAAGT-GTGTGTCA	9057
QY	178	-----	178
Db	9058	GTGSAAGTTGGGGGGGTGTCAATGAGGAAGGGCAGAGCTCCAGAGACAGCTTGGCAGC	9117
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Db	9478	CAGGCTGCCAGGCTGACACAGAAGGCTCTGGGCGCTCCCTGGATACCTGGGATCT	9537
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QY	178	-----	178
Db	9598	CCTCCACCTTCACCTCCGCGCCCGAGCTTCCACCCCTTCCACCCGCGCTCCGCGCC	9657
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QY	271	Tyr-----	271
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Dh		282	GCTAAGGCTCCGTGAAGCCTCGAGACGATCTTCGCCGCCGAGAGAGAAGTAAACGGCCCCG	341
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Dh		342	TTGGCGCTCCGCGCTTACTACTGCGGCGCATCGCTCACTACGACGACGCGACGCCGCCGCGAG	401
Oy		97	SerLeuSerSerApCySpheLeuthrVAlleuLeuglLyIsLeuGlInlysSerPhe---	115
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Dh		462	CGCACGACACATCTGCCTGCTCAAAGCGGCTATGAGAAGTTTTCTCCGAATTCCCGAA	521
Oy		135	LeucyAgInglYlysserThreu-----ValProThrCysIleser	148
Dh		522	TTCTGTTCTTAAACCAAGGCCCTGGAGGCATCCACC GCCGTTCCGCCAGGCGCA	581
Oy		149	GIAPro-----CysleuProValAla-----AsnIlleglyPro	155
Dh		582	GAGCGCTTGGACCTGACCTGACAGCTCTCTGTGGACCCCACTAACAGACAGAGAGGTCCT	641
Oy		160	ThraYglleuProAsnleuTyrlensglYcysglInargApvalleuAmlysglIneu	179
Dh		642	GTCGAGATCT	701
Oy		180	IleglInlaAnslYlleglYTrValleuAnaIaserTYrThyCysProIAsPProasp	199
Dh		702	CTGAGAGCCCTGGGCATCAACGGCTGTTGAATGTCTCTCGAGCTGCCAAAC---CAC	758
Oy		200	PheIleProgluseriHsPheleuArvalProValIasnapSerPheCysglInlylle	219
Dh		759	TTTGAAGACACTATGATCAAGATGCATCCCAGGTGAAGATACACAGAGCCGAGCATC	818
Oy		220	LeuProThrleuNapbysserValIAsPheIIegluWbAlalyAlaseraAnglyCys	239
Dh		819	AGCTCCGTGTCATGGAAGCATAGATCATGATGCCGTGAAGACCTCGGTGGCGC	878
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Dh		879	GTCGTGTCGACACGCGAGCGGCATCTCGCGTGGCGCAACATCTGCTGCTTACTG	938
Oy		260	MettylearYMetarPwterSerleuNapgluaIATyratrpheVallysglInlyAsxpro	279
Dh		939	ATGATGACGAACACGGGTGAGCGTGGAGAGGCTTCGAGTTCTGTTAAGCAGCGCGCAGC	998
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 RESULT 14 US-09-702-705-803 Sequence 803, Application US/09702705 Patent No. 6504010 GENERAL INFORMATION: APPLICANT: Wang, Tonglong APPLICANT: Bangur, Chaitanya S. APPLICANT: Lodes, Michael A. APPLICANT: Fanger, Gary APPLICANT: Vedvick, Tom APPLICANT: Carter, Darrick APPLICANT: Retter, Marc APPLICANT: Mannion, Jane TITLE OF INVENTION: Pan, Liqun TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND FILE REFERENCE: DIAGNOSIS OF LUNG CANCER CURRENT APPLICATION NUMBER: US/09/702,705 CURRENT FILING DATE: 2000-10-30 NUMBER OF SEQ ID NOS: 1833 SOFTWARE: PaetSEQ for Windows Version 3.0 SEQ ID NO 803				

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: TYPE: DNA
: ORGANISM: Homo sapien
US-09-702-705-803

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Query Match: 27.17 Indels: 22
DB: 4 Gaps: 8

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Qy 77 ValAspLLeaPcysSerGlnLysValValValTyrAspGlnSerSerGlnAspValAla 96
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Qy 97 SerLeuSerSerArgPcysPheLeuThrValLeuLeuGlyLysLeuGluLysSerPhe-- 115
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Qy 116 ---AsnSerValHisLeuLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeu 134
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Qy 149 GlnPro-----CysLeuProValAla-----AsnLLeuLysPro 159
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Qy 160 ThrArgLLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLLeuAnLysGluLeu 179
Db 642 GTGAGATCTTCCCTCTCTACTCTGGCAGGTGCTACCATGCTGGCGGAGAGCATG 701
Qy 180 LLeuGlnAsnGlyLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeuLLeu 199
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comphen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: February 14, 2005, 10:56:55 / Search time 403.187 Seconds
(without alignments)
4419.632 Million cell updates/sec

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Searched: 5378673 seqs, 2950229984 residues
Total number of hits satisfying chosen parameters: 10757346

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1552	99.2	1998	US-10-377-072-27	Sequence 27, Appl1
3	1552	99.2	1998	US-10-377-072-27	Sequence 27, Appl1
4	1552	99.2	2071	US-10-072-012-257	Sequence 257, Appl1
5	1552	99.2	2732	US-10-168-506-2	Sequence 2, Appl1
6	1552	99.2	3059	US-10-257-026-1	Sequence 1, Appl1
7	1552	99.2	3496	US-09-964-277-1	Sequence 1, Appl1
8	1552	99.2	3521	US-10-370-715B-261	Sequence 261, Appl1
9	1552	99.2	3544	US-09-816-494-1	Sequence 1, Appl1
10	1552	99.2	3544	US-10-377-072-25	Sequence 25, Appl1
11	1552	99.2	3544	US-10-377-072-25	Sequence 25, Appl1
12	1552	99.2	3625	US-10-425-114-26234	Sequence 26234, Appl1
13	1552	99.2	3766	US-10-343-357-17	Sequence 17, Appl1
14	1552	99.2	4790	US-10-648-593-115	Sequence 115, Appl1
15	1552	99.2	5145	US-10-357-930-20824	Sequence 20824, Appl1
16	1552	99.2	5145	US-10-357-930-20969	Sequence 20969, Appl1
17	1552	99.2	5145	US-10-357-930-21071	Sequence 21071, Appl1
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20	1552	99.2	5145	US-10-357-930-21307	Sequence 21307, Appl1
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22	1552	99.2	5145	US-10-357-930-26669	Sequence 26669, Appl1
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24	1552	99.2	5145	US-10-357-930-26912	Sequence 26912, Appl1
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32	1194.5	76.4	3332	US-09-964-277-20	Sequence 20, Appl1
33	985	63.0	2453	US-10-005-858-1	Sequence 1, Appl1
34	943	60.3	2476	US-10-220-120-28	Sequence 28, Appl1
35	837	53.5	2039	US-10-072-012-265	Sequence 265, Appl1
36	724	46.3	418	US-10-357-930-11243	Sequence 11243, Appl1
37	724	46.3	461	US-10-357-930-12416	Sequence 12416, Appl1
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39	724	46.3	461	US-10-357-930-11346	Sequence 11346, Appl1
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44	602	38.5	346	US-10-357-930-11236	Sequence 11236, Appl1
45	602	38.5	377	US-10-357-930-32409	Sequence 32409, Appl1

ALIGNMENTS

RESULT 1
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Sequence 3, Application US/09816494
Patient No. US20020034807A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
FILE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
FILE REFERENCE: 10448-030002
CURRENT APPLICATION NUMBER: US/09/816,494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,858
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens
US-09-816-494-3

Alignment Scores:

Pred. No.:	9,31e-193	Length:	1998
Score:	1552.00	Matches:	300
Percent Similarity:	99.67%	Conservative:	1
Best Local Similarity:	99.34%	Mismatches:	1
Query Match:	99.23%	Indels:	0
DB:	9	Gaps:	0

US-10-029-345a-109_COPY_1_302 (1-302) x US-09-816-494-3 (1-1998)

QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGln 20
DB 1 ATGGCCCATGAGATGATGTTGAACTCAATTTGTTACGAGAGTTGGTCTGCTGGAGAA 60
QY 21 SerGlyThrGluLeuValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40
DB 61 AGTGGAAACGGAAAAAGTGTGCTTAATGTATGATGCCGCGCATTTGTGGAAATACATATCCTCC 120
QY 41 HisIleLeuGluAlaIleAsnIleAsnGlySerIleuMetIleuMetIleuArgLeuGlnGln 60
DB 121 CACATTTTGGAAAGCCATTATATCACTCTCCAACTTATGAGCGAAGTTGCAACAG 180
QY 61 AspIleValIleuIleThrGluLeuIleGlnHisSerAlaIleHisIleValAspIleAsp 80
DB 181 GACAAAGTGTATATACAGAGCTCATCCAGCATTTGACGAAACATPAGGTTGACATTTGAT 240
QY 81 CysSerGlnLeuValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
DB 241 TGCAGTCAGAAAGGTGTATGTTTACATCAAACTCCCAAGATGTGCTCTCTCTCTTCA 300
QY 101 AspCysPheLeuThrValLeuLeuGluIleGluValSerPheAsnSerValHisIleu 120
DB 301 GACTGTTTCTACCTGACTTCTCTGGGTAACTGGAGAAAGCTTCACTCTTTCACCTG 360
QY 121 LeuAlaGlyIlePheAlaGlnPheSerArgCysPheProGlyLeuCysGlnGlyIleSer 140
DB 361 CTTCGACGGGGGTTGCTGAGTTCTCTGTTTCCCTGTTTCCCTGGGCTCTGTAAGAAATCC 420
QY 141 ThrIleuValProThrCysIleSerGlnProCysIleuProValAlaAsnIleGlyProThr 160
DB 421 ACTCTAGTCTCTACCTGACATTTCTAGCTTCTTAACTCTTAACTCTTAACTCTTAACTCT 480
QY 161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnIleGlyLeuIle 180
DB 481 CGAATTTCTTCCCAATCTTTATCTTGGCTGCCAGCAGATGCTCTCAACAGAGACTGATG 540
QY 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProIlePheAspPhe 200
DB 541 CAGCAGAAATGGGATTTGTTATGTGTTAAATGCCACCAATACCTGTCCAAAGCCTGACTTT 600
QY 201 IleProGlnUserHisPheLeuArgValProValAsnAspSerPheCysGlnIleIleu 220
DB 601 ATCCCGAGTCTCATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 221 ProTyrLeuAspIleSerValAspPheIleGlnValAlaIleSerAsnGlyCysVal 240
DB 661 CCGTGTGGTGGCAATCATGATGATTTCAATGAGAAAGAAAGCCTCCAAATGATGATGTT 720
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
DB 721 CTAGTGCACTGTTTGTGCTGGGATCTCCCGCTCCGCAACCATGCTATGCGCTACATCATG 780
QY 261 LysArgMetAspMetSerLeuAspGlnAlaTyrArgPheValIleGlnIleuArgProThr 280
DB 781 AAGAGAGATGACATGTCTTTAGATGAACTTACCAATTTGTGAAAAAGAAAGAAAGCTTCT 840
QY 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluIleValIleIleAsn 300
DB 841 ATATCTCCAAACTTCAATTTCTGGGCCAATCTCTGACATATGAGAAAGAAATTTAGAAC 900
QY 301 GlnThr 302
|||||

DB 901 CAGACT 906

RESULT 2

US-10-377-072-27

Sequence 27, Application US/10377072

Publication No. US20040009501A1

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals Inc.

APPLICANT: Curtis, Rory A.J.

APPLICANT: Logan, Thomas Joseph

APPLICANT: Glucksmann, Maria A.

APPLICANT: Meyers, Rachel E.

APPLICANT: Williamson, Mark J.

APPLICANT: Rudolph-Owen, Laura A.

APPLICANT: Chun, Miyoung

APPLICANT: Tsai, Feng-Ying

TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,

TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES

FILE REFERENCE: MP103-0180NM1M

CURRENT APPLICATION NUMBER: US/10/377,072

CURRENT FILING DATE: 2003-02-27

PRIOR APPLICATION NUMBER: US 09/895,860

PRIOR FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US 60/215,370

PRIOR FILING DATE: 2000-06-29

PRIOR APPLICATION NUMBER: US 09/723,806

PRIOR FILING DATE: 2000-11-28

PRIOR APPLICATION NUMBER: US 60/187,455

PRIOR FILING DATE: 2000-03-07

PRIOR APPLICATION NUMBER: US 09/843,297

PRIOR FILING DATE: 2001-04-25

PRIOR APPLICATION NUMBER: US 60/199,801

PRIOR FILING DATE: 2000-04-26

PRIOR APPLICATION NUMBER: US 09/861,801

PRIOR FILING DATE: 2001-05-21

PRIOR APPLICATION NUMBER: US 60/205,508

PRIOR FILING DATE: 2000-05-19

PRIOR APPLICATION NUMBER: US 09/816,494

PRIOR FILING DATE: 2001-03-23

PRIOR APPLICATION NUMBER: US 09/815,419

PRIOR FILING DATE: 2001-03-22

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 114

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 27

LENGTH: 1998

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(1998)

US-10-377-072-27

Alignment Scores:

Pred. No.:	9,31e-193	Length:	1998
Score:	1552.00	Matches:	300
Percent Similarity:	99.67%	Conservative:	1
Best Local Similarity:	99.34%	Mismatches:	1
Query Match:	99.23%	Indels:	0
DB:	17	Gaps:	0

US-10-029-345a-109_COPY_1_302 (1-302) x US-10-377-072-27 (1-1998)

QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGln 20
DB 1 ATGGCCCATGAGATGATGTTGAACTCAATTTGTTACGAGAGTTGGTCTGCTGGAGAA 60
QY 21 SerGlyThrGluLeuValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40
DB 61 AGTGGAAACGGAAAAAGTGTGCTTAATGTATGATGCCGCGCATTTGTGGAAATACATATCCTCC 120
QY 41 HisIleLeuGluAlaIleAsnIleAsnGlySerIleuMetIleuMetIleuArgLeuGlnGln 60

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DB 121 CACATTTGGAGGACCATTAATATCAATGCTCCAAAGCTTATAGAGGAGTTGCAACAG 180
QY 61 Aaplysvallleuilethgluleuileglnhisseralalyahislyvalaspiileap 80
DB 181 GACAAAGTTTATTAACAGAGCTCAATCCAGCATTCAGCAAACTAAGATTACATTGAT 240
QY 81 CysSerGlnlyValValValValTyraSpGlnSerSerGlnaApValAlaSerLeuSer 100
DB 241 TGCACATCGAAGAGTTGTAGTTTACATCAAAAGCTCCAAAGATGTCCTCTCTCTTCA 300
QY 101 AapCySpheLeuThrValleuLeuGlylyLeuGlnlySerPheAsnSerValHisLeu 120
DB 301 GACTGTTTCTCAGTCACTTCTGGGTAAACGAGAGAAGCTTCAACTCTGTCACTG 360
QY 121 LeuAlaGlylyPheAlaGlnPheSerArgCySpheProGlyLeuCyGlnGlylySer 140
DB 361 CTGGAGAGGAGTTGTAGTTCTCTGTTTCTCTGTTTCTCTGAGGAGGAGGAGGAGGAG 420
QY 141 ThrLeuValProThrCysIleSerGlnProCySpLeuProValAlaAsnIleGlyProThr 160
DB 421 ACTGATGTCCTCACTGATTTCTCAGCTTCTTACCTGTTGCCAACCTTGGGCAACC 480
QY 161 ArgIleLeuProAsnLeuTyrlenglyCySpGlnArgAspValLeuAsnlyGlnLeu 180
DB 481 CGAATTTCTCCAACTTTATCTTGGGCTGCCAGCGAGATGCTCTCAACAGAGGAGTATG 540
QY 181 GlnGlnAsnGlylyIleGlyTyrlValleuAsnAlaSerTyrlThrCySpProlyProAspPhe 200
DB 541 CAGCGAATGGAGATTGTATGTGTAAATGCCACCAATACCTGTCTCAAAAGCTGACTTT 600
QY 201 IleProGlnSerHisPheLeuArgValProValaAsnSerPheCyGlnlyValleu 220
DB 601 ATCCCGAGTCTCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 221 ProTyrLeuAspLySerSerValAspPheIleGlylyValAlaSerAsnlyCyVal 240
DB 661 CCGTGTGTCGACAAATCACTGATATTTCATTGAGAAAGCAAAAGCTCCAAAGATGTTGT 720
QY 241 LeuValHisCySpLeuAlaGlylyIleSerArgSerAlaThrIleAlaIleAlaTyrlleMet 260
DB 721 CTAGTGCACTGTTTGTGGGATCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 780
QY 261 LysArgMetAspMetSerLeuAspGlnAlaTyraSpPheVallyGlnlyValAspProThr 280
DB 781 AAGAGAGAGGACATCTTTAGATAGAGCTTACAGATTGTGAAAGAAAAGAAAGAAAGCT 840
QY 281 IleSerProAsnPheAsnPheLeuGlylyLeuLeuAspTyrlGlylySerIleIleYAsn 300
DB 841 ATATCTCCAACTTCAATTTTCTGGGCCAACTCTCGACTATGAGAGAGATTAAAGAAC 900
QY 301 GlnThr 302
DB 901 CAGACT 906
RESULT 3
US-10-377-072-27
; Sequence 27, Application US/10377072
; Publication No. US2004015721A9
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Logsen, Thomas Joseph
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williams, Mark J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Chun, Miyoung
; APPLICANT: Teal, Fong-Ying
; TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
; FILE REFERENCE: MP103-0180NMIM
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; CURRENT APPLICATION NUMBER: US/10/377,072
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US 09/895,860
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/215,370
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/723,806
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,455
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/843,297
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 60/199,801
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/816,494
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 09/815,419
; PRIOR FILING DATE: 2001-03-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (1998)
US-10-377-072-27
Alignment Scores:
Pred. No.: 9,31e-193 Length: 1998
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
Gaps: 0
US-10-029-345a-109_COPY_1_302 (1-302) x US-10-377-072-27 (1-1998)
QY 1 MetAlaHisGlnMetIleGlyThrcGlnIleValThrGlnValGlnValAlaLeuGln 20
DB 1 ATGGCCCATGAGATGATTGGAATCAATTTGTTACTGAGAGGTTGGCTCTCTGGAA 60
QY 21 SerGlyThrGlnlyValleuLeuIleAspSerArgProPheValGlnTyraAsnThrSer 40
DB 61 AGTGAAGGAAAGAGTCTGCTAATTGATAGCCGCAATTTGTGAATACATACATCC 120
QY 41 HisIleLeuGlnAlaIleAsnIleAsnCySerLyLeuMetLyArgArgLeuGln 60
DB 121 CACATTTGGAGGACCATTAATATCAATGCTCCAAAGCTTATAGAGGAGTTGCAACAG 180
QY 61 Aaplysvallleuilethgluleuileglnhisseralalyahislyvalaspiileap 80
DB 181 GACAAAGTTTATTAACAGAGCTCAATCCAGCATTCAGCAAACTAAGATTACATTGAT 240
QY 81 CysSerGlnlyValValValValTyraSpGlnSerSerGlnaApValAlaSerLeuSer 100
DB 241 TGCACATCGAAGAGTTGTAGTTTACATCAAAAGCTCCAAAGATGTCCTCTCTCTTCA 300
QY 101 AapCySpheLeuThrValleuLeuGlylyLeuGlnlySerPheAsnSerValHisLeu 120
DB 301 GACTGTTTCTCAGTCACTTCTGGGTAAACGAGAGAAGCTTCAACTCTGTCACTG 360
QY 121 LeuAlaGlylyPheAlaGlnPheSerArgCySpheProGlyLeuCyGlnGlylySer 140
DB 361 CTGGAGAGGAGTTGTAGTTCTCTGTTTCTCTGTTTCTCTGAGGAGGAGGAGGAGGAG 420
QY 141 ThrLeuValProThrCysIleSerGlnProCySpLeuProValAlaAsnIleGlyProThr 160
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Db 421 ACTCTAGTCCCTACGATTTCTGACCTTGCTTCCGTGGCCAACTTGGGCCAAC 480
Qy 161 Arg11LeuProAsnLeuTyrLeuGlyCySGlnArgAspValLeuAsnLysGluLeu 180
Db 481 CGAATCTTCCCAATCTTTATCTTGAGCTGCAGCGAGATGTCTCAACAGAGCTGAG 540
Qy 181 GlnGlnAsnGly11eg1YrValLeuAsnAlaSerTyrThrCysProLysProAspPhe 200
Db 541 CAGCAAAATGGGATTTGTTATGTGTTAAATGCCAGAAATCTGTCCAAAGCTGACTT 600
Qy 201 11eProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGlnLys11eLeu 220
Db 601 ATCCCGAGCTCATCTTCTCGCTGCTGCTGGAAGAAGACGCTTTGTGAGAAAATTTG 660
Qy 221 ProTProLysAspLysSerValAspPhe11eg1LysValAlaLysSerAsnGlyCysVal 240
Db 661 CCGTGGTGGACAAATCAATTAATTCATGATGAGAAAGAAAGCCCTCCAAATGATGTGT 720
Qy 241 LeuValHisCysLeuAlaGly11eSerArgSerAlaThr11eAla11eAlaTyr11eMet 260
Db 721 CTAGTGCACTGTTTACGTGGATCTCCCGCTCCGCAACATGCTATGCTCACTCATG 780
Qy 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGlnLysArgProThr 280
Db 781 AAGAGATGACATGTCTTATGATGAGCTTACAGATTGTGAAGAAAAGAAAGACTACT 840
Qy 281 11eSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGlnLysLys11eLysAsn 300
Db 841 AATCTCCAACTTCAATTTCTTGAGGCCAACTCTGAGCTATGAGAAAGAAATTAAGAC 900
Qy 301 GlnThr 302
Db 901 CAGACT 906

RESULT 4
US-10-072-012-257
; Sequence 257, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spyrek, Kimberly
; APPLICANT: Zernusen, Bryan
; APPLICANT: Patkurajan, Weera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grossie, William M.
; APPLICANT: Alsebrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
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; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 257
; LENGTH: 2071
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-012-257

Alignment Scores:
Pred. No.: 9,89e-193 Length: 2071
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Mismatches: 1
Best Local Similarity: 99.34% Indels: 0
Query Match: 99.23% Gaps: 0
DB: 17

US-10-029-345a-109_copy_1_302 (1-302) x US-10-072-012-257 (1-2071)
Qy 1 MetAlaHisGluMet11eg1YrGln11eVal1ThrGluArgLeuValAlaLeuLeuGlu 20
Db 61 ATGGCCATAGAGATGATGGAACCAATGTTACTGAGAGTTGGCTGCTGCGGAA 120
Qy 21 SerGlyThrGlnLysValLeuLeu11eAspSerArgProPheValGluTyrAsnThrSer 40
Db 121 AGTGAACGGAAGAAAGCTGCTTATGATGACCGGCACTTTGTGAAATTCATACATCC 180
Qy 41 His11eLeuGlnAla11eAsn11eAsnCysSer11eLeuMet11eArgArgLeuGln 60
Db 181 CACATTTTGAAGCATTAATATCACTGCTCCAAAGTTATGAAGCAAGTTGCAACAG 240
Qy 61 AspLysValLeuLeuThrGlnLeu11eg1HisSerAlaSerHisLysValAsp11eAsp 80
Db 241 GACAAAGTTAATTAACAGAGCTCATCCAGCATTCACGAAACATTAAGTTGACATTGAT 300
Qy 81 CysSerGlnLysValVal11eAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db 301 TGCAGTCAGAAAGTTGATGATTAAGATCAAGATCCCAAGATGTGCTCTCTCTTCA 360
Qy 101 AspCysPheLeuThrValLeuLeuGlyLysLeuGlnLysSerPheAsnSerValHisLeu 120
Db 361 GACTGTTTCTCACTGATCTTGAGTAACTGGAAGAGAGCTTCAACTGTTCACTG 420
Qy 121 LeuAlaGly11eLeuAlaGluPheSerArgCysPheProGlyLeuGlyGlySer 140
Db 421 CTTCAGAGTGGTGTGCTGAGTCTCTCGTTGTTCCCTGCGCTGTGAGGAAATATCC 480
Qy 141 ThrLeuValProThrCys11eSerGlnProCysLeuProValAlaAsn11eg1ProThr 160
Db 481 ACTCTAGTCCCTACGATTTCTGACCTTGCTTACCTGTTCCCAACATGGGCCAAC 540
Qy 161 Arg11LeuProAsnLeuTyrLeuGlyCySGlnArgAspValLeuAsnLysGluLeu 180
Db 541 CGAATCTTCCCAATCTTTATCTTGAGCTGCAGCGAGATGTCTCAACAGAGCTGAG 600
Qy 181 GlnGlnAsnGly11eg1YrValLeuAsnAlaSerTyrThrCysProLysProAspPhe 200
Db 601 CAGCAAAATGGGATTTGTTATGTGTTAAATGCCAGAAATCTGTCCAAAGCTGACTT 660
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Qy 201 ILeProgiUserHisPheLeuAryValProValAaenAspSerPheCysGluValIleLeu 220
Db 661 ATCCCGAGTGTCAATTCCTGGGTGCTGCTGGATGACAGCTTTTGTGAGAAAATTTTG 720
Qy 221 ProTripleuAapLySerValAspPheIleGluValAlaValAspSerHisGlyCysVal 240
Db 721 CCGGTGTGGACAAATCAGTATTCATTTGAGAAAGCAAAAGCCTCCAAATGAGATGTGT 780
Qy 241 LeuValHisCysPheAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
Db 781 CTAGTCTGCTGTTTACTGGGATCTCCGCTCCGACATGCTATGCTTACACTCAG 840
Qy 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValGlyLysArgProThr 280
Db 841 AAGGAGATGACATCTCTTATGATGACCTTACATTTGTGAAAAGAAAAAGACTTACT 900
Qy 281 ILeSerProAsnPheAsnPheLeuGlyGluLeuAspTyrGluLysValIleLysAsn 300
Db 901 ATATCTCCAAACTTCATATTTCTGGGCCAACTCCTGACATATGAGAAAGATTAAAGAC 960
Qy 301 GlnThr 302
Db 961 CAGACT 966

RESULT 5

US-10-168-506-2
; Sequence 2, Application US/10168506
; Publication No. US20040053229A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY D.
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: MAYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSHANAM, SUCHA
; APPLICANT: HILL, RON
; APPLICANT: FLANAGAN, PETER
; TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
; FILE REFERENCE: 038602/1351
; CURRENT APPLICATION NUMBER: US/10/168,506
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: PCT/US00/34736
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-168-506-2

Alignment Scores:

Pred. No.: 1,57e-192 Length: 2732
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservatve: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 17 Gaps: 0

US-10-029-345a-109_COPY_1_302 (1-302) x US-10-168-506-2 (1-2732)

Qy 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
Db 538 ATGGCCCATGAGATGATGGAACTCAAAATGTTACTGTGAGAGGTGGCTCTGCTGGAA 597
Qy 21 SerGlyThrGluValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40
Db 598 AGTGAAGAGAAAAGTGTCTGTAATGATGACGGCCATTTGTGAATTAACAATCATCC 657
Qy 41 HisIleLeuGluAlaIleAsnIleAsnCysSerIlySleMetLysArgArgLeuGln 60
Db 658 CACATTTTGGAAAGCCATTAAATCACTGCTCCAAAGCTTATGAAAGGTTGCAACAG 717
Qy 61 AspLysValLeuIleThrGluLeuIleGlnHisSerAlaLysIleValAspIleAsp 80

Db 718 GACAAAGTAAATTACAGAGCTCATCCAGATTCAGGAAACATAGGTTGACATTGAT 777
Qy 81 CysSerGlyLysValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSer 100
Db 778 TGCAGTCAGAAAGTTGATGTTACATCAAAAGCTCCAAAGATGTGCTCTCTCTTCA 837
Qy 101 AspCysPheLeuThrValLeuLeuGlyLysLeuGluLysSerPheAsnSerValHisLeu 120
Db 838 GACTGTTTCTCAGTCTCTTCTGGTAACTGAGAAAGACTTCAACTCTTCACTG 897
Qy 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyLysSer 140
Db 898 CTGGAGGTGGATTGGCTGAGATTCCTGTTGTTCCCTGGCCCTGTGAAAGAAATCC 957
Qy 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Db 958 ACTTATGTCCTTACCTGATTCATGAGCTTGCTTACCTGTTGCCAAACATTTGGGCAAC 1017
Qy 161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnLysGluLeuIle 180
Db 1018 CGAATTCCTCCATCTTATCTTGGCTGCCAGGAGATGCTTCAACAAGAGCTGATG 1077
Qy 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProLysProAspPhe 200
Db 1078 CAGAGAAATGGGATTTGTTATGTTAATGCAAGCAATACCTGTCCAAAGCTGACTTT 1137
Qy 201 ILeProgiUserHisPheLeuAryValProValAaenAspSerPheCysGluValIleLeu 220
Db 1138 ATCCCGAGTGTCAATTTCTGGGTGCTGCTGGATGACAGCTTTTGTGAGAAAATTTTG 1197
Qy 221 ProTripleuAapLySerValAspPheIleGluValAlaValAspSerHisGlyCysVal 240
Db 1198 CCGGTGTGGACAAATCAGTATTCATTTGAGAAAGCAAAAGCCTCCAAATGAGATGTGT 1257
Qy 241 LeuValHisCysPheAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
Db 1258 CTAGTCTGCTGTTTACTGGGATCTCCGCTCCGACATGCTATGCTTACACTCAG 1317
Qy 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValGlyLysArgProThr 280
Db 1318 AAGGAGATGACATGCTCTTATGATGACCTTACATTTGTGAAAAGAAAAAGACTTACT 1377
Qy 281 ILeSerProAsnPheAsnPheLeuGlyGluLeuAspTyrGluLysValIleLysAsn 300
Db 1378 ATATCTCCAAACTTCATATTTCTGGGCCAACTCCTGACATATGAGAAAGATTAAAGAC 1437
Qy 301 GlnThr 302
Db 1438 CAGACT 1443

RESULT 6

US-10-257-026-1
; Sequence 1, Application US/10257026
; Publication No. US20040086859A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: New dual specificity phosphatase
; FILE REFERENCE: DUSP10KDS
; CURRENT APPLICATION NUMBER: US/10/257,026
; CURRENT FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3059
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (127)..(2121)
US-10-257-026-1

Alignment Scores:

Pred. No.: 1,9e-192 Length: 3059
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 17 Gaps: 0

US-10-029-345A-109_COPY_1_302 (1-302) x US-10-257-026-1 (1-3059)

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QY 1 MetAlaHisGluMetIleGlyThrGlnIleValIleThrGluArgLeuValAlaLeuGlu 20
Db 127 ATGGCCCATGAATGATTAAGTCAATTAATGTTACTGAGAGGTGGTGGCTCTGCTGAA 186
QY 21 SerGlyThrGluValLeuLeuIleAspSerArgProPheValGluTrpAsnThrSer 40
Db 187 AGTGGAAACGGAAGAAAGTGTCTGCTAAATGATAGCCGGCCATTTGTGGAAATCAATCATCC 246
QY 41 HisIleLeuGluAlaIleAsnIleAsnGlySerIleLeuMetIleArgLeuGlnGln 60
Db 247 CACATTTTGGAAAGCATTAATATCAATGCTCCAAAGCTTATGAGGAAGTTGCAACAG 306
QY 61 AspIleValLeuIleThrGluLeuIleGlnHisSerAlaValHisIleValAspIleAsp 80
Db 307 GACAAAGTGTAAATTAACAGAGCTCATCCAGCATTCAGCGAAACATTAAGGTGAATGAT 366
QY 81 CysSerGlnIleValIleValIleTrpAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db 367 TGCAGTCAAGAGGTGTAGTTTACATCAATCAAGCTCCAAAGATGTTGCCCTCTCTTCA 426
QY 101 AspCysPheLeuThrValLeuLeuGluIleValLeuGluIleValSerPheAsnSerValHisLeu 120
Db 427 GACTGTTTTCTACGTACTCTCGGTGGAACGAGGAAGAGCTTCAACTGTCTTCACTG 486
QY 121 LeuAlaGlyIleGlyPheAlaGluPheSerArgCysPheProGlyLeuGluGlnIleValSer 140
Db 487 CTTCGAGGTGGGTTGCTGAGTTCCTGCTGTTTCTCCGCTCTGCGAAGGAAATCC 546
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Db 547 ACTCAGTCCCTACCTGATTTCTCAGCCTTGCTTACCTGTTGCCAATCGGCGCAACC 606
QY 161 ArgIleLeuProAsnLeuTrpLeuGluIleCysGlnArgAspValLeuAsnIleGluLeu 180
Db 607 GCAATTTCTCCAAATCTTATCTTGCGCCAGCGAGATGCTTCAAGAAAGAGCTGATG 666
QY 181 GlnGlnAsnGlyIleGlyTrpValLeuAsnIleAspTrpThrCysProIleProAspPhe 200
Db 667 CAGCAGATGGGATTTGATTATGTGTAAATGCCAGCAATACCTGTCCAAAGCTGACTTT 726
QY 201 IleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluIleLeu 220
Db 727 ATCCCGAGTCTCATTTCTCGTGTGCTGATGACAGCTTTTGAGAAATTTTG 786
QY 221 ProTrpLeuAspIleValSerValAspPheIleGluIleValIleValIleValIleVal 240
Db 787 CCGGTGTGGCAATATCAATGATTTCTTGAAGAAAGAAAGCTCCAAAGGATGTGT 846
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIleValIleMet 260
Db 847 CTAGTGCACTGTTTATAGTGGGATCTCCGCTCCGCGCAATCCGTTATGCTTACATCATG 906
QY 261 LysArgMetAspMetSerLeuAspGluAlaTrpArgPheValIleGluIleValArgProThr 280
Db 907 AAGGAGTGGACATGCTTTAGATGAGCTTACAGATTTTGAAAGAAAGAAAGCACTACT 966
QY 281 IleSerProAsnPheAsnPheLeuGluIleLeuMetAspTrpGluIleValIleValAsn 300
Db 967 ATATCTCAAACTTCAATTTCTGCGCAACTCTGCACTATGAGAAAGAAATTAAGAAC 1026
QY 301 GlnThr 302
Db 1027 CAGACT 1032
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RESULT 7
US-09-964-277-1

/ Sequence 1, Application US/09964277

/ Patent No. US20020137170A1

/ GENERAL INFORMATION:

/ APPLICANT: Lucite, Ralf M.

/ APPLICANT: Wei, Bo

/ TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE

/ FILE REFERENCE: 200125,434

/ CURRENT APPLICATION NUMBER: US/09/964,277

/ CURRENT FILING DATE: 2001-09-25

/ NUMBER OF SEQ ID NOS: 22

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 1

/ LENGTH: 3496

/ TYPE: DNA

/ ORGANISM: Homo sapiens

US-09-964-277-1

Alignment Scores:

Pred. No.: 2,38e-192 Length: 3496
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 9 Gaps: 0

US-10-029-345A-109_COPY_1_302 (1-302) x US-09-964-277-1 (1-3496)

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QY 1 MetAlaHisGluMetIleGlyThrGlnIleValIleThrGluArgLeuValAlaLeuGlu 20
Db 562 ATGGCCCATGAATGATTAAGTCAATTAATGTTACTGAGAGGTGGTGGCTCTGCTGAA 621
QY 21 SerGlyThrGluValLeuLeuIleAspSerArgProPheValGluTrpAsnThrSer 40
Db 622 AGTGGAAACGGAAGAAAGTGTCTGCTAAATGATAGCCGGCCATTTGTGGAAATCAATCATCC 681
QY 41 HisIleLeuGluAlaIleAsnIleAsnGlySerIleLeuMetIleArgLeuGlnGln 60
Db 682 CACATTTTGGAAAGCATTAATATCAATGCTCCAAAGCTTATGAGGAAGAGTTCGCAACAG 741
QY 61 AspIleValLeuIleThrGluLeuIleGlnHisSerAlaValHisIleValAspIleAsp 80
Db 742 GACAAAGTGTAAATTAACAGAGCTCATCCAGATTCAGCGAAACATTAAGGTTGACATGAT 801
QY 81 CysSerGlnIleValIleValIleTrpAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db 802 TGCAGTCAAGAGGTGTAGTTTACAGATCAAGCTCCAAAGATGTGCTCTCTCTTCA 861
QY 101 AspCysPheLeuThrValLeuLeuGluIleValSerPheAsnSerValHisLeu 120
Db 862 GACTGTTTTCTACCTGATTTCTGGGTGAATCTGGAAGAGAGCTTCAACTGTTCACCTG 921
QY 121 LeuAlaGlyIleGlyPheAlaGluPheSerArgCysPheProGlyLeuGluGlnIleValSer 140
Db 922 CTTCGAGGTGGGTTGCTGAGTTCCTCGTGTGTTCTCCGCTCTGCGAAGGAAATCC 981
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Db 982 ACTTATCTCCATCACTGATTTCTAGCCTTGCTTACCTGTTGCTCCAAACATTTGGCCCAACC 1041
QY 161 ArgIleLeuProAsnLeuTrpLeuGluIleCysGlnArgAspValLeuAsnIleGluLeu 180
Db 1042 CGAATTTCTCCAAATCTTATCTTGGTGCGCAAGAGATGTCTTCAAGAGAGCTGATG 1101
QY 181 GlnGlnAsnGlyIleGlyTrpValLeuAsnIleAspTrpThrCysProIleProAspPhe 200
Db 1102 CACAGAGATGGGATTTGATTATGTGTAAATGCCAGCAATACCTGTCCAAAGCTGACTTT 1161
QY 201 IleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluIleLeu 220
Db 1162 ATCCCGAGTCTCATTTCTCGTGTGCTGATGACAGCTTTTGAGAAATTTTG 1221
```

QY	221	ProTIRpleuAspLysSerValaAspPheIleGluValaAlaLysAlaSerAsnGlyCYVal	240
Db	1222	CCGTCGTTGGACAAATCAAGTACATTTCATTGAGAAAGCAAAAGCTCCAAAGATGTGT	1281
QY	241	LeuValHisValLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet	260
Db	1282	CTAGGCACTGTTTGTGCTGGGATCTCCCGCTCCGACACATCGCTATGCGCCATCACTCATG	1341
QY	261	LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValIleGluLysAspProThr	280
Db	1342	AAGAGGATGGACATCTCTTTAGATGAAGCTTTCAGATTGTGAAAGAAAAAGACCTTACT	1401
QY	281	IleSerProAsnPheAsnPheLeuGlyGlnIleuLeuAspTyrGluLysAlaIleLysAsn	300
Db	1402	ATATCTCAAACTTCAATTTTCTGGGCAACTCTGACTATGAGAAAGATTAAGAAC	1461
QY	301	GlnThr 302	
Db	1462	CAGACT 1467	

RESULT 8

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US-10-370-715B-261
; Sequence 261, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
;   Patin Docket Preview
;   APPLICANT: BODARY, SARAH C.
;   APPLICANT: CLARK, HILARY
;   APPLICANT: BRISDELL, HUNTE
;   APPLICANT: JACKMAN, JANET
;   APPLICANT: SCHOENFELD, TILL R.
;   APPLICANT: WILLIAMS, P. MICKEY
;   APPLICANT: WOOD, WILLIAM I.
;   APPLICANT: WU, THOMAS D.
;   TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
;   TITLE OF INVENTION: Related Diseases
;   FILE REFERENCE: PI948R1-US
;   CURRENT APPLICATION NUMBER: US/10/370,715B
;   CURRENT FILING DATE: 2003-02-21
;   NUMBER OF SEQ ID NOS: 742
;   SEQ ID NO 261:
;     LENGTH: 3521
;     TYPE: DNA
;   ORGANISM: Homo sapien
US-10-370-715B-261

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Alignment Scores:

Pred. No.:	2,41e-192	length:	3521
Score:	1552.00	Matches:	300
Percent Similarity:	99.67%	Conservative:	1
Best Local Similarity:	99.34	Mismatches:	1
Query Match:	99.23%	Indels:	0
DB:	18	Gaps:	0

US-10-029-345A-109_COPY_1_302 (1-302) X US-10-370-715B-261 (1-3521)

Qy	1	MeAlaHisGluMetIleGlyThrGlnIleValIleThnGluArgLeuValAlaLeuLeuGlu	20
Db	564	ATGGCCCATGAGTAAATGGTCAATATTGTACGAGAGGTGTGGCTCTCTGGAA	6223
Qy	21	SerGlyThrGluValLeuLeuIleLeuSerArgProPheValGluTyrAsnThrSer	40
Db	624	AGTGGACCGGAAAAAGCTGCTGATTATGATTAGCGCGCATTTGTGGATTCAATACATCC	6833
Qy	41	HisIleLeuGluIleAlaLeuIleAsnIleAsnGlySerIleValMetIleValArgLeuGlnGln	60
Db	684	CACATTTTGGACCCATTAATATCACTCTCCAGCTTAGAACCGGAAAGGTGTCAACAG	7433
Qy	61	AspIleValLeuIleLeuThrGluLeuIleGlnHisSerAlaIleValHisIleValAspIleAsp	80
Db	744	GACCAATGTTATTATTCACAGCTCATCCAGCATTCAGCGAACCAATTAAGGTGGACATTGAT	8003
Qy	81	CysSerGlnIleValValIleTyrAspGlnSerSerGlnIlePheValAlaSerLeuSerSer	100

Db	804	TGCACTCAGAAAGTTGTAGTTACATCAAGCTCCCAAGATGTTGCCTCTCTCTTCA	863
Qy	101	AspCysPheLeuThrValLeuLeuGlyLysLeuGluLysSerPheAsnSerValHisLeu	120
Db	864	GACTGTTTTCATCTGACTTCTGGGGTAACTGAGAAAGACTTCAACTCTGTCACCTG	923
Qy	121	LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyLysSer	140
Db	924	CTTGCAGAGTGGAGTTGCTGAGCTTCTCTGTTGTTTCCCTGGCTCTGGAGAAATCC	983
Qy	141	ThrLeuValProThrCysHisSerGlnProCysLeuProValAlaAsnIleGlyProThr	160
Db	964	ACTCTAGTCCCTCACTGCAATTTCTCAGCCTTGCTTACCTGTTGCCAACTTGGGCCACC	104
Qy	161	ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnLysGluLeuIle	180
Db	1044	CGAATTTCTCCCAATCTTTATCTTGGCTGCCAGCAGATGTCCTCAACAAGAGCTGATG	1104
Qy	181	GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProLysProAspPhe	200
Db	1104	CAGCAGAAATGGAGATTGTATGTGTTAATGCGCAATACCTGTGCCAAAGCTGACTTT	1164
Qy	201	IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIleLeu	220
Db	1164	ATCCCGAGCTCATTTCTCGGTGTGCTGTGAATGACAGCTTTTGAGAAAAATTTTG	1224
Qy	221	ProTrpLeuAspLysSerValAspPheIleGluLysAlaLysAlaSerAsnGlyCysVal	240
Db	1224	CCGTGGTTGGCAAAATCACTGATTTTCAATGAGAAAGCAAAAGCTCCCAATGAGATGTGT	1284
Qy	241	LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet	260
Db	1284	CTAGTGCACTGTTAGCTGGGATCTCCGCTCCGCCACATCGCTATGCGCTACATCATG	1344
Qy	261	LysArgMetAspMetSerLeuAspGlnAlaTyrArgPheValIleGluLysArgProThr	280
Db	1344	AAGAGGATGACATGCTTTAGATGAAAGCTTACAGATTGTGAAAGAAAGAAAGACTTACT	1404
Qy	281	IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGluLysIleLysAsn	300
Db	1404	ATATCTCCAAACTTCAATTTCTGGGCCAACTCTCGAGCTATGAGAAAGATTTAAGAAC	1464
Qy	301	GlnThr 302	
Db	1464	CAGACT 1469	
RESULT 9			
US-09-816-494-1			
/ Sequence 1, Application US/09816494			
/ Patent No. US20020034807A1			
/ GENERAL INFORMATION:			
/ APPLICANT: Meyers, Rachel A.			
/ TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY			
/ FILE REFERENCE: 10448-030002			
/ CURRENT APPLICATION NUMBER: US/09/816,494			
/ CURRENT FILING DATE: 2001-03-23			
/ PRIOR APPLICATION NUMBER: US 60/191,858			
/ PRIOR FILING DATE: 2000-03-24			
/ NUMBER OF SEQ ID NOS: 10			
/ SOFTWARE: FastSeq for Windows Version 4.0			
/ SEQ ID NO 1			
/ LENGTH: 3544			
/ TYPE: DNA			
/ ORGANISM: Homo sapiens			
/ FEATURE:			
/ NAME/KEY: CDS			
/ LOCATION: (589) ... (2583)			
US-09-816-494-1			
Alignment Scores:			
Pred. No.: 2,43e-192 Length: 3544			

Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 0
Query Match: 99.23% Indels: 0
DB: 9 Gaps: 0

US-10-029-345A-109_COPY_1_302 (1-302) x US-09-816-494-1 (1-3544)

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OY 1 MetAlaH:EGlUmeTlleglYThrGlnIleValThGluArgLeuValAlaLeuEnglu 20
DB 589 ATGGCCCATGAGATGATTGGAATCTCAATTTGTTACTGAGAGGTTGGCTCTGCTGGAA 648
OY 21 SerGlyThrGluYsValLeuLeuIleAspSerArgProPheValGluTyraAnthSer 40
DB 649 AGTGGAAACGAAAAAGTGTCTTAATGTATGATGCGGCGCATTTGTGGAATACATCATCC 708
OY 41 HisIleLeuGluAlaIleAsnIleAsnCySerIlySleuMetIlyArgArgLeuGlnGln 60
DB 709 CACATTTTGGAGCCATTATATCACTGCTCCAGCTTATGAAAGGAGTTGCAACAG 768
OY 61 AspIysValLeuIleThrGluLeuIleGlnHisSerAlaIysHisIlyValAspIleAsp 80
DB 769 GACAAAGTTTAAATTCAGAGCTCATCCAGCTTCCAGCAACATAGGTTTACATTGAT 828
OY 81 CysSerGlnIysValValValIlyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
DB 829 TGCAGTCCAGAAAGTTGATGATTACGATCAAGCTCCCAAGATGTTGCCCTCTCTTCA 888
OY 101 AspCysPheLeuThrValLeuLeuGluYsLeuGluYsSerPheAsnSerValHisIleu 120
DB 889 GACTGTTTCTACGTACTTCTGGGTAACGTGGAAGAGCTTCAACTCTGTTACCTG 948
OY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuCyGluGlyYsSer 140
DB 949 CTTCGAGGTGGGTTTGTCTGAGTCTCTCTGTTTCCCTGGCTCTGGAAGAAATCC 1008
OY 141 ThrIleuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
DB 1009 ACTTAGTCCCTACCTGATTTCTCAGCCTTCTTACCTGTTGCCAATGGGCAACC 1068
OY 161 ArgIleuProAsnLeuTyrlleuGlyCysGlnArgAspValLeuAsnIysGluLeuIle 180
DB 1069 GCAATTTCTCCCAATCTTATCTGTGCTGCCAGCAGATGTCCTCAACAAAGAGCTGATG 1128
OY 181 GlnGlnAsnGlyIleGlyTyrlValLeuAsnAlaSerTyrlThrCysProIysProAspPhe 200
DB 1129 CAGCAGATGGGATTGTTATCTGTTAAATGCCACATACCTGTCCAAAGCTGACTTT 1188
OY 201 IleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluYsIleLeu 220
DB 1189 ATCCCCGAGTCTCATTTCTCGTGTGCTGATGACAGCTTTTGAGAAATTTTG 1248
OY 221 ProTrpLeuAspIysSerValAspPheIleGluYsAlaIlyAsnIleAsnGlyCysVal 240
DB 1249 CCGGTGTGGCAAAATTCAGTATTCATGTAGAAAGAAAGCCTCCAAATGAGATGTTT 1308
OY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrlleuMet 260
DB 1309 CTAGTGCACTGTTTATGCTGGATCTCCGCTCCGCAACATCGCTATGCTTACATCAG 1368
OY 261 LysArgMetAspMetSerLeuAspGluAlaTyrlArgPheValIysGluYsArgProThr 280
DB 1369 AAGGAGATGACATGCTTTAGATGATGACATTAAGATTTTGAAAGAAAAAGACTTACT 1428
OY 281 IleSerProAsnPheAsnPheLeuGluYsIleuLeuAspTyrlGluYsIlyIleYsAsn 300
DB 1429 ATATCTCCAAACTTCAATTTCTGTGGCCAACTCTCGACTATGAGAAAGATTAAGAAC 1488
OY 301 GlnThr 302
DB 1489 CAGACT 1494
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RESULT 10

US-10-377-072-25

/ Sequence 25, Application US/10377072
/ Publication No. US20040009501A1

/ GENERAL INFORMATION:

/ APPLICANT: Millennium Pharmaceuticals Inc.

/ APPLICANT: Curtis, Roy A.J.

/ APPLICANT: Logan, Thomas Joseph

/ APPLICANT: Glucksmann, Maria A.

/ APPLICANT: Meyers, Rachel E.

/ APPLICANT: Williamson, Mark J.

/ APPLICANT: Rudolph-Owen, Laura A.

/ APPLICANT: Chun, Miyoung

/ APPLICANT: Tsai, Fong-Ying

/ TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,

/ TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES

/ TITLE OF INVENTION: AND USES THEREFOR

/ FILE REFERENCE: MP103-0180NMIM

/ CURRENT APPLICATION NUMBER: US/10/377, 072

/ CURRENT FILING DATE: 2003-02-27

/ PRIOR APPLICATION NUMBER: US 09/895,860

/ PRIOR FILING DATE: 2001-06-29

/ PRIOR APPLICATION NUMBER: US 60/215,370

/ PRIOR FILING DATE: 2000-06-29

/ PRIOR APPLICATION NUMBER: US 09/723,806

/ PRIOR FILING DATE: 2000-11-28

/ PRIOR APPLICATION NUMBER: US 60/187,455

/ PRIOR FILING DATE: 2000-03-07

/ PRIOR APPLICATION NUMBER: US 09/843,297

/ PRIOR FILING DATE: 2001-04-25

/ PRIOR APPLICATION NUMBER: US 60/199,801

/ PRIOR FILING DATE: 2000-04-26

/ PRIOR APPLICATION NUMBER: US 09/861,801

/ PRIOR FILING DATE: 2001-05-21

/ PRIOR APPLICATION NUMBER: US 60/205,508

/ PRIOR FILING DATE: 2000-05-19

/ PRIOR APPLICATION NUMBER: US 09/816,494

/ PRIOR FILING DATE: 2001-03-23

/ PRIOR APPLICATION NUMBER: US 09/815,419

/ PRIOR FILING DATE: 2001-03-22

/ Remaining Prior Application data removed - See File Wrapper or PALM.

/ NUMBER OF SEQ ID NOS: 114

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 25

/ LENGTH: 3544

/ TYPE: DNA

/ ORGANISM: Homo Sapiens

/ FEATURE:

/ NAME/KEY: CDS

/ LOCATION: (589) ... (2586)

US-10-377-072-25

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

2.43e-192 Length: 3544

1552.00 Matches: 300

99.67% Conservative: 1

99.34% Mismatches: 1

99.23% Indels: 0

17 Gaps: 0

US-10-029-345A-109_COPY_1_302 (1-302) x US-10-377-072-25 (1-3544)

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OY 1 MetAlaH:EGlUmeTlleglYThrGlnIleValThGluArgLeuValAlaLeuEnglu 20
DB 589 ATGGCCCATGAGATGATTGGAATCTCAATTTGTTACTGAGAGGTTGGCTCTGCTGGAA 648
OY 21 SerGlyThrGluYsValLeuLeuIleAspSerArgProPheValGluTyraAnthSer 40
DB 649 AGTGGAAACGAAAAAGTGTCTTAATGTATGATGCGGCGCATTTGTGGAATACATCATCC 708
OY 41 HisIleLeuGluAlaIleAsnIleAsnCySerIlySleuMetIlyArgArgLeuGlnGln 60
DB 709 CACATTTTGGAGCCATTATATCACTGCTCCAACTTATGAAAGGAGTTGCAACAG 768
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Qy	61	AspLeuValLeuIleThrGluLeuIleGlnHisSerAlaIleHisIleValAspIleAsp	80
Db	769	GACAAAGCTTATTATTCAGAGCTCATCCAGCATTCAGCAACATATAGGTGACATTGAT	828
Qy	81	CysSerGlnIleValIleValIleValIleValIleValIleValIleValIleValIleVal	100
Db	829	TGCAGTCAGAAAGTGTGATGATTACGATCAAAAGCTCCAAAGATGTTGCTCTCTTCA	888
Qy	101	AspCysPheLeuThrValIleuLeuGlyIleValGluIleSerPheAsnSerValHisLeu	120
Db	889	GACTGTTTTCCTACCTGACTCTTCGGGTTAACTGGAGAAAGAGCTTCAACTCTGTTCACTCG	948
Qy	121	LeuAlaGlyIlePheAlaGluPheSerArgCysPheProGlyIleuGlyGlyIleValSer	140
Db	949	CTTGCAAGGGGTGTGCTGAGTTCTCTCTGTTTCCCTGGGCTCTGTAAAGGAAATCC	1008
Qy	141	ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr	160
Db	1009	ACTCTAGTCCCTACCTGATTTCTCAGCTTCTTACCTGTGGCCAACTGGGCCAACC	1068
Qy	161	ArgIleLeuProAsnIleuTyrluGlyCysGlnArgAspValIleuAsnIleGluLeuIle	180
Db	1069	CGAATTCTTCCCAATCTTATCTTGAGCTCCAGCGAGATGTCCTCAACAAGAGCTGATG	1128
Qy	181	GlnGlnAsnGlyIleGlyTyrluValIleuAsnAlaSerTyrluCysProIleProAspPhe	200
Db	1129	CAGCAAGAAATGGATGGTATGTATGTTAAATGCGAGAAATACCTGTCCAAAGCTGACTTT	1188
Qy	201	IleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluIleValIleu	220
Db	1189	ATCCCGAGTCTCATTTCTCGCTGTGCTGTGATGACAGCTTTGTGAGAAATTTTG	1248
Qy	221	ProTyrLeuAspIleSerValAspPheIleGluValAlaIleValAsnGlyCysVal	240
Db	1249	CCGTGTTGGACAAATCAGTAGATTTCATTGAGAAAGCAAAAGCTCCCATGAGATGTGTT	1308
Qy	241	LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrluMet	260
Db	1309	CTAGTGCACTGTTTGTGCTGGAGTCTCCGCTCCGCAACATGCTATCCCTCAACATCAG	1368
Qy	261	LysArgMetAspMetSerLeuAspGluAlaTyrluArgPheValIleGluIleValAspProThr	280
Db	1369	AAGAGATGACATGCTCTTATGATGAGCTTTCAGATTGTGTAAAGAAAAAGACTTACT	1428
Qy	281	IleSerProAsnPheAsnPheLeuGlyGlnIleuLeuAspTyrluIleValIleValAsn	300
Db	1429	ATATCTCCAAACTTCATTTTCTGGGCCAACTCTGGAATTATGAGAAAGATTTAAGAAC	1488
Qy	301	GlnThr 302	
Db	1489	CAGACT 1494	

RESULT 11
 US-10-377-072-25
 Sequence 25, Application US/10377072
 Publication No. US20040157221A9
 GENERAL INFORMATION:
 APPLICANT: Millennium Pharmaceuticals Inc.
 APPLICANT: Curtis, Rory A.J.
 APPLICANT: Logan, Thomas Joseph
 APPLICANT: Glucksmann, Maria A.
 APPLICANT: Meyers, Rachel E.
 APPLICANT: Williamson, Mark J.
 APPLICANT: Rudolph-Owen, Laura A.
 APPLICANT: Chun, Miyoung
 APPLICANT: Tsai, Fong-Ying
 TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
 TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
 FILE REFERENCE: MP103-0180NMIM
 CURRENT APPLICATION NUMBER: US/10/377, 072
 PRIOR APPLICATION NUMBER: US 09/895, 860

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1 PRIOR FILING DATE: 2001-06-29
2 PRIOR APPLICATION NUMBER: US 60/215,370
3 PRIOR FILING DATE: 2000-06-29
4 PRIOR APPLICATION NUMBER: US 09/723,806
5 PRIOR FILING DATE: 2000-11-28
6 PRIOR APPLICATION NUMBER: US 60/187,455
7 PRIOR FILING DATE: 2000-03-07
8 PRIOR APPLICATION NUMBER: US 09/843,297
9 PRIOR FILING DATE: 2001-04-25
10 PRIOR APPLICATION NUMBER: US 60/199,801
11 PRIOR FILING DATE: 2000-04-26
12 PRIOR APPLICATION NUMBER: US 09/861,801
13 PRIOR FILING DATE: 2001-05-21
14 PRIOR APPLICATION NUMBER: US 60/205,508
15 PRIOR FILING DATE: 2000-05-19
16 PRIOR APPLICATION NUMBER: US 09/816,494
17 PRIOR FILING DATE: 2001-03-23
18 PRIOR APPLICATION NUMBER: US 09/815,419
19 PRIOR FILING DATE: 2001-03-22
20 Remaining Prior Application data removed - See File Wrapper or PALM
21 NUMBER OF SEQ ID NOS: 114
22 SOFTWARE: FastSeq for Windows Version 4.0
23 SEQ ID NO 25
24 LENGTH: 3544
25 TYPE: DNA
26 ORGANISM: Homo Sapiens
27 FEATURE:
28 NAME/KEY: CDS
29 LOCATION: (589)...(2586)
30 US-10-377-072--25

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Alignment Scores:

Pred. No.:	2,436-122	Length:	3544
Score:	1552.00	Matches:	300
Percent Similarity:	99.67%	Conservative:	1
Best Local Similarity:	99.34%	Mismatches:	134
Query Match:	99.23%	Indels:	0
DB:	18	Gaps:	0

US-10-029-345A-109_COPY_1_302 (1-302) X US-10-377-072-25 (1-3544)

Qy	1	MetLAHSGIMETLIGLYTHNGINLLEVALTHRGIVAGLEUVALALEUENLEUGIU	20
Db	589	ATGGCCCATGAGATGATTGGAACCTCAATGTGTACTGAGAGGTTGATGGCTTGCTGGAA	648
Qy	21	SerGIyThrgIuLyVaIleuLeuIleAspSerArProPheValGIuTyzAnThrSer	40
Db	649	AGTGGAAACGAAAAAGTGCCTGCTTAATTGATAGCCGGCATTTGTGGAAATACAAATCATCC	708
Qy	41	HisIleleuGIuAlaIleAsnIleAsnCySerLyLeuMetLyAlaArgLeuGINgin	60
Db	709	CACATTTTGGAGGCATTAAATATCAACGCTCCCAAGCTTAATGAAACGGAAGTTGGCAACAG	768
Qy	61	AspLyVaIleuIleThnGIuLeuIleGINHisSerAlaLySHIleValAspIleAsp	80
Db	769	GACAAAGCTTAATTACAGAGCTCATCCAGACTTCACGGAAACATTAAGCTTACATTGAT	828
Qy	81	CysSerGIuLyVaIleValTyIAspGINSerSerGIuAspValAlaSerLeuSerSer	100
Db	829	TGCAGTCCGAAAGGTTGTAGTTACGATCAAAAGCTCCCAAGATGTGGCCTCTCTCCCTTCA	888
Qy	101	AspCyAspPheLeuThrValleuLeuGIyLySileuGIuLySerPheAsnSerVaIHisLeu	120
Db	889	GACGTGTTTTCACCTGACCTGACTCTGGGTAACCTGAGAAAGAGCTTCAACTCTGTTCACCTG	948
Qy	121	LeuAlaGIyGIyPheAlaGIuPheSerArGCSpPheProGIyLeuCySeGIuGIyLySer	140
Db	949	CTTCAGAGTGGGTTGTGCTGAGGTTCTCTGCTGTTTCCCTGGCCCTCTGGAAGAAATCC	1008
Qy	141	ThrlieuValProThrCySileSerGINProCySleuProValAlaAsnIleGIyProThr	160
Db	1009	ACTGTAGTCCCTACTCTGCATTTTCACGCTTGCTTAACCTGTGGCCAAATTTGGGCAACC	1068

QY 161 Arg1LeuProAsnLeuTyrLeuGlyCysGlnAArgAspValLeuAsnLysGluLeu 180
|||
Db 1069 CGAATTCCTCCAACTTTATCTTGTGCTGCCAGCAGATGCTCTCAACAAGAGCTGATG 1128
|||
QY 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProLysProAspPhe 200
|||
Db 1129 CAGCAGATGGGATGTGTTATGTGTTAAATGCGACCAATACCTGTCCAAAGCCTGACTTT 1188
|||
QY 201 IleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlnLysIleLeu 220
|||
Db 1189 ATCCCGAGTCCATCTTCCGTGCTGCTGGAATGACAGCTTTTGAGAAAAATTTTG 1248
|||
QY 221 ProTLeuAspLysSerValAspPheIleGlnLysAlaLysAlaSerAsnGlyCysVal 240
|||
Db 1249 CGGTGTTGGACAAATCAGTATGATTTCAATTGGAAGAAGAAAGCCTCCAAATGAGTGT 1308
|||
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
|||
Db 1309 CTAGTGCACGTGTTAGCTGGGATCTCCGCTCCGACCATGCTATGCGCTACATCATG 1368
|||
QY 261 LysArgMetAspMetSerLeuAspGlnAlaTyrArgPheValLysGlnLysArgProThr 280
|||
Db 1369 AAGAGGATGACATGCTTTAGATGAACTTACAGATTTGGAAGAAAAAGACCTTACT 1428
|||
QY 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuAspTyrGlnLysIleLysAsn 300
|||
Db 1429 ATATCTCCAAACTTCAATTTTCTGGGCCAATCTCCGACTATGAGAAAGATTAAAGAC 1488
|||
QY 301 GlnThr 302
|||
Db 1489 CAGACT 1494
|||

RESULT 12

US-10-425-114-26234
; Sequence 26234, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 26234
; LENGTH: 3625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4119-028-H6_FLI
; US-10-425-114-26234

Alignment Scores:

Pred. No.: 2,53e-192 Length: 3625
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 17 Gaps: 0

US-10-029-345A-109_COPY_1_302 (1-302) x US-10-425-114-26234 (1-3625)

QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGlnArgLeuValAlaLeuLeuGln 20
|||
Db 692 ATGCCCATGAGATGATTGGAACCTCAATTCTTACTGAGAGGTTGGTGGCTCTGCGAA 751
|||
QY 21 SerGlyThrGlnLysValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40
|||

Db 752 AGTGAAGCGAAAAAGTCTGCTAATTGATAGCCGCCCATTTGTGAAATACATATCATCC 811
|||
QY 41 HisIleLeuGlnAlaIleAsnIleAsnGlySerIleuMetLysArgArgLeuGln 60
|||
Db 812 CACATTTTGAAGCCATTAAATATCAACTGCTCCAGGCTTATGAAGCGGAAGGTTCACAG 871
|||
QY 61 AspLysValLeuIleThrGlnLeuIleGlnHisSerAlaLysHisLysValAspIleAsp 80
|||
Db 872 GACAAAGTTTAAATTACAGAGCTATCCAGATTCAGCGAAACATTAAGTTGACATTGAT 931
|||
QY 81 CysSerGlnLysValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
|||
Db 932 TGCACTGAGAAAGTTGATGATTAAGATCAAGACTCCCAAGATGTGCTCTCTCTTCA 991
|||
QY 101 AspCysPheLeuThrValIleLeuGlyLysLeuGlnLysSerPheAsnSerValHisLeu 120
|||
Db 992 GACTGTTTCTCAGCTGATCTTCTGGTAACTGGAGAAAGACCTTCACTGTTCCACTG 1051
|||
QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuCysGlnLysLysSer 140
|||
Db 1052 CTTCGAGGTGGGTTTCTGCTGAGTCTCTCGTTGTTCCCTGGCTCTGTGAAGAAAAATCC 1111
|||
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
|||
Db 1112 ACTCTAGCCCTTACCTGCATTTCTCAGCCTTGCTTACTCGTTGCCAATTGGGCCCAACC 1171
|||
QY 161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnLysGlnLeu 180
|||
Db 1172 CGAATTCCTCCAACTTTATCTTGTGCTGCGACGAGATGCTCCAAAGAGCTGATG 1231
|||
QY 181 GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyrThrCysProLysProAspPhe 200
|||
Db 1232 CAGCAGATGGGATGTGTTATGTGTTAAATGCCAGCAATACCTGTCCAAAGCCTGACTTT 1291
|||
QY 201 IleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGlnLysIleLeu 220
|||
Db 1292 ATCCCGAGTCCATCTTCCGTGCTGCTGCTGTAATGACAGCTTTGTGAAAAATTTTG 1351
|||
QY 221 ProTLeuAspLysSerValAspPheIleGlnLysAlaLysAlaSerAsnGlyCysVal 240
|||
Db 1352 CCGGTGTTGACAAATCAGTATGATTTCAATTGAGAAACAAAGCCTCCAAAGGATGTGT 1411
|||
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
|||
Db 1412 CTATGCACTGTTTAGCTGGAGATCTCCGCTCCGCCACATCGCTATCGCTATCATG 1471
|||
QY 261 LysArgMetAspMetSerLeuAspGlnAlaTyrArgPheValLysGlnLysArgProThr 280
|||
Db 1472 AAGAGATGACATGCTTTAGATGAAAGCTTACAGATTTGTGAAGAAAAAGACCTTACT 1531
|||
QY 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuAspTyrGlnLysLysIleLysAsn 300
|||
Db 1532 ATATCTCCAAACTTCAATTTTCTGGGCCAATCTCGATGATATGAGAAAGATTAAAGAC 1591
|||
QY 301 GlnThr 302
|||
Db 1592 CAGACT 1597
|||

RESULT 13

US-10-343-357-17
; Sequence 17, Application US/10343357
; Publication No. US20040058341A1
; GENERAL INFORMATION:
; APPLICANT: INCTE GENOMICS, INC.; TANG, Y.Tom
; APPLICANT: ELIOTY, Vicki S.; RAMKUMAR, Jayalaxmi
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: WANG, Yumei E.; STEWART, Elizabeth A.
; APPLICANT: GANDHI, Ameena R.; ARVIZU, Chandra S.
; APPLICANT: LEE, Ernestine A.; HARALID, April J.A.
; APPLICANT: LU, Dyrng Alina M.; TRIBOULEY, Catherine M.
; APPLICANT: GRIFFIN, Jennifer A.; BAUGHN, Marian R.
; APPLICANT: YUE, Henry; WARREN, Bridget A.
; APPLICANT: NGUYEN, Daniel B.; CHAWLA, Narinder K.

```

APPLICANT: KEARNEY, Liam
TITLE OF INVENTION: PROTEIN PHOSPHATASES
FILE REFERENCE: PI-0173 PCT
CURRENT APPLICATION NUMBER: US/10/343,357
PRIOR FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: PCT/US01/23716
PRIOR FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: US 60/221,679
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/223,272
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/224,309
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: US 60/226,728
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: US 60/229,254
PRIOR FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: US 60/231,366
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PERL Program
SEQ ID NO: 17
LENGTH: 3766
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040058341A1 7480570CB1
US-10-343-357-17

Alignment Scores:
Pred. No.: 2,69e-192 Length: 3766
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
Gaps: 0
DB: 17

US-10-029-345a-109_copy_1_302 (1-302) x US-10-343-357-17 (1-3766)
QY 1 MetAlahisglumetiieglythrglnilevalthrgluargleuvalaleuenglun 20
Db 538 ATGCCCCATGAGATGATGGAACCAATTGTACTGAGAGGTGTGGCTCTGCGAA 597
QY 21 SerGlythrGluValValleuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
Db 598 AGTGAACGGAAGAGTCTCTAATTGATGACCGGCATTTGTGGAATACAAATACATCC 657
QY 41 HislleuGlualaleAsnileAsnileAsnileAsnileAsnileAsnileAsnile 60
Db 658 CACATTTGGAAAGCATTATATCTCACTGCTCCAAAGCTTATGAAAGCGAAGTTGCAACG 717
QY 61 AsplyValleuilethrgluLeuileglnhisseralalyshislyValAspilleap 80
Db 718 GACAAAGTTAATATACAGAGCTCATCCAGCATTCAGGAAACATTAAGTTGACATTGAT 777
QY 81 CysSerGlnlyValValValValValValValValValValValValValValVal 100
Db 778 TGCAGTCGAAAGTGTGATTGATTCATCAAGCTCCCAAGATGTTGCTCTCTCTTCA 837
QY 101 AspCysPheLeuThrValleuLeuLeuGlyValLeuGlyValSerPheAsnSerValHisleu 120
Db 838 GACTGTTTCTCACTGATCTCTGAGTAACTGAGAAAGAGCTTCACTCTGTTCACTG 897
QY 121 LeuAlaGlyValPheAlaGlyPheSerArgCysPheProGlyLeuGlyValSer 140
Db 898 CTTCAGAGTGGGTTTGTGAGAGTCTCTGTTGTTTCCCTGGCCTCTGGAAGAAATCC 957
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnileGlyProThr 160
Db 958 ACTTAGTCCCTACCTGCAATTTCTCAGCTTGTCTTACCTGTTGCCAATATTGGGCAACC 1017
QY 161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValleuAsnlyGluLeuile 180

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Db 1018 CGAATTTCCCAATCTTATCTTGCGCCAGCAGATGCTCACAAGAGCTGATG 1077
QY 181 GlnGlnAnGlyIleGlyTyrValleuAsnIleSerTyrThrCysProlySerPhe 200
Db 1078 CAGCAGAAATGGAGTGTATGTGTAAATGACCAATACCTGTGCAAAAGCTTACATT 1137
QY 201 IleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGlyValHisleu 220
Db 1138 ATCCCGAGTCTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1197
QY 221 ProTyrLeuAspIleValAspPheIleGlyValAlaValAlaSerAsnGlyCysVal 240
Db 1198 CGGTGTTGGAACAATCAGTATGATTTCAATTGGAAGAAAGAGCTCCCAATGATGTGT 1257
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
Db 1258 CTAGTCACTGTATTAGTGGGATCTCCCGCTCCGACCATCTGCTATGCTTACATG 1317
QY 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValIleGlyLysArgProThr 280
Db 1318 AAGAGATGACATGTCTTTGATGATGACCTTACAGATTTGGAAGAAAGAAAGACTTACT 1377
QY 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspIleGlyLysIleLysAsn 300
Db 1378 ATATCTCAAACTTCAATTTCTGGGCCAATCTCGATGATGAGAAAGATTAAGAAC 1437
QY 301 GlnThr 302
Db 1438 CAGACT 1443

RESULT 14
US-10-648-593-115
; Sequence 115, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,365
; PRIOR FILING DATE: 2002-08-27
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: Patent version 3.2
; SEQ ID NO 115
; LENGTH: 4790
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-648-593-115

Alignment Scores:
Pred. No.: 4.03e-192 Length: 4790
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
Gaps: 0
DB: 18

US-10-029-345a-109_copy_1_302 (1-302) x US-10-648-593-115 (1-4790)
QY 1 MetAlahisglumetiieglythrglnilevalthrgluargleuvalaleuenglun 20
Db 184 ATGCCCCATGAGATGATGGAACCAATTGTACTGAGAGGTGTGGCTCTGCGAA 243
QY 21 SerGlythrGluValValleuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
Db 244 AGTGAACGGAAGAGTCTCTAATTGATGACCGGCATTTGTGGAATACAAATACATCC 303
QY 41 HislleuGlualaleAsnileAsnileAsnileAsnileAsnileAsnileAsnile 60

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Db 304 CACATTTTGGAGGCCATTATATCACTGCTCCCAAGCTTATGAGCAAGTTGCAACAG 363
Qy AsplysValleu1leThGluLeu1leg1nHisSer1a1yeh1slyValAsp1leasp 80
Db 364 GACAAAGTGTATATACAGAGCTCATCCAGCAATTCAGCAAAACATTAAGTGAATATAT 423
Qy CysSerGlnuysValValValTyraSpGlnSerSerGlnAspValAlaSerLeuSer 100
Db 424 TGCACATCAGAAAGTTGATGTTACATCAAACTCCCAAGATGTTGCTCTCTCTTCA 483
Qy AspCysPheLeuThValLeuLeuGlyLyLeuGlnuysSerPheAsnSerValHisLeu 120
Db 484 GACTGTTTCTCACCTGTACTCTCTGGTAAACTGGAGAAAGCTTCAACTCTGTTCACTG 543
Qy Leu1aGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuCysGlnuysSer 140
Db 544 CTTCAGAGTGGGTGTGCTGAGTCTCTGTTGTTTCCCTGGGCTCTGAGAGAAATCC 603
Qy 141 ThrLeuValProThrCys1leSerGlnProCysLeuProValAlaAsn1leg1yProThr 160
Db 604 ACTTAGTCCCTACCTGATTTCTCAGCCTTGCTTACCTGTTGCCAATGCGCAAC 663
Qy 161 Arg1leuProAsnLeuTyrlleuGlyCysGlna1ArgAspValLeuAsnlyGluLeu 180
Db 664 CGAATTTCTCCCAATCTTATCTTGCTGCCAGCAGAGATGCTTCACAAAGAGCTGAT 723
Qy 181 GlnGlnaGlny1leg1yTyraValLeuAsn1aSerTyrlThCysProLyProAspPhe 200
Db 724 CAGCAAAATGGGATTTGTTATGTTAAATGCAACAAATACCTGTCACAAAGCTGACTT 783
Qy 201 IleProGlnuSerHisPheLeuArgValProValAsnAspSerPheCysGlnuys1leu 220
Db 784 ATCCCGAGTCTCATTTCTGCTGCTGCTGCTGATGATGACAGTTTGTGAGAAATTTG 843
Qy 221 ProTrpLeuAspLySerSerValAspPhe1leg1yValAlaValAsn1yCysVal 240
Db 844 CCGTGTGTGCAATCAGATGATTTCAATGAGAAAGCAAAAGCTCCAAATGATGTGT 903
Qy 241 LeuValHisCysLeuAlaGly1leSerArgSerAlaThr1leAla1leTyrlleMet 260
Db 904 CTAGTGCATGTTTATGCTGGAGATCTCCGCTCCGACACATGCTATGCTCTACATCATG 963
Qy 261 LysArgMetAspMetSerLeuAspGluAlaTyraPheValLySGluLyArgProThr 280
Db 964 AAGAGATGACATGCTTTAGATGACCTTACAGATTTGTGAAAGAAAGAAAGCTACT 1023
Qy 281 IleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrlGluLySylleLysAsn 300
Db 1024 ATATCTCCAACTCAATTTCTGTGGCCAACTCTGAGCTATGAGAGAGATTAAGAAC 1083
Qy 301 GlnThr 302
Db 1084 CAGACT 1089

RESULT 15
US-10-357-930-20824
; Sequence 20824, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: KRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357, 930
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862

; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20824
; LENGTH: 5145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc.feature
; LOCATION: 1, 5144, 5145
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-20824

Alignment Scores:
Pred. No.: 4,546-192 Length: 5145
Score: 1552.00 Matches: 300
Percent Similarity: 99.67% Conservative: 1
Best Local Similarity: 99.34% Mismatches: 1
Query Match: 99.23% Indels: 0
DB: 18 Gaps: 0

US-10-029-345a-109_COPY_1_302 (1-302) x US-10-357-930-20824 (1-5145)

Qy 1 MetaHisGluMet1leg1yThrGln1eValThrGluArgLeuValAlaLeuLeuGln 20
Db 589 ATGCCCATGATGATGATTTGCAATCTCAATTTGTTACTAGAGTTGGTGGCTCTGCGAA 648
Qy 21 SerGlyThrGluysValLeuLeu1leAspSerArgProPheValGluTyraSer 40
Db 649 AGTGAACGGAAGAAAGTGTGCTATGATGATGACCGGCAATTTGGATCAATATACATCC 708
Qy 41 His1leLeuGlnAla1leAsn1leAsn1leAsn1leAsn1leAsn1leAsn1leAsn 60
Db 709 CACATTTTGGAAAGCATTAATATCACTGCTCCAAAGCTTGTGAAGCAAGTTGCAACAG 768
Qy 61 AsplysValleu1leThGluLeu1leg1nHisSer1a1yeh1slyValAsp1leasp 80
Db 769 GACAAAGTGTATATACAGAGCTCATCAGCATTTACGCAAAACATTAAGTTGACATTTGAT 828
Qy 81 CysSerGlnuysValValValTyraSpGlnSerSerGlnAspValAlaSerLeuSer 100
Db 829 TGCAGTCAGAAAGTTGATGTTACGATCAAAAGCTCCCAAGATGTGCTCTCTCTTCA 888
Qy 101 AspCysPheLeuThrValLeuLeuGlyLyLeuGlnuysSerPheAsnSerValHisLeu 120
Db 889 GACTGTTTCTCACCTGTACTCTGGTAAACTGGAGAAAGCTTCAACTCTGTTCACTG 948
Qy 121 Leu1aGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuCysGlnuysSer 140
Db 949 CTTCAGAGTGGGTGTGCTGAGTCTCTGTTGTTTCCCTGGGCTCTGAGAGAAATCC 1008
Qy 141 ThrLeuValProThrCys1leSerGlnProCysLeuProValAlaAsn1leg1yProThr 160
Db 1009 ACTTAGTCCCTACCTGATTTCTCAGCCTTGCTTACCTGTGCAACATTTGGGCAAC 1068
Qy 161 Arg1leuProAsnLeuTyrlleuGlyCysGlna1ArgAspValLeuAsnlyGluLeu 180
Db 1069 CGAATTTCTCCCAATCTTATCTTGCTGCCAGCAGATGCTTCACAAAGAGCTGATG 1128
Qy 181 GlnGlnaGlny1leg1yTyraValLeuAsn1aSerTyrlThCysProLyProAspPhe 200
Db 1129 CAGCAAAATGGGATTTGTTATGTTAAATGCAACAAATACCTGTCACAAAGCTGACTTT 1188
Qy 201 IleProGlnuSerHisPheLeuArgValProValAsnAspSerPheCysGlnuys1leu 220

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 9, 2005, 12:12:08 ; Search time 45 Seconds
(without alignments)
1103.147 Million cell updates/sec

Title: US-10-029-345A-109

Perfect score: 665

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 50

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	472	71.0	665	4	US-09-816-494-2

ALIGNMENTS

RESULT 1
US-09-816-494-2
; Sequence 2, Application US/09816494
; Patent No. 6664089
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; PRIOR APPLICATION NUMBER: 2001-03-23
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-816-494-2

Query Match 71.0%; Score 472; DB 4; Length 665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	254	IAIAYIMRMDMSLDEAARFVYERKPTISPNFNLGQLDYKKIKNOTGASGPKLKL	313
DB	254	IAIAYIMRMDMSLDEAARFVYERKPTISPNFNLGQLDYKKIKNOTGASGPKLKL	313
QY	314	LHLEKPNPVPVAVSEGGKSETPPLSPCADSATSBAAQRPVHPASVSPSPVQPSLLED	373
DB	314	LHLEKPNPVPVAVSEGGKSETPPLSPCADSATSBAAQRPVHPASVSPSPVQPSLLED	373
QY	374	SPLVQALSGHLISADRLSDSNKLKRSFSLDIKSVSYASMAASLHGFSSEDALEYKPS	433
DB	374	SPLVQALSGHLISADRLSDSNKLKRSFSLDIKSVSYASMAASLHGFSSEDALEYKPS	433
QY	434	TLIDGTNKLCOFSPVQELSEQTPETSPDKEASIPKLIQTARPSDSQKRLHSVRTSSSG	493
DB	434	TLIDGTNKLCOFSPVQELSEQTPETSPDKEASIPKLIQTARPSDSQKRLHSVRTSSSG	493
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DB	494	TAQRSLSPILHRSGSVEDNHYHTSFLFGLSTSQOHLTKSAGLKKMHSIDILAPQSTPBL	553
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DB	554	TSSWYFATESHSHFYASAIYGGASAYSCGLPTCGDQVYSVRRQKPSDRADSRGW	613
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Job time : 45 secs

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QY	260	edIySaRgweAspSerSetleuapgluAlaYrAargPheVallysgIulYsArpProT	280
Db	779	TGAAGAGATGACATGCTTCTTAAATGAACTTCAAGATTGTGTGAAGAAAAAGACTA	838
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QY	300	enGIrThGlYAlAsErGlYProLySeSerLeuLylleuLuhIleuGlulYsProA	320
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QY	340	roCYaIaAsPSeSerAlathrSerGlulAlaIagIyInaGProValHsProAlAsErV	360
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QY	380	enSerGlYleuHIsleuSerAlaAsPArgleuGluAsPSeAsnYsleuYAsrGSeP	400
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QY	420	heSeSerSeSerGluAsPAlaLeuGluTYrTYrLYeProSeerThThleuAsPglYThCa	440
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Db	1799	GGCAGAAAGCCMATGACAGAGCTGAGCTGCGGAGACTGGCAATGAAGAGAGCCCTTTG	1855
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US-09-816-494-1
? Sequence 1, Application US/09816494
? Patent No. 6664089
? GENERAL INFORMATION:
? APPLICANT: Meyers, Rachel A.
? TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
? TIME OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
? FILE REFERENCE: 10448-030002
? CURRENT APPLICATION NUMBER: US/09/816,494
? CURRENT FILING DATE: 2001-03-23
? PRIOR APPLICATION NUMBER: US 60/191,858
? PRIOR FILING DATE: 2000-03-24
? NUMBER OF SEQ ID NOS: 10
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 1
? LENGTH: 3544
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (589)...(2583)
US-09-816-494-1

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QY 81 CysSerGlnLyValValValLyTraspGlnSerSerGlnAspValAlaSerLeuSerSer 100
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Title: US-10-029-345a-109

Sequence: 1 MAHEMIGTIVTERLVALL.....LGKVGSGSGSFGSMETIEVS 665

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Word size : 50

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	472	71.0	665	US-09-816-494-2	Sequence 2, Appl
3	472	71.0	665	US-09-864-277-2	Sequence 2, Appl
4	472	71.0	665	US-10-094-749-2312	Sequence 2312, Ap
5	472	71.0	665	US-10-377-072-26	Sequence 26, Appl
6	472	71.0	665	US-10-072-012-680	Sequence 680, App
7	472	71.0	665	US-10-072-012-681	Sequence 681, App
8	472	71.0	665	US-10-168-506-14	Sequence 14, Appl
9	472	71.0	665	US-10-343-357-7	Sequence 7, Appl
10	472	71.0	665	US-10-257-026-2	Sequence 2, Appl
11	472	71.0	665	US-10-648-593-240	Sequence 240, App
12	472	71.0	665	US-10-648-593-247	Sequence 247, App
13	472	71.0	665	US-10-377-072-26	Sequence 26, Appl

14	472	71.0	690	US-10-072-012-679	Sequence 679, App
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16	472	71.0	690	US-10-425-114-54204	Sequence 54204, A
17	394	59.2	680	US-10-072-012-256	Sequence 256, App
18	304	45.7	662	US-10-072-012-258	Sequence 258, App
19	258	38.8	672	US-10-296-115-1259	Sequence 1259, App
20	152	22.9	253	US-10-108-260A-4872	Sequence 4872, Ap
21	108	16.2	155	US-09-964-277-7	Sequence 7, Appl
22	67	10.1	660	US-10-072-012-682	Sequence 682, App
23	64	9.6	677	US-10-072-012-683	Sequence 683, App
24	56	8.4	88	US-09-764-853-578	Sequence 578, App

ALIGNMENTS

RESULT 1
US-09-964-277-21
; Sequence 21, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Lucite, Ralf M.
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-277-21

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Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	286	TLIDGTNKLCCPSPIQELSEOTPEPSPDKEASIPKULOTARPDSQSKLISVRSSSG	345
QY	494	TAORSLSPHRSQSVEDVYHTSFLGSLSTSOQHLTKSAGLKGWHSIILAPOTSTPUL	553
DB	346	TAORSLSPHRSQSVEDVYHTSFLGSLSTSOQHLTKSAGLKGWHSIILAPOTSTPUL	405
QY	554	TSSWYFATESHFPYASAIYGSASYSAYSCGQLPTCGDQVYSVRRQKPSDRADSRSG	613
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US-09-816-494-2
; Sequence 2, Application US/09816494
; Patent No. US20020034807A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
; TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
; FILE REFERENCE: 10448-030002
; CURRENT APPLICATION NUMBER: US/09/816,494
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,858
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-816-494-2

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Query Match      71.0%; Score 472; DB 9; Length 665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

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US-09-964-277-2
; Sequence 2, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ralf M.
; APPLICANT: Wei, Ralf M.
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125,434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
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; TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-964-277-2

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Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 494 TAQRSLSPLRSGSVEDNYHTSFLFGLSTSQHLLTKSAGLGLKGMHSDILAPQSTPSL 553
DB 494 TAQRSLSPLRSGSVEDNYHTSFLFGLSTSQHLLTKSAGLGLKGMHSDILAPQSTPSL 553
QY 554 TSSWYFATESHSHFYASAIYGSASAYSASCSQLPTCGDQVYSVRRQKPSDRADSRSSW 613
DB 554 TSSWYFATESHSHFYASAIYGSASAYSASCSQLPTCGDQVYSVRRQKPSDRADSRSSW 613
QY 614 HESPEKQFKRRSCQMEFGESIMSENRREELGKVGQSOSFSFGSMELIIVS 665
DB 614 HESPEKQFKRRSCQMEFGESIMSENRREELGKVGQSOSFSFGSMELIIVS 665

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RESULT 4

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US-10-094-749-2312
; Sequence 2312, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUTUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHITO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 08435/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: PatentIn Ver. 2.1

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SEQ ID NO 2312
 LENGTH: 665
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-094-749-2312

Query Match 71.0%; Score 472; DB 15; Length 665;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

194 TCPKDFIPESHFLRPVNDSECEKILPWLKSVDFIEKAKASNCVIVHCLAGISRSAT 253
 194 TCPKDFIPESHFLRPVNDSECEKILPWLKSVDFIEKAKASNCVIVHCLAGISRSAT 253
 254 IAIATIMKMDMSLDEARFVYKEKPTTISPNFNLGQLLDYKTKIKNOTGASGPKSKKL 313
 254 IAIATIMKMDMSLDEARFVYKEKPTTISPNFNLGQLLDYKTKIKNOTGASGPKSKKL 313
 314 IHLKPNPEVPVAVSEGGQKSETPLSPPCADSATSEAGORPVHPASVSPVSPSLIED 373
 314 IHLKPNPEVPVAVSEGGQKSETPLSPPCADSATSEAGORPVHPASVSPVSPSLIED 373
 374 SPLVALSGHLMSADRLSDSNLTKRSFSLDIKSVSYASMAASLHGFSSEDALEYKPS 433
 374 SPLVALSGHLMSADRLSDSNLTKRSFSLDIKSVSYASMAASLHGFSSEDALEYKPS 433
 434 TTLDTGNKLCOPSPVOELSEOTPEPSPDKEASIPKKTQTARPSDSQSKLHVSRTSSSG 493
 434 TTLDTGNKLCOPSPVOELSEOTPEPSPDKEASIPKKTQTARPSDSQSKLHVSRTSSSG 493
 494 TAORSLSLPLHRSVGVNDYHTSFLGLSTSOOHLTKSAGLKGWHSIDILAPOTSTPSL 553
 494 TAORSLSLPLHRSVGVNDYHTSFLGLSTSOOHLTKSAGLKGWHSIDILAPOTSTPSL 553
 554 TSSWFFATESSHFYASAIYGGASAYSAYSCQLPTCGQVYSVRRROKPSDRADSRBW 613
 554 TSSWFFATESSHFYASAIYGGASAYSAYSCQLPTCGQVYSVRRROKPSDRADSRBW 613
 614 HESPEPEKQFKRRSCOMEGESIMENRREBELGKVGSGSSPFGSMETIEVS 665
 614 HESPEPEKQFKRRSCOMEGESIMENRREBELGKVGSGSSPFGSMETIEVS 665

RESULT 5
 US-10-377-072-26
 Sequence 26, Application US/10377072
 Publication No. US2004009501A1
 GENERAL INFORMATION:
 APPLICANT: Millennium Pharmaceuticals Inc.
 APPLICANT: Curtis, Rory A.J.
 APPLICANT: Logan, Thomas Joseph
 APPLICANT: Glucksmann, Maria A.
 APPLICANT: Meyers, Rachel E.
 APPLICANT: Williamson, Mark J.
 APPLICANT: Rudolph-Owen, Laura A.
 APPLICANT: Teal, Feng-Ying
 TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
 TITLE OF INVENTION: 36692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
 FILE REFERENCE: MP103-0180NMIM
 CURRENT APPLICATION NUMBER: US/10/377,072
 CURRENT FILING DATE: 2003-02-27
 PRIOR APPLICATION NUMBER: US 09/895,860
 PRIOR FILING DATE: 2001-06-29
 PRIOR APPLICATION NUMBER: US 60/215,370
 PRIOR FILING DATE: 2000-06-29
 PRIOR APPLICATION NUMBER: US 09/723,806
 PRIOR FILING DATE: 2000-11-28
 PRIOR APPLICATION NUMBER: US 60/187,455
 PRIOR FILING DATE: 2000-03-07
 PRIOR APPLICATION NUMBER: US 09/843,297
 PRIOR FILING DATE: 2001-04-25

PRIOR APPLICATION NUMBER: US 60/199,801
 PRIOR FILING DATE: 2000-04-26
 PRIOR APPLICATION NUMBER: US 09/861,801
 PRIOR FILING DATE: 2001-05-21
 PRIOR APPLICATION NUMBER: US 60/205,508
 PRIOR FILING DATE: 2000-05-19
 PRIOR APPLICATION NUMBER: US 09/816,494
 PRIOR FILING DATE: 2001-03-23
 PRIOR APPLICATION NUMBER: US 09/815,419
 PRIOR FILING DATE: 2001-03-22
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 114
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 26
 LENGTH: 665
 TYPE: PRT
 ORGANISM: Homo Sapiens
 US-10-377-072-26

Query Match 71.0%; Score 472; DB 15; Length 665;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

194 TCPKDFIPESHFLRPVNDSECEKILPWLKSVDFIEKAKASNCVIVHCLAGISRSAT 253
 194 TCPKDFIPESHFLRPVNDSECEKILPWLKSVDFIEKAKASNCVIVHCLAGISRSAT 253
 254 IAIATIMKMDMSLDEARFVYKEKPTTISPNFNLGQLLDYKTKIKNOTGASGPKSKKL 313
 254 IAIATIMKMDMSLDEARFVYKEKPTTISPNFNLGQLLDYKTKIKNOTGASGPKSKKL 313
 314 IHLKPNPEVPVAVSEGGQKSETPLSPPCADSATSEAGORPVHPASVSPVSPSLIED 373
 314 IHLKPNPEVPVAVSEGGQKSETPLSPPCADSATSEAGORPVHPASVSPVSPSLIED 373
 374 SPLVALSGHLMSADRLSDSNLTKRSFSLDIKSVSYASMAASLHGFSSEDALEYKPS 433
 374 SPLVALSGHLMSADRLSDSNLTKRSFSLDIKSVSYASMAASLHGFSSEDALEYKPS 433
 434 TTLDTGNKLCOPSPVOELSEOTPEPSPDKEASIPKKTQTARPSDSQSKLHVSRTSSSG 493
 434 TTLDTGNKLCOPSPVOELSEOTPEPSPDKEASIPKKTQTARPSDSQSKLHVSRTSSSG 493
 494 TAORSLSLPLHRSVGVNDYHTSFLGLSTSOOHLTKSAGLKGWHSIDILAPOTSTPSL 553
 494 TAORSLSLPLHRSVGVNDYHTSFLGLSTSOOHLTKSAGLKGWHSIDILAPOTSTPSL 553
 554 TSSWFFATESSHFYASAIYGGASAYSAYSCQLPTCGQVYSVRRROKPSDRADSRBW 613
 554 TSSWFFATESSHFYASAIYGGASAYSAYSCQLPTCGQVYSVRRROKPSDRADSRBW 613
 614 HESPEPEKQFKRRSCOMEGESIMENRREBELGKVGSGSSPFGSMETIEVS 665
 614 HESPEPEKQFKRRSCOMEGESIMENRREBELGKVGSGSSPFGSMETIEVS 665

RESULT 6
 US-10-072-012-680
 Sequence 680, Application US/10072012
 Publication No. US2004003493A1
 GENERAL INFORMATION:
 APPLICANT: Tcheurev, Velizar
 APPLICANT: Spytek, Kimberly
 APPLICANT: Zernusen, Bryan
 APPLICANT: Patcurajan, Meera
 APPLICANT: Shimkets, Richard
 APPLICANT: Li, Li
 APPLICANT: Gangoli, Bsha
 APPLICANT: Padigaru, Muralidhara
 APPLICANT: Anderson, David W.
 APPLICANT: Rastelli, Luca
 APPLICANT: Miller, Charles E.
 APPLICANT: Gerlach, Valerie

```

; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Coleman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 680
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-680

Query Match          71.0%; Score 472; DB 15; Length 665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 TCPKPFIPESHRLRVPVNDSECEKILPWLKSVDFIERAKASNGCVLVHCLAGISRAT 253
    |||||
Db 194 TCPKPFIPESHRLRVPVNDSECEKILPWLKSVDFIERAKASNGCVLVHCLAGISRAT 253

QY 254 IAIAYIMKEMDMSLDEAYRFPVKEKRPITSPNENFLGQLLDYEKKINQGTGASGPKSKL 313
    |||||
Db 254 IAIAYIMKEMDMSLDEAYRFPVKEKRPITSPNENFLGQLLDYEKKINQGTGASGPKSKL 313

QY 314 LHEKNEVNPANSEGGOKSETPPLSPPCADSAESAAGRPVPAVPSPVQPSLLD 373
    |||||
Db 314 LHEKNEVNPANSEGGOKSETPPLSPPCADSAESAAGRPVPAVPSPVQPSLLD 373

QY 374 SPLVQALSGILHSADLEDSNKLKRSFSLDIKSVSYASMAASIHGSSSEDALEYKKS 433
    |||||
Db 374 SPLVQALSGILHSADLEDSNKLKRSFSLDIKSVSYASMAASIHGSSSEDALEYKKS 433

QY 434 TTLDTGNKLCQSPVQELSEQTPETSPDYKEASIPKLTOTARPDSQSRLHSVRTSSG 493
    |||||
Db 434 TTLDTGNKLCQSPVQELSEQTPETSPDYKEASIPKLTOTARPDSQSRLHSVRTSSG 493

QY 494 TAORSLSLPLHSGSVEDNYHNSFLGLSTSOOHLTKSGILGKGMHSDIILAPQSTPSL 553
    |||||
Db 494 TAORSLSLPLHSGSVEDNYHNSFLGLSTSOOHLTKSGILGKGMHSDIILAPQSTPSL 553

QY 554 TSSWYFATESSHFYASAIYGGASYSAYSCSQLPTCGQVYSVRRRQKPSDRADRSRW 613
    |||||
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Db 554 TSSWYFATESSHFYASAIYGGASYSAYSCSQLPTCGQVYSVRRRQKPSDRADRSRW 613
    |||||
QY 614 HESPEKQFKRRSCOMERGESIMENSREBELGVGQSSPSGSMETIEVS 665
    |||||
Db 614 HESPEKQFKRRSCOMERGESIMENSREBELGVGQSSPSGSMETIEVS 665

RESULT 7
US-10-072-012-681
; Sequence 681, Application US/10072012
; Publication No. US2004003493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zernusen, Bryan
; APPLICANT: Patcurajan, Weera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Bsha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Coleman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 681
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-681

Query Match          71.0%; Score 472; DB 15; Length 665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 194 TCPKPDFIESHFLRVPVNDSPCEKILPMLDKSVDFIERAKASNGCVLVHCLAGISRAT 253
DB 194 TCPKPDFIESHFLRVPVNDSPCEKILPMLDKSVDFIERAKASNGCVLVHCLAGISRAT 253
QY 254 IAIAYIMKMDMSLDAYRPFVKEKPTISPNFNLCOQLDYEEKIKNOGTGASGPKSKLX 313
DB 254 IAIAYIMKMDMSLDAYRPFVKEKPTISPNFNLCOQLDYEEKIKNOGTGASGPKSKLX 313
QY 314 LHEKNEBPVAVSEGGOKSETPPLSPCADSATSEAGORPVHPASVPSPVQPSLLBD 373
DB 314 LHEKNEBPVAVSEGGOKSETPPLSPCADSATSEAGORPVHPASVPSPVQPSLLBD 373
QY 374 SPLVQALSGLHLSADRLBDSNKLKRSFSLDIKSVSYSASMAASLHGFSSEDLLEYXKS 433
DB 374 SPLVQALSGLHLSADRLBDSNKLKRSFSLDIKSVSYSASMAASLHGFSSEDLLEYXKS 433
QY 434 TTLDTGNKLCQSPVOELSEQTPETSPPDKEASIPKKLOTARPDSQSKRLHSVRTSSG 493
DB 434 TTLDTGNKLCQSPVOELSEQTPETSPPDKEASIPKKLOTARPDSQSKRLHSVRTSSG 493
QY 494 TQORSLSPLHRSVGVEDNYHTSFLFGLSTSOQHLTKSAGLGKWHSDIILAPQISTPST 553
DB 494 TQORSLSPLHRSVGVEDNYHTSFLFGLSTSOQHLTKSAGLGKWHSDIILAPQISTPST 553
QY 554 TSSWYFATESHPSYASAIYGSASYSAYSCSQLPTCGQOYVSVRROKPSDRADRRSM 613
DB 554 TSSWYFATESHPSYASAIYGSASYSAYSCSQLPTCGQOYVSVRROKPSDRADRRSM 613
QY 614 HESPEPKQFKRRSCOMEFGESIMSENRSREELGKVGSGSFSGSMELIEVS 665
DB 614 HESPEPKQFKRRSCOMEFGESIMSENRSREELGKVGSGSFSGSMELIEVS 665

RESULT 8

US-10-168-506-14
Sequence 14, Application US/10168506
Publication No. US20040053229A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY D.
APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHITE, DAVID
APPLICANT: MANNING, GERARD
APPLICANT: SUDASANAM, SUCHA
APPLICANT: HILL, RON
APPLICANT: FLANAGAN, PETER
TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
FILE REFERENCE: 038602/1351
CURRENT APPLICATION NUMBER: US/10/168,506
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: PCT/US00/34736
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 665
TYPE: PRT
ORGANISM: Homo sapiens
US-10-168-506-14

Query Match 71.0%; Score 472; DB 15; Length 665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 TCPKPDFIESHFLRVPVNDSPCEKILPMLDKSVDFIERAKASNGCVLVHCLAGISRAT 253
DB 194 TCPKPDFIESHFLRVPVNDSPCEKILPMLDKSVDFIERAKASNGCVLVHCLAGISRAT 253
QY 254 IAIAYIMKMDMSLDAYRPFVKEKPTISPNFNLCOQLDYEEKIKNOGTGASGPKSKLX 313
DB 254 IAIAYIMKMDMSLDAYRPFVKEKPTISPNFNLCOQLDYEEKIKNOGTGASGPKSKLX 313
QY 314 LHEKNEBPVAVSEGGOKSETPPLSPCADSATSEAGORPVHPASVPSPVQPSLLBD 373
DB 314 LHEKNEBPVAVSEGGOKSETPPLSPCADSATSEAGORPVHPASVPSPVQPSLLBD 373

DB 314 LHEKNEBPVAVSEGGOKSETPPLSPCADSATSEAGORPVHPASVPSPVQPSLLBD 373
QY 374 SPLVQALSGLHLSADRLBDSNKLKRSFSLDIKSVSYSASMAASLHGFSSEDLLEYXKS 433
DB 374 SPLVQALSGLHLSADRLBDSNKLKRSFSLDIKSVSYSASMAASLHGFSSEDLLEYXKS 433
QY 434 TTLDTGNKLCQSPVOELSEQTPETSPPDKEASIPKKLOTARPDSQSKRLHSVRTSSG 493
DB 434 TTLDTGNKLCQSPVOELSEQTPETSPPDKEASIPKKLOTARPDSQSKRLHSVRTSSG 493
QY 494 TQORSLSPLHRSVGVEDNYHTSFLFGLSTSOQHLTKSAGLGKWHSDIILAPQISTPST 553
DB 494 TQORSLSPLHRSVGVEDNYHTSFLFGLSTSOQHLTKSAGLGKWHSDIILAPQISTPST 553
QY 554 TSSWYFATESHPSYASAIYGSASYSAYSCSQLPTCGQOYVSVRROKPSDRADRRSM 613
DB 554 TSSWYFATESHPSYASAIYGSASYSAYSCSQLPTCGQOYVSVRROKPSDRADRRSM 613
QY 614 HESPEPKQFKRRSCOMEFGESIMSENRSREELGKVGSGSFSGSMELIEVS 665
DB 614 HESPEPKQFKRRSCOMEFGESIMSENRSREELGKVGSGSFSGSMELIEVS 665

RESULT 9

US-10-343-357-7
Sequence 7, Application US/10343357
Publication No. US20040058341A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.; TANG, Y.Tom
APPLICANT: BLIOT, Vlckl S.; RAMKUMAR, Jayalaxmi
APPLICANT: YAO, Monique G.; BUREFORD, Neil
APPLICANT: WANG, Yumel E.; STEWART, Elizabeth A.
APPLICANT: GANDHI, Ameesha R.; ARVIZU, Chandra S.
APPLICANT: LEE, Ernestine A.; HAPALITA, April J.A.
APPLICANT: LU, Dying Aina M.; TRIBOLEY, Catherine M.
APPLICANT: GRIFFIN, Jennifer A.; BAUGHN, Mariah R.
APPLICANT: YUE, Henry; WARREN, Bridget A.
APPLICANT: NGUYEN, Daniel B.; CHAVLA, Nandinder K.
APPLICANT: KEARNEY, Liam
TITLE OF INVENTION: PROTEIN PHOSPHATASES
FILE REFERENCE: PI-0173 PCT
CURRENT APPLICATION NUMBER: US/10/343,357
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: PCT/US01/23716
PRIOR FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: US 60/221,679
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/223,272
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/224,309
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: US 60/226,728
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: US 60/229,254
PRIOR FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: US 60/231,366
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PERL Program
SEQ ID NO 7
LENGTH: 665
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US20040058341A1 7480570CD1
US-10-343-357-7

Query Match 71.0%; Score 472; DB 15; Length 665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 TCPKPDFIESHFLRVPVNDSPCEKILPMLDKSVDFIERAKASNGCVLVHCLAGISRAT 253
DB 194 TCPKPDFIESHFLRVPVNDSPCEKILPMLDKSVDFIERAKASNGCVLVHCLAGISRAT 253

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Db 194 TCKPKDFIPESHFLRVPVNDSCFKILPWLDKSVDFIEKAKASNGCVLVHCLAGISRAT 253
Qy 254 IAIAYIMKMDMSLDEAYRFVYKERTPTISPNFNFLGQLLDYEKKIKNOTGASGPKSKLT 313
Db 254 IAIAYIMKMDMSLDEAYRFVYKERTPTISPNFNFLGQLLDYEKKIKNOTGASGPKSKLT 313
Qy 314 IHLERKNEVPVAVSEGGQKSETPLSPPCADSATSEAAQORPVHPASVPSVPQPSLLED 373
Db 314 IHLERKNEVPVAVSEGGQKSETPLSPPCADSATSEAAQORPVHPASVPSVPQPSLLED 373
Qy 374 SPLVQALSGLIHSADRLBDSNKLKRSFSLDIKSVYSASMAASLHGFSSSEDALEYKXS 433
Db 374 SPLVQALSGLIHSADRLBDSNKLKRSFSLDIKSVYSASMAASLHGFSSSEDALEYKXS 433
Qy 434 TTLDTGNKLCQFSPVQELSEQTPETSPDKKEASIPKCLQTARPSDSQSKRLHSVRTSSG 493
Db 434 TTLDTGNKLCQFSPVQELSEQTPETSPDKKEASIPKCLQTARPSDSQSKRLHSVRTSSG 493
Qy 494 TQORSLSPLRSGSVEDNYHTSFLFGLSTSOQHLTKSAGLKGWHSIDLAPOTSTPSL 553
Db 494 TQORSLSPLRSGSVEDNYHTSFLFGLSTSOQHLTKSAGLKGWHSIDLAPOTSTPSL 553
Qy 554 TSSWFATESSHFYASAIYGGASAYSAYSCQLPTCGQOYVSVRRQKPSDRADSRSM 613
Db 554 TSSWFATESSHFYASAIYGGASAYSAYSCQLPTCGQOYVSVRRQKPSDRADSRSM 613
Qy 614 HESPEKQFKRRSCOMERGESIMSENRREELGKVGQSOSFSGSMEIIEVS 665
Db 614 HESPEKQFKRRSCOMERGESIMSENRREELGKVGQSOSFSGSMEIIEVS 665
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RESULT 10

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US-10-257-026-2
; Sequence 2, Application US/10257026
; Publication No. US20040086859A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: New dual specificity phosphatase
; FILE REFERENCE: DUSP10KDS
; CURRENT APPLICATION NUMBER: US/10/257,026
; CURRENT FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-257-026-2
```

Query Match 71.0%; Score 472; DB 15; Length 665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 194 TCKPKDFIPESHFLRVPVNDSCFKILPWLDKSVDFIEKAKASNGCVLVHCLAGISRAT 253
Db 194 TCKPKDFIPESHFLRVPVNDSCFKILPWLDKSVDFIEKAKASNGCVLVHCLAGISRAT 253
Qy 254 IAIAYIMKMDMSLDEAYRFVYKERTPTISPNFNFLGQLLDYEKKIKNOTGASGPKSKLT 313
Db 254 IAIAYIMKMDMSLDEAYRFVYKERTPTISPNFNFLGQLLDYEKKIKNOTGASGPKSKLT 313
Qy 314 IHLERKNEVPVAVSEGGQKSETPLSPPCADSATSEAAQORPVHPASVPSVPQPSLLED 373
Db 314 IHLERKNEVPVAVSEGGQKSETPLSPPCADSATSEAAQORPVHPASVPSVPQPSLLED 373
Qy 374 SPLVQALSGLIHSADRLBDSNKLKRSFSLDIKSVYSASMAASLHGFSSSEDALEYKXS 433
Db 374 SPLVQALSGLIHSADRLBDSNKLKRSFSLDIKSVYSASMAASLHGFSSSEDALEYKXS 433
Qy 434 TTLDTGNKLCQFSPVQELSEQTPETSPDKKEASIPKCLQTARPSDSQSKRLHSVRTSSG 493
Db 434 TTLDTGNKLCQFSPVQELSEQTPETSPDKKEASIPKCLQTARPSDSQSKRLHSVRTSSG 493
```

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Qy 494 TQORSLSPLRSGSVEDNYHTSFLFGLSTSOQHLTKSAGLKGWHSIDLAPOTSTPSL 553
Db 494 TQORSLSPLRSGSVEDNYHTSFLFGLSTSOQHLTKSAGLKGWHSIDLAPOTSTPSL 553
Qy 554 TSSWFATESSHFYASAIYGGASAYSAYSCQLPTCGQOYVSVRRQKPSDRADSRSM 613
Db 554 TSSWFATESSHFYASAIYGGASAYSAYSCQLPTCGQOYVSVRRQKPSDRADSRSM 613
Qy 614 HESPEKQFKRRSCOMERGESIMSENRREELGKVGQSOSFSGSMEIIEVS 665
Db 614 HESPEKQFKRRSCOMERGESIMSENRREELGKVGQSOSFSGSMEIIEVS 665
```

RESULT 11

```
US-10-648-593-240
; Sequence 240, Application US/10648593
; Publication No. US20040106132A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCE: D0273 NP
; CURRENT APPLICATION NUMBER: US/10/648,593
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: 60/406,385
; NUMBER OF SEQ ID NOS: 557
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 240
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-593-240
```

Query Match 71.0%; Score 472; DB 16; Length 665;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 194 TCKPKDFIPESHFLRVPVNDSCFKILPWLDKSVDFIEKAKASNGCVLVHCLAGISRAT 253
Db 194 TCKPKDFIPESHFLRVPVNDSCFKILPWLDKSVDFIEKAKASNGCVLVHCLAGISRAT 253
Qy 254 IAIAYIMKMDMSLDEAYRFVYKERTPTISPNFNFLGQLLDYEKKIKNOTGASGPKSKLT 313
Db 254 IAIAYIMKMDMSLDEAYRFVYKERTPTISPNFNFLGQLLDYEKKIKNOTGASGPKSKLT 313
Qy 314 IHLERKNEVPVAVSEGGQKSETPLSPPCADSATSEAAQORPVHPASVPSVPQPSLLED 373
Db 314 IHLERKNEVPVAVSEGGQKSETPLSPPCADSATSEAAQORPVHPASVPSVPQPSLLED 373
Qy 374 SPLVQALSGLIHSADRLBDSNKLKRSFSLDIKSVYSASMAASLHGFSSSEDALEYKXS 433
Db 374 SPLVQALSGLIHSADRLBDSNKLKRSFSLDIKSVYSASMAASLHGFSSSEDALEYKXS 433
Qy 434 TTLDTGNKLCQFSPVQELSEQTPETSPDKKEASIPKCLQTARPSDSQSKRLHSVRTSSG 493
Db 434 TTLDTGNKLCQFSPVQELSEQTPETSPDKKEASIPKCLQTARPSDSQSKRLHSVRTSSG 493
Qy 494 TQORSLSPLRSGSVEDNYHTSFLFGLSTSOQHLTKSAGLKGWHSIDLAPOTSTPSL 553
Db 494 TQORSLSPLRSGSVEDNYHTSFLFGLSTSOQHLTKSAGLKGWHSIDLAPOTSTPSL 553
Qy 554 TSSWFATESSHFYASAIYGGASAYSAYSCQLPTCGQOYVSVRRQKPSDRADSRSM 613
Db 554 TSSWFATESSHFYASAIYGGASAYSAYSCQLPTCGQOYVSVRRQKPSDRADSRSM 613
Qy 614 HESPEKQFKRRSCOMERGESIMSENRREELGKVGQSOSFSGSMEIIEVS 665
Db 614 HESPEKQFKRRSCOMERGESIMSENRREELGKVGQSOSFSGSMEIIEVS 665
```

RESULT 12
 US-10-648-593-247
 ; Sequence 247, Application US/10648593
 ; Publication No. US20040106132A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
 ; INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
 ; TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
 ; FILE REFERENCE: D0273 NP
 ; CURRENT APPLICATION NUMBER: US/10/648,593
 ; CURRENT FILING DATE: 2003-08-26
 ; PRIOR APPLICATION NUMBER: 60/406,385
 ; PRIOR FILING DATE: 2002-08-27
 ; NUMBER OF SEQ ID NOS: 557
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 247
 ; LENGTH: 665
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-648-593-247

Query Match 71.0%; Score 472; DB 16; Length 665;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	194	TCPKDFTIPESHFLRPVNDSECEKILPWLKSVDFIEKAKSNGCVLVHCLAGISRAT	253
DB	194	TCPKDFTIPESHFLRPVNDSECEKILPWLKSVDFIEKAKSNGCVLVHCLAGISRAT	253
QY	254	IAIAYIMKMDMSLDEAYRFVKEKRPRTISPNFNFLGQLLDYKIKINQOGASGPKSKLT	313
DB	254	IAIAYIMKMDMSLDEAYRFVKEKRPRTISPNFNFLGQLLDYKIKINQOGASGPKSKLT	313
QY	314	LHLEKPNBEPVAVSEGGQKSETPPLSPCADSATSEAGQRPVHPASVPSVQPSLLD	373
DB	314	LHLEKPNBEPVAVSEGGQKSETPPLSPCADSATSEAGQRPVHPASVPSVQPSLLD	373
QY	374	SPLVALSGHLISADRLBDSNKLKRSFSLDIKSVSYASMAASLHGFSSEDALEYKXS	433
DB	374	SPLVALSGHLISADRLBDSNKLKRSFSLDIKSVSYASMAASLHGFSSEDALEYKXS	433
QY	434	TLLDGTNKLCOFSPVOELSEQTPETSPDKKASIPKKQOTAPRPSQSRLHSVRTSSG	493
DB	434	TLLDGTNKLCOFSPVOELSEQTPETSPDKKASIPKKQOTAPRPSQSRLHSVRTSSG	493
QY	494	TAQRSLSPLRSGSVEDNYHTSFLGLSTSOQHLTKSAGLKGWHSIDILAPOTSTPST	553
DB	494	TAQRSLSPLRSGSVEDNYHTSFLGLSTSOQHLTKSAGLKGWHSIDILAPOTSTPST	553
QY	554	TSSWTFATSSHIFYASAIYGGASAYSCSQLPTCGQVYSVRRQKPSDRADSRRW	613
DB	554	TSSWTFATSSHIFYASAIYGGASAYSCSQLPTCGQVYSVRRQKPSDRADSRRW	613
QY	614	HEESPFEKQFKRRSCOMERGESIMENRSREELGKVGSSSPSGSMETIEVS	665
DB	614	HEESPFEKQFKRRSCOMERGESIMENRSREELGKVGSSSPSGSMETIEVS	665

RESULT 13
 US-10-377-072-26
 ; Sequence 26, Application US/10377072
 ; Publication No. US20040157221A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals Inc.
 ; APPLICANT: Curtis, Rory A.J.
 ; APPLICANT: Logan, Thomas Joseph
 ; APPLICANT: Gluckmann, Maria A.
 ; APPLICANT: Meyers, Rachel E.
 ; APPLICANT: Williamson, Mark J.
 ; APPLICANT: Rudolph-Owen, Laura A.
 ; APPLICANT: Chun, Miyoung
 ; APPLICANT: Tsai, Fong-Ying

; TITLE OF INVENTION: NOVEL, 25869, 25934, 26335, 50365, 21117,
 ; TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
 ; TITLE OF INVENTION: AND USES THEREFOR
 ; FILE REFERENCE: MP103-0180NM1M
 ; CURRENT APPLICATION NUMBER: US/10/377,072
 ; CURRENT FILING DATE: 2003-02-27
 ; PRIOR APPLICATION NUMBER: US 09/895,860
 ; PRIOR FILING DATE: 2001-06-29
 ; PRIOR APPLICATION NUMBER: US 60/215,370
 ; PRIOR FILING DATE: 2000-06-29
 ; PRIOR APPLICATION NUMBER: US 09/723,806
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: US 60/187,455
 ; PRIOR FILING DATE: 2000-03-07
 ; PRIOR APPLICATION NUMBER: US 09/843,297
 ; PRIOR FILING DATE: 2001-04-25
 ; PRIOR APPLICATION NUMBER: US 60/199,801
 ; PRIOR FILING DATE: 2000-04-26
 ; PRIOR APPLICATION NUMBER: US 09/861,801
 ; PRIOR FILING DATE: 2001-05-21
 ; PRIOR APPLICATION NUMBER: US 60/205,508
 ; PRIOR FILING DATE: 2000-05-19
 ; PRIOR APPLICATION NUMBER: US 09/816,494
 ; PRIOR FILING DATE: 2001-03-23
 ; PRIOR APPLICATION NUMBER: US 09/815,419
 ; PRIOR FILING DATE: 2001-03-22
 ; Remaining Prior Application data removed - See file wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 114
 ; SOFTWARE: FaeltSeq for Windows Version 4.0
 ; SEQ ID NO 26
 ; LENGTH: 665
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-377-072-26

Query Match 71.0%; Score 472; DB 16; Length 665;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	194	TCPKDFTIPESHFLRPVNDSECEKILPWLKSVDFIEKAKSNGCVLVHCLAGISRAT	253
DB	194	TCPKDFTIPESHFLRPVNDSECEKILPWLKSVDFIEKAKSNGCVLVHCLAGISRAT	253
QY	254	IAIAYIMKMDMSLDEAYRFVKEKRPRTISPNFNFLGQLLDYKIKINQOGASGPKSKLT	313
DB	254	IAIAYIMKMDMSLDEAYRFVKEKRPRTISPNFNFLGQLLDYKIKINQOGASGPKSKLT	313
QY	314	LHLEKPNBEPVAVSEGGQKSETPPLSPCADSATSEAGQRPVHPASVPSVQPSLLD	373
DB	314	LHLEKPNBEPVAVSEGGQKSETPPLSPCADSATSEAGQRPVHPASVPSVQPSLLD	373
QY	374	SPLVALSGHLISADRLBDSNKLKRSFSLDIKSVSYASMAASLHGFSSEDALEYKXS	433
DB	374	SPLVALSGHLISADRLBDSNKLKRSFSLDIKSVSYASMAASLHGFSSEDALEYKXS	433
QY	434	TLLDGTNKLCOFSPVOELSEQTPETSPDKKASIPKKQOTAPRPSQSRLHSVRTSSG	493
DB	434	TLLDGTNKLCOFSPVOELSEQTPETSPDKKASIPKKQOTAPRPSQSRLHSVRTSSG	493
QY	494	TAQRSLSPLRSGSVEDNYHTSFLGLSTSOQHLTKSAGLKGWHSIDILAPOTSTPST	553
DB	494	TAQRSLSPLRSGSVEDNYHTSFLGLSTSOQHLTKSAGLKGWHSIDILAPOTSTPST	553
QY	554	TSSWTFATSSHIFYASAIYGGASAYSCSQLPTCGQVYSVRRQKPSDRADSRRW	613
DB	554	TSSWTFATSSHIFYASAIYGGASAYSCSQLPTCGQVYSVRRQKPSDRADSRRW	613
QY	614	HEESPFEKQFKRRSCOMERGESIMENRSREELGKVGSSSPSGSMETIEVS	665
DB	614	HEESPFEKQFKRRSCOMERGESIMENRSREELGKVGSSSPSGSMETIEVS	665

RESULT 14

/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/267,459
/ PRIOR FILING DATE: 2001-02-08
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 703
/ LENGTH: 690
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-072-012-703

Query Match 71.0%; Score 472; DB 15; Length 690;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 TCPKPDFIPESHFLRPVNDSECEKILPWLKSVDFIEKAKASNCVTVHCLAGISRSAT 253
DB 219 TCPKPDFIPESHFLRPVNDSECEKILPWLKSVDFIEKAKASNCVTVHCLAGISRSAT 278
QY 254 IAIAYIMRMDMSLDEAVRFVKEKRPITSPNPNFLGQLLDYRKIKNOGASGPKSKKL 313
DB 279 IAIAYIMRMDMSLDEAVRFVKEKRPITSPNPNFLGQLLDYRKIKNOGASGPKSKKL 338
QY 314 LHLKPNBPVPAVSEGGOKSETPLSPPCADSATSEAGORPVHPASVPSVPVPSILED 373
DB 339 LHLKPNBPVPAVSEGGOKSETPLSPPCADSATSEAGORPVHPASVPSVPVPSILED 398
QY 374 SPLVALSGLHLSADRLSDSNLKRKPSLIDIKSVSYASMAASLHGFSSEDALEYKPS 433
DB 399 SPLVALSGLHLSADRLSDSNLKRKPSLIDIKSVSYASMAASLHGFSSEDALEYKPS 458
QY 434 TTLDTGNTLCCPSPVQELSEQTPETSPDKEASIPKLOTAPSPDSQSKRLHSVTSSSG 493
DB 459 TTLDTGNTLCCPSPVQELSEQTPETSPDKEASIPKLOTAPSPDSQSKRLHSVTSSSG 518
QY 494 TAQRSLSPHRSAGVEDNYHTSFLGLSTSQOHLTKSAGLKGWHSIDILAPOTSTPSL 553
DB 519 TAQRSLSPHRSAGVEDNYHTSFLGLSTSQOHLTKSAGLKGWHSIDILAPOTSTPSL 578
QY 554 TSSWYFATESSHFYASAIYGGASAYSQSLPTCGDQVYSVRRROKPSDRADSRSM 613
DB 579 TSSWYFATESSHFYASAIYGGASAYSQSLPTCGDQVYSVRRROKPSDRADSRSM 638
QY 614 HESPEKQFKRRSCOMERGESIMENRREELGKVGSSSFGSGMEIIEVS 665
DB 639 HESPEKQFKRRSCOMERGESIMENRREELGKVGSSSFGSGMEIIEVS 690

RESULT 16
US-10-425-114-54204

/ Sequence 54204, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jindong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E.
/ APPLICANT: Tabacka, Jack B.
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53313)B
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO: 54204
/ LENGTH: 690
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: Clone ID: LIB4119-028-H6_F11.pap
US-10-425-114-54204

Query Match 71.0%; Score 472; DB 15; Length 690;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 TCPKPDFIPESHFLRPVNDSECEKILPWLKSVDFIEKAKASNCVTVHCLAGISRSAT 253
DB 219 TCPKPDFIPESHFLRPVNDSECEKILPWLKSVDFIEKAKASNCVTVHCLAGISRSAT 278
QY 254 IAIAYIMRMDMSLDEAVRFVKEKRPITSPNPNFLGQLLDYRKIKNOGASGPKSKKL 313
DB 279 IAIAYIMRMDMSLDEAVRFVKEKRPITSPNPNFLGQLLDYRKIKNOGASGPKSKKL 338
QY 314 LHLKPNBPVPAVSEGGOKSETPLSPPCADSATSEAGORPVHPASVPSVPVPSILED 373
DB 339 LHLKPNBPVPAVSEGGOKSETPLSPPCADSATSEAGORPVHPASVPSVPVPSILED 398
QY 374 SPLVALSGLHLSADRLSDSNLKRKPSLIDIKSVSYASMAASLHGFSSEDALEYKPS 433
DB 399 SPLVALSGLHLSADRLSDSNLKRKPSLIDIKSVSYASMAASLHGFSSEDALEYKPS 458
QY 434 TTLDTGNTLCCPSPVQELSEQTPETSPDKEASIPKLOTAPSPDSQSKRLHSVTSSSG 493
DB 459 TTLDTGNTLCCPSPVQELSEQTPETSPDKEASIPKLOTAPSPDSQSKRLHSVTSSSG 518
QY 494 TAQRSLSPHRSAGVEDNYHTSFLGLSTSQOHLTKSAGLKGWHSIDILAPOTSTPSL 553
DB 519 TAQRSLSPHRSAGVEDNYHTSFLGLSTSQOHLTKSAGLKGWHSIDILAPOTSTPSL 578
QY 554 TSSWYFATESSHFYASAIYGGASAYSQSLPTCGDQVYSVRRROKPSDRADSRSM 613
DB 579 TSSWYFATESSHFYASAIYGGASAYSQSLPTCGDQVYSVRRROKPSDRADSRSM 638
QY 614 HESPEKQFKRRSCOMERGESIMENRREELGKVGSSSFGSGMEIIEVS 665
DB 639 HESPEKQFKRRSCOMERGESIMENRREELGKVGSSSFGSGMEIIEVS 690

RESULT 17
US-10-072-012-256

/ Sequence 256, Application US/10072012
/ Publication No. US2004003493A1
/ GENERAL INFORMATION:
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Zernusen, Bryan
/ APPLICANT: Patuturajan, Weera
/ APPLICANT: Shimkets, Richard
/ APPLICANT: Li, Li
/ APPLICANT: Gangolli, Esba
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Anderson, David W.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Tapiet, Jr., Raymond J.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Coleman, Steven D.
/ APPLICANT: Wolenc, Adam R.
/ APPLICANT: Pena, Carol E. A.
/ APPLICANT: Futrak, Katarzyna
/ APPLICANT: Grose, William M.
/ APPLICANT: Alsdbrook II, John P.
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Rieger, Daniel K.
/ APPLICANT: Burgess, Catherine E.
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-258
/ CURRENT APPLICATION NUMBER: US/10/072,012
/ CURRENT FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: 60/265,102
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/265,514

```

; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 256
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Homo sapiens
us-10-072-012-256

Query Match      59.2%; Score 394; DB 15; Length 680;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 RFVKSRPTISNPNFNLGGLDYEKKIKNQTGASGPKSLKLLHLEKPNBPVPAVSEGGQ 331
DB 267 RFVKSRPTISNPNFNLGGLDYEKKIKNQTGASGPKSLKLLHLEKPNBPVPAVSEGGQ 346
QY 332 KSETPLSPCCADSATSEAAQGRPVHPASVSVSVQPSLLEDSPLVQALSGHLSDADRL 391
DB 347 KSETPLSPCCADSATSEAAQGRPVHPASVSVSVQPSLLEDSPLVQALSGHLSDADRL 406
QY 332 DSNKTKRSPSLDIKVSYSASMAASLHGSSSEDALEYKPKSTTLDGNTKLCQFSPVQDL 451
DB 407 DSNKTKRSPSLDIKVSYSASMAASLHGSSSEDALEYKPKSTTLDGNTKLCQFSPVQDL 466
QY 452 SEQTPETSPDKKEASIPKKLQTPAPPSDSQSKRLHSVRTSSSGTAORSLSPHRSQVVD 511
DB 467 SEQTPETSPDKKEASIPKKLQTPAPPSDSQSKRLHSVRTSSSGTAORSLSPHRSQVVD 526
QY 512 NYHTSFLFGLSTSQOHLTKSAGLGLKGMHSDILAPQSTPSTLTSWYFATSSSHFYASA 571
DB 527 NYHTSFLFGLSTSQOHLTKSAGLGLKGMHSDILAPQSTPSTLTSWYFATSSSHFYASA 586
QY 572 IYGSASASVAYSCSQLPTCGDOVYSVRROKPSDRADSRSMHEBPFKQPKRRSCOME 631
DB 587 IYGSASASVAYSCSQLPTCGDOVYSVRROKPSDRADSRSMHEBPFKQPKRRSCOME 646
QY 632 FGEISIMSENRREBELGKVGSSSFGSGSMELIEVS 665
DB 647 FGEISIMSENRREBELGKVGSSSFGSGSMELIEVS 680

RESULT 18
us-10-072-012-258
; Sequence 258, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: zernusen, Bryan
; APPLICANT: Patrujan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
```

```

; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gueev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 258
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
us-10-072-012-258

Query Match      45.7%; Score 304; DB 15; Length 662;
Best Local Similarity 100.0%; Pred. No. 1,4e-278;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 SVPSVQPSLLEDSPLVQALSGHLSDADRLSDSNKTKRSPSLDIKVSYSASMAASLHGFS 421
DB 359 SVPSVQPSLLEDSPLVQALSGHLSDADRLSDSNKTKRSPSLDIKVSYSASMAASLHGFS 418
QY 422 SEEDALEYKPKSTTLDGNTKLCQFSPVQDLSEQTPETSPDKKEASIPKKLQTPAPPSDSQS 481
DB 419 SEEDALEYKPKSTTLDGNTKLCQFSPVQDLSEQTPETSPDKKEASIPKKLQTPAPPSDSQS 478
QY 482 KRLHSVRTSSSGTAORSLSPHRSQVVDNYHTSFLFGLSTSQOHLTKSAGLGLKGMHS 541
DB 479 KRLHSVRTSSSGTAORSLSPHRSQVVDNYHTSFLFGLSTSQOHLTKSAGLGLKGMHS 538
QY 542 DILAPQSTPSTLTSWYFATSSSHFYASATYGSASVAYSCSQLPTCGDOVYSVRRO 601
DB 539 DILAPQSTPSTLTSWYFATSSSHFYASATYGSASVAYSCSQLPTCGDOVYSVRRO 598
QY 602 KPSDRADSRSMHEBPFKQPKRRSCOMEFGEISIMSENRREBELGKVGSSSFGSGSMEL 661
DB 599 KPSDRADSRSMHEBPFKQPKRRSCOMERGESIMSENRREBELGKVGSSSFGSGSMEL 658
QY 662 IEVS 665
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Db 659 IEVS 662

RESULT 19

US-10-296-115-1259
; Sequence 1259, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ. ID NOS: 1478
; SEQ ID NO 1259
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(672)
; OTHER INFORMATION: Xaa = any amino acid or other as shown in Table 3
US-10-296-115-1259

Query Match 38.8%; Score 258; DB 15; Length 672;
Best Local Similarity 100.0%; Pred. No. 5e-235;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 TCPKPDFIPESHFLRPVNDSECEKILPWLKSVDFIEKAKSNGCVLHCLAGISRSAT 253
Db 201 TCPKPDFIPESHFLRPVNDSECEKILPWLKSVDFIEKAKSNGCVLHCLAGISRSAT 260
QY 254 IAIAYIMKRMDSLDEAYRFVKEKRPITSPNPNFLGQLLDYKIKNQTAGSKPKTL 313
Db 261 IAIAYIMKRMDSLDEAYRFVKEKRPITSPNPNFLGQLLDYKIKNQTAGSKPKTL 320
QY 314 LHLKPNPEPPVAVSEGGQKSETPLSPPCADSATSEAAQGRPVHPASVPSVQPSLLED 373
Db 321 LHLKPNPEPPVAVSEGGQKSETPLSPPCADSATSEAAQGRPVHPASVPSVQPSLLED 380
QY 374 SPVVALSGHLHSARLEDSNKLKRSFSLDTSVSYSSASMAASLHGFSSESSEALTYKPS 433
Db 381 SPVVALSGHLHSARLEDSNKLKRSFSLDTSVSYSSASMAASLHGFSSESSEALTYKPS 440
QY 434 TTLDTGNKLCOPSPVOEL 451
Db 441 TTLDTGNKLCOPSPVOEL 458

RESULT 20

US-10-108-260A-4872
; Sequence 4872, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4872
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4872

Query Match 22.9%; Score 152; DB 15; Length 253;
Best Local Similarity 99.6%; Pred. No. 4.6e-135;

Matches 252; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 413 MAASLHGFSSESSEALTYKPSLTLDTGNKLCOPSPVOELSEOTPTSPDKESASIPKIQ 472
Db 1 MAASLHGFSSESSEALTYKPSLTLDTGNKLCOPSPVOELSEOTPTSPDKESASIPKIQ 60
QY 473 TARPDSOSKRLHSVRTSSGTAQRSLSPHLRSGSVEDNVTSTFLGLSTSQHLYKSA 532
Db 61 TARPDSOSKRLHSVRTSSGTAQRSLSPHLRSGSVEDNVTSTFLGLSTSQHLYKSA 120
QY 533 GLGLGKMSDILAPQSTPSTLTSVYPATSSHPYASAIYGSASYSAYSCSQLPCTGD 592
Db 121 GLGLGKMSDILAPQSTPSTLTSVYPATSSHPYASAIYGSASYSAYSCSQLPCTGD 180
QY 593 QVYSVRRQKPSDRADRSRWSHEESPFEKQFRRCQWFEFGSINSNRREELKVGSG 652
Db 181 QVYSVRRQKPSDRADRSRWSHEESPFEKQFRRCQWFEFGSINSNRREELKVGSG 240
QY 653 SFFSGSMELIEVS 665
Db 241 SFFSGSMELIEVS 253

RESULT 21

US-09-964-277-7
; Sequence 7, Application US/09964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Lucite, Ralf M.
; APPLICANT: Wei, Bo
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125,434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-277-7

Query Match 16.2%; Score 108; DB 9; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.3e-93;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 TCPKPDFIPESHFLRPVNDSECEKILPWLKSVDFIEKAKSNGCVLHCLAGISRSAT 253
Db 48 TCPKPDFIPESHFLRPVNDSECEKILPWLKSVDFIEKAKSNGCVLHCLAGISRSAT 107
QY 254 IAIAYIMKRMDSLDEAYRFVKEKRPITSPNPNFLGQLLDYKIKNQ 301
Db 108 IAIAYIMKRMDSLDEAYRFVKEKRPITSPNPNFLGQLLDYKIKNQ 155

RESULT 22

US-10-072-012-682
; Sequence 682, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernyev, Vellizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zetrisen, Bryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esna
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Raetelli, Luca
; APPLICANT: Miller, Charles B.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.

APPLICANT: Gusev, Vladimir Y.
APPLICANT: Coleman, Steven D.
APPLICANT: Molenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 682
LENGTH: 660
TYPE: PRT
ORGANISM: Mus musculus
US-10-072-012-682

Query Match 10.1%; Score 67; DB 15; Length 660;
Best Local Similarity 100.0%; Pred. No. 3.2e-54;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 15 LVALLSGTEKVLILDSRPFEYNTSHLEAININCSKIMKRRLOODKVLITELIOHSAK 74
QY 75 HKVDIDC 81
DB 75 HKVDIDC 81
RESULT 23
US-10-072-012-683
Sequence 683, Application US/10072012
Publication No. US2004003343A1
GENERAL INFORMATION:
APPLICANT: Tchenev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zernusen, Bryan
APPLICANT: Patcurajan, Meera
APPLICANT: Shinkets, Richard
APPLICANT: Li, Li
APPLICANT: Gangoli, Esna
APPLICANT: Padigaru, Muralihara
APPLICANT: Anderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Miller, Charles E.
APPLICANT: Gerlach, Valerie

APPLICANT: Taupier Jr, Raymond J.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Coleman, Steven D.
APPLICANT: Molenc, Adam R.
APPLICANT: Pena, Carol E. A
APPLICANT: Furtak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: US/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
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PRIOR APPLICATION NUMBER: 60/266,406
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PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 683
LENGTH: 677
TYPE: PRT
ORGANISM: Mus musculus
US-10-072-012-683

Query Match 9.6%; Score 64; DB 15; Length 677;
Best Local Similarity 100.0%; Pred. No. 2.2e-51;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 114 SFNSVHLAAGFAEFRCFPGACEGKSTVPTCISOPCLPVANIGPTTILPNLYIGCORD 173
DB 114 SFNSVHLAAGFAEFRCFPGACEGKSTVPTCISOPCLPVANIGPTTILPNLYIGCORD 173
QY 174 VLNK 177
DB 174 VLNK 177
RESULT 24
US-09-764-853-578
Sequence 578, Application US/09764853
Patent No. US20020090672A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJ206
CURRENT APPLICATION NUMBER: US/09/764,853
PRIOR FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 939
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 578
LENGTH: 88
TYPE: PRT

; ORGANISM: Homo sapiens
US-09-764-853-578

Query Match 8.4%; Score 56; DB 9; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.4e-44;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAHEMIGTQIVTERLVALLSGSTKYLIDSRPFVEYNTSHILEAININCSKLMKR 56
|||
Db 26 MAHEMIGTQIVTERLVALLSGSTKYLIDSRPFVEYNTSHILEAININCSKLMKR 81

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 14, 2005, 13:42:21 ; Search time 845 Seconds

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Title: US-10-029-345a-109

Perfect score: 665
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5378673 seqs, 295022984 residues

Word size: 75

Total number of hits satisfying chosen parameters: 39

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Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

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-FAPOP=6 -FAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELop=6 -DELEXT=7

Database : Published Applications NA.*

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22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	472	71.0	1998	17	US-10-377-072-27
3	472	71.0	1998	18	US-10-377-072-27
4	472	71.0	2102	17	US-10-094-749-673
5	472	71.0	2732	17	US-10-168-506-2
6	472	71.0	2966	17	US-10-296-115-520
7	472	71.0	3059	17	US-10-257-026-1
8	472	71.0	3332	9	US-09-964-277-20
9	472	71.0	3496	9	US-09-964-277-1
10	472	71.0	3521	18	US-10-370-715B-261
11	472	71.0	3544	9	US-09-816-494-1
12	472	71.0	3544	17	US-10-377-072-25
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14	472	71.0	3625	17	US-10-425-114-26234
15	472	71.0	3766	17	US-10-343-357-17
16	472	71.0	4790	18	US-10-648-593-115
17	472	71.0	5145	18	US-10-357-930-20824
18	472	71.0	5145	18	US-10-357-930-20969
19	472	71.0	5145	18	US-10-357-930-21071
20	472	71.0	5145	18	US-10-357-930-21083
21	472	71.0	5145	18	US-10-357-930-21303
22	472	71.0	5145	18	US-10-357-930-21307
23	472	71.0	5145	18	US-10-357-930-22820
24	472	71.0	5145	18	US-10-357-930-26669
25	472	71.0	5145	18	US-10-357-930-26815
26	472	71.0	5145	18	US-10-357-930-26912
27	472	71.0	5145	18	US-10-357-930-26923
28	472	71.0	5145	18	US-10-357-930-27145
29	472	71.0	5145	18	US-10-357-930-27149
30	472	71.0	5145	18	US-10-357-930-28675
31	408	61.4	2200	17	US-10-072-012-255
32	304	45.7	2071	17	US-10-072-012-257
33	178	26.8	1916	17	US-10-108-260A-2429
34	138	20.8	4625	18	US-10-357-930-10717
35	137	20.6	467	18	US-10-357-930-31909
36	137	20.6	467	18	US-10-357-930-40868
37	137	20.6	467	18	US-10-357-930-41017
38	133	20.0	408	18	US-10-357-930-10898
39	132	19.8	438	18	US-10-357-930-32077

ALIGNMENTS

RESULT 1
US-09-816-494-3
Sequence 3, Application US/09816494
Patent No. US20020034807A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
FILE REFERENCE: 10448-030002
CURRENT APPLICATION NUMBER: US/09/816,494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/191,858
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo sapiens
US-09-816-494-3

Alignment Scores:
Pred. No.: 0
Score: 472.00
Percent Similarity: 99.40%
Best Local Similarity: 99.40%
Length: 1998
Matches: 663
Conservative: 0
Mismatches: 2

Query Match: 70.98% Indels: 4
DB: 9 Gaps: 0

US-10-029-345A-109 (1-665) x US-09-816-494-3 (1-1998)

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DB 61 AGTGGACGGAAGAAAAGCTGCTACTATTTGATAGCCGGCATTGGGAAATCAATACATCC 120
QY 41 HisIleLeuGluValAlaIleAsnIleAsnCySerIleuWetIysValGluLeuGln 60
DB 121 CACATTTTGGAAAGCATTAATATCACTGCTCCAAAGCTTATGAGAGCAAGGTTGCAACAG 180
QY 61 AspIysValLeuIleThrGluLeuIleGlnHisSerAlaIysHisIysValAspIleAsp 80
DB 181 GACAAAGTTTAAATTACAGACCTCATCAGCATTCAGCAAAACATAAGTTGACATTGAT 240
QY 81 CysSerGlnYsValValIYrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
DB 241 TGCAGTCAGAAAGTTGATGTTACATCAAAAGCTCCCAAGATGTGCTCTCTCTTCA 300
QY 101 AspCySphenThrValLeuLeuGlyIlyLeuGluYsSerPheAsnSerValHisLeu 120
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DB 659 TGCCTGTGGTGGACAAATCAATGATTAATTCATTGAGAAAGCAAAAGCTCCATAGAGTGG 718
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QY 260 eIlyAspMetAspMetSerLeuAspGluAlaIYrArgPheValIysGluYsArgProT 280
DB 779 TGAAGAGATGACACTGTCTTTAGATGAAGCTTACAGATTGTGAAAGAAAAAGACCTA 838
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DB 959 ATGAACCTGCTCCTGCTGTCTAGAGGGTGAACAGAAAAGCAAGAGCGCCCTCAGTCCAC 1018

QY 340 rOCyAlaAspSerAlaThrSerGluAlaAlaGlyIlyAspProValHisProAlaSer 360
DB 1019 CCGTGGCCACTCTGTACTTACATGAGGCAAGCAAGCAAAAGCCCTGATCCCGCAGGG 1078
QY 360 aIProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAla 380
DB 1079 TGGCCAGCGTGGCCAGCGTGCAGCGTGTGATAGGACAGCCCGCTGTATCAGCGCG 1138
QY 380 euSerGIYleuHisIleuSerAlaAspArgLeuGluAspSerAsnIysIleuYsArgSerP 400
DB 1139 TCAGTGGGCTGCACCTGTCCGAGACAGGCTGAAAGACAAATTAAGCTCAAGCGTTCT 1198
QY 400 heSerLeuAspIleYsSerValSerTYrSerAlaSerMetAlaIleSerLeuHisGlyP 420
DB 1199 TCTCTGTGATATCAATCAATGATTCAATTCAGCCAGCATGGCAGATCTTACATGGCT 1258
QY 420 heSerSerSerGluAspAlaLeuGluTYrTYrIlyAspProSerThrThrLeuAspGlyTh 440
DB 1259 TCTCCTCATCAGAAAGTCTTGGAAATACTACAAACCTTCCACTCTGTGATGGACCA 1318
QY 440 snIlyLeuCySglnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerP 460
DB 1319 ACAAGCTATGCAAGTTCTCCCTGTTCAGAAACTATCGAGCAAGCTCCGAAACAGATC 1378
QY 460 roAspIysGluGluAlaSerIleProIysIlyLeuGlnThrAlaArgProSerAspSerG 480
DB 1379 CTGATTAAGAGAGAGCAAGCATCCCAAGAGCTGACAGCCCGCAGGCTTCAACAGACC 1438
QY 480 IAserIysArgLeuHisIserValArgThrSerSerSerGlyThrAlaGlnAspSerLeu 500
DB 1439 AGAGCAAGGAGATTGCTGCTGTCAGAAACAGACAGCTGAGCCGCGCAAGGCTCTTT 1498
QY 500 euSerProLeuHisAspSerGlySerValGluAspAsnTYrHisThrSerPheLeuPheG 520
DB 1499 TATCTCAGCTGATCAGAGTGGAGGCTGAGAGCAATTAACACACACTTCCTTTGG 1558
QY 520 IYleuSerThrSerGlnGlnHisIleuThrIysSerAlaGlyLeuGlyIlyYsGlyTYrH 540
DB 1559 GCCTTTCACAGCAGCAGCAGCACTTCAGCAAGCTGCTGCGGCTTTAAGGGCTGGC 1618
QY 540 IAserAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTPYrPheA 560
DB 1619 ACTCGATATCTTGGCCCCCAGACCTTACCTTACCTTCCCTGACAGCAGCACTGTATTTG 1678
QY 560 IeThrGlnSerSerHisPheTYrSerAlaSerAlaIleTYrGlyIlySerAlaSerTYrs 580
DB 1679 CCAAGAGTCTTACACTTCTACTCTGCTCAGCCATCTACGAGGCAAGTCACTTACT 1738
QY 580 eAlaTYrSerCySserGlnLeuProThrCySgIlyAspGlnValTYrSerValArgArg 600
DB 1739 CTGCTTACAGCTCAGCAGCAGCTGCCACTTGGCGGAGAACAAAGTCTATTTCTGTGCGCAGGC 1798
QY 600 rGlnIlySProSerAspArgAlaAspSerArgArgSerTPHISgIlyGluYsSerProPheG 620
DB 1799 GGCAGAAAGCCAAATGACAGCTGACTCGCGGAGCTGGCAATTAAGAGAGCCCTTTG 1858
QY 620 IuYsGlnPheIysArgArgSerCySgIlymeGluPheGlyGluSerIleMetSerGluA 640
DB 1859 AAAAGAGATTTAACGCAAGACTGCCAAATGGAATTTGAGAGAGCAATCATTCAGAGA 1918
QY 640 snArgSerArgGluLeuGlyIlyValGlySserGlnSerSerPheSerGlySerMetG 660
DB 1919 ACAAGTACGGGAAGAGCTGGGAAAGTGGGCAGTCACTATGCTTTTGGGCGAGCATGG 1978
QY 660 IuIleIleGluValSer 665
DB 1979 AAATCATTAAGTCTCC 1995

RESULT 2
US-10-377-072-27
; Sequence 27, Application US/10377072
; Publication No. US2004009501A1
; GENERAL INFORMATION:

```

APPLICANT: Millennium Pharmaceuticals Inc.
APPLICANT: Curtis, Rory A.J.
APPLICANT: Logan, Thomas Joseph
APPLICANT: Glucksmann, Maria A.
APPLICANT: Meyers, Rachel E.
APPLICANT: Williams, Mark J.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Chun, Myoung
APPLICANT: Tsai, Fong-Ying
TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
FILE REFERENCE: MP103-0180NMIM
CURRENT APPLICATION NUMBER: US/10/377,072
CURRENT FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: US 09/895,860
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,370
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/723,806
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/187,455
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/843,297
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: US 60/199,801
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: US 09/861,801
PRIOR FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/205,508
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/816,494
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/815,419
PRIOR FILING DATE: 2001-03-22
Remaining prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27
LENGTH: 1998
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1998)
US-10-377-072-27

Alignment Scores:
Pred. No.: 0
Score: 472.00
Percent Similarity: 99.40%
Best Local Similarity: 99.40%
Query Match: 70.98%
Length: 1998
Matches: 663
Conservative: 0
Mismatch: 2
Indels: 4
Gaps: 0

US-10-029-345a-109 (1-665) x US-10-377-072-27 (1-1998)
QY 1 MetAlHlsglUmetlleglYthrglnllevAlthGluArgleuValAlaleuLeugln 20
DB 1 ATGGCCCATGAGTGTGATGGAATGTAATGTAAGTGTGAGAGTGTGCTGCTGGA 60
QY 21 SerGlyThrglUyValleuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
DB 61 AGTGAACCGAAGAAAGTGTGCTAATGTAATGTAAGTGTGGAATGTAATGTAATG 120
QY 41 HlelLeuGlUalaleuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
DB 121 CACATTTTGGAAACCTTAATATCACTGCTCAACCTTAATGAGGAGTTGCAACG 180
QY 61 AspLyValleuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
DB 181 GACAAAGTGTATTAATACAGAGCTCATCCAGCATTCAGCGAAACATTAAGTTG 240

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QY 81 CySerGlnLyValValValYrApgInSerSerGlnAAspValAlaSerLeuSer 100
DB 241 TGCAGTCAGAAAGTTGTATTAATACATCAAACTCCAGAAAGTTGCCCTCTCTTCA 300
QY 101 AspCyPheLeuThrValleuLeuGlyLyLeuGlnLySerPheAsnSerValHleu 120
DB 301 GACTGTTTCTCACTGATCTTCTGGGTAAACGTGGAGAAAGCTTCAACTCTGTCAC 360
QY 121 LeuAlaGlyGlyPheAlaGlnPheSerArgPheProGlyLeuCyGlnGlyLySer 140
DB 361 CTTCAGAGGTGGTGTGATGTTCTCTGTTTCTGCTGCTGCTGTAAGAAATCC 420
QY 141 ThrLeuValProThrCyLeuSerGlnProCyLeuProValAlaAsnIleGlyProThr 160
DB 421 ACTCTAGTCCCTACCTGCACTTCTCAAGCTTCTTACCTGTTGCCAACCTGGCCAAC 480
QY 161 ArgIleLeuProAsnLeuTyrLeuGlyCyGlnArgAspValleuAsnLyGlnLeu 180
DB 481 CGAATTCCTCCAACTTATATCTGGCTGCCAGGAGTCTCTCAACAGAGCTGAT- 539
QY 181 -GlnGlnAnglylIleGlyTyrValleuAsnAlaSerTyr-ThrCyPProLyProAsp 200
DB 540 GGAGCAGATGGGATGTTATGTGTAAATGCCAGCA-TACCTGTCCAAAGCTGACT 598
QY 200 HeIlProGlnSerHisPheLeuArgValProValAsnAspSerPheCyGlnLyIle 220
DB 599 TTAATCCGAGTCTCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 658
QY 220 euProTyrLeuAspLySerValAspPheIleGlnLyValLyAsnSerAnglyCyav 240
DB 659 TCCCGGTGGTGAACATCAATGATGATTCATGAGAAACAAAGCTCCATATGATG 718
QY 240 AlLeuValHleCySerLeuAlaGlyIleSerArgSerAlaThrIleAlaIleA 260
DB 719 TTCTAGTGACGTGTTAGTGGATCTCCGCTCCGCAACATCGCTACCTATATCA 778
QY 260 eLyArgMetAspMetSerLeuAspGlnAlaTyrArgPheValLyGlnLyAspPro 280
DB 779 TGAAGAGATGACATGCTTTAGATGAACTTACAGATTGTGAAGAAAGAAAGCTTA 838
QY 280 hrIleSerProAsnPheAsnPheLeuGlnLyLeuLeuAspTyrGlnLyIleLy 300
DB 839 CTATATCTCCAACTTCAATTTCTGGGCCAATCTCTGGAATGAGAGAAATTAAGA 898
QY 300 AnglInThrglyAlaSerGlyProLySerLyLeuLyLeuLeuHleuGlnLyPPro 320
DB 899 ACCAGACTGAGCATCAGGCGCAAGAGCAAACTCAAGCTGTGCACTGGAGAAACCA 958
QY 320 AngLyProValProAlaValSerGlnGlyGlyGlnLySerGlnLyProLeuSerPro 340
DB 959 ATGAACTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1018
QY 340 roCyAlaAspSerAlaThrSerGlnAlaAlaGlyGlnArgProValHisProAlaSer 360
DB 1019 CCTGTGCGGACTCTGCTACCTCAGAGGAGCAGAGCAAAAGCCCGGATCCCGCAG 1078
QY 360 AlProSerValProSerValGlnProSerLeuLeuGlnAspSerProLeuValGlnAl 380
DB 1079 TCCCAAGCGTGGCCAGCGCGCGCTGCTGTGAGAGCAGCCCGCTGATACAGGCC 1138
QY 380 euSerGlyLeuHleuSerAlaAspArgLeuGlnAspSerAsnLyLeuLyAspSer 400
DB 1139 TCAATGGGCTGCACTGTTCGAGACAGGCTGGAAGACAGCAATTAAGCTCAAGCTT 1198
QY 400 HeSerLeuAspIleLySerValSerTyrSerAlaSerMetAlaAlaSerLeuHle 420
DB 1199 TCTCTCGGATATCAATCAAGTTTCATATTCAGCCAGCATGCGACATCTTACATG 1258
QY 420 HeSerSerSerGlnAspAlaLeuGlyTyrTyrLyPProSerThrThrLeuAspGly 440
DB 1259 TCTCTCTATCAAAATGCTTGGATCTCAAACTTCCACTCTGATGAGGAGCA 1318
QY 440 snLyLeuCyGlnPheSerProValGlnGlnLeuSerGlnGlnThrProGlnThrSer 460

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Db 1319 ACAAGCTATGCCAGTTCCTCCCTGTCAGAACTATCGGAGCAACTCCGGAACCAAGTC 1378
QY 460 rGAspLysgluLuuLaaSerLleProlYsLseuGlnThraLaaPProSerAspSerG 480
Db 1379 CTGATTAAGAGGAGAACCCAGCATTCCTCCAGGAAGCTGAGAACCGGACGCTTCAGACAGCC 1438
QY 480 lnseryLysgluLuuLaaSerValArgThrsersersergLynThraLaglnaLysSerleuL 500
Db 1439 AGAGCAAGCGATTTGATTCGCTCAGAACCCAGCAAGCTGACCGCCAGAGGCTCCCTTT 1498
QY 500 euserProleuHiLargSerGlySeryValLueAspAanyrHsThrserserPheLuePheG 520
Db 1499 TATCTCCATGATCAGAGTGGAGCGCTGGAGGACATTTACCAACACAGCTTCCTTTTCG 1558
QY 520 lyeuserThrserserglnHnHleuthrLysSerLaglyLseuGlyLysLysglYTPH 540
Db 1559 GCGCTTCCACAGCCAGCAAGCACTCAGAAAGTCTGCTGCGCTGAGGCTTAAAGGCTGAGC 1618
QY 540 lsserAapLleLuuLaaProlnThrsersThrsProserLeuthrserserTPyrPhea 560
Db 1619 ACTCGATATCTTGGCCCCCAGACCTTAACCTTCCTTGACCAAGAGCTGGATTTTG 1678
QY 560 lathrgLyserserserHisPheYrSeraLaserLaleYrGlyLyseraLaserYrs 580
Db 1679 CCACAGAGTCTCACACTTCTACTCTGCTCAGCCATTAACGAGGAGGCTCCAGTTACT 1738
QY 580 exPalaYrSerCyserSerGlnLueProthCyserGlyAspGlnValYrSeraLArgArG 600
Db 1739 CTGCTTACAGCTGACAGCCAGCTGCCCCACTTGGCGAGACACAGTCTATTTCTGCGAGGC 1798
QY 600 rGglnLysProserAspArgLaaAspSerArgArGserTPHsGlnGlnserProbeg 620
Db 1799 GCGAGAGCCAGTACAGAGCTGACTCGCGCGAGGCTGGCAAGGAGGAGGAGGAGGAGGAGG 1858
QY 620 luluYsGlnPheLysArgArGserCyserGlnMetGlnPheGlyLysSerLleMetSerGln 640
Db 1859 AAAAGAGATTAAAGCAGAAAGCTGCCAAATGAAATTTGGAGAGAGATATGTCAGAGA 1918
QY 640 snArgSerArgGlnLueLueGlyLysValGlyserGlnserSerPheSerGlySerMetG 660
Db 1919 ACAAGTCAAGGAGAGAGCTGGGGAAGTGGGAGAGTGGAGTACTTTTTCGGGAGCATGG 1978
QY 660 lulleLleGlnValiser 665
Db 1979 AAATCATTTGAGGTCTCC 1995

RESULT 3
US-10-377-072-27
/ Sequence 27, Application US/10377072
/ Publication No. US20040157221A9
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals Inc.
/ APPLICANT: Curtis, Roy A.J.
/ APPLICANT: Logan, Thomas Joseph
/ APPLICANT: Gluckemann, Maria A.
/ APPLICANT: Meyers, Rachel E.
/ APPLICANT: Williamson, Mark J.
/ APPLICANT: Rudolph-Owen, Laura A.
/ APPLICANT: Chun, Miyoung
/ APPLICANT: Tsai, Feng-Ying
/ TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
/ TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
/ FILE REFERENCE: MP103-0180NM1M
/ CURRENT APPLICATION NUMBER: US/10/377.072
/ PRIOR APPLICATION NUMBER: US 09/895,860
/ PRIOR FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: US 60/215,370
/ PRIOR FILING DATE: 2000-06-29
/ PRIOR APPLICATION NUMBER: US 09/723,806
/ PRIOR FILING DATE: 2000-11-28
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/ PRIOR APPLICATION NUMBER: US 60/187,455
/ PRIOR FILING DATE: 2000-03-07
/ PRIOR APPLICATION NUMBER: US 09/843,297
/ PRIOR FILING DATE: 2001-04-25
/ PRIOR APPLICATION NUMBER: US 60/199,801
/ PRIOR FILING DATE: 2000-04-26
/ PRIOR APPLICATION NUMBER: US 09/861,801
/ PRIOR FILING DATE: 2001-05-21
/ PRIOR APPLICATION NUMBER: US 60/205,508
/ PRIOR FILING DATE: 2000-05-19
/ PRIOR APPLICATION NUMBER: US 09/816,494
/ PRIOR FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: US 09/815,419
/ PRIOR FILING DATE: 2001-03-22
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 27
/ LENGTH: 1998
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(1998)
US-10-377-072-27

Alignment Scores:
Pred. No.: 0
Score: 472.00
Percent Similarity: 99.40%
Best Local Similarity: 99.40%
Query Match: 70.98%
DB: 18
Gaps: 0

US-10-029-345A-109 (1-665) x US-10-377-072-27 (1-1998)
QY 1 MetAlaHisgluMetlleGlyThrGlnlleValThrGlnArgLuuValAlaLueLueGln 20
Db 1 ATGGCCATAGATGATGATGAACTCAAAATGTTACTGAGAGGTTGGTGGCTGCTGAGAA 60
QY 21 SerGlyThrGlnLysValLueLueLleAspSerArgPhePheValGlnYrAsnThSer 40
Db 61 AGTGAACCGAAAGAGTCTGCTGATTAATGATGACCGGCAATTTGGAAATACAAATACATCC 120
QY 41 HislleLueGlnuAlaLleasnLleasnCyserLysLueMetLysArgArgLueGlnGln 60
Db 121 CACATTTTGAAGCCATTAATATCAACTGCTCCAAAGCTTATGAGAGGAGGTTGCAAG 180
QY 61 AspLysValLleuLleThrGlnLueLleGlnHisSerLalysHslusValaAspLleAsp 80
Db 181 GACAAAGTGTATTAACAGAGCTCATCCAGATTCAGCGAAACATTAAGGTTGACATTGAT 240
QY 81 CyserGlnLysValLleValLleValLleYrAspGlnserSerGlnAspValAlaserLueSer 100
Db 241 TCGATCGAAGAGTGTATTAACAGAGCTCATCCAGATTCAGCGAAACATTAAGGTTGAT 300
QY 101 AspCyserLueThrValLleLueLueGlyLysLueLueLysSerPheAsnSerValHisLue 120
Db 301 GACTGTTTTCACATGATCTTCTGGTAACTGAGAGAGGCTTCAACTCTGTTCACTCG 360
QY 121 LueLaglyGlyPheAlaGlnPheSerArgCyAspPheGlyLueCyGlnGlyLysSer 140
Db 361 CTGAGAGTGGTGTGCTGAGTCTCTCGTGTGTTCCCTGGGCTCTGTGAAGGAATTC 420
QY 141 ThrLuuValProthCyserLysSerGlnProCyserLueProValAlaAsnLleGlyProThr 160
Db 421 ACTCTAGTCCCTACCTGATCTTCTGAGCTTGTCTTACCTGTTGCCAAGATGGGCAACC 480
QY 161 ArgLleLueProAsnLueYrLueGlyCyserGlnArgAspValLleuAsnLysGlnLueLle 180
Db 481 CGAATCTTCCCAATCTTATCTGCTGCGAGGAGAGTCTCTCAAGAGAGCTGAT- 539
QY 181 -GlnGlnAsnGlylleGlyYrValLueAsnLaserYr-ThrCyserProLysProAsp 200
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Db      540 GCAGCAGAAATGGATGTTATGTATGTTAATGCCACAA-TACCTGTCCAAAGCTGACT 598
Qy      200 helLeProGluSerHisPheLeuArgValProValIAsnAspSerPheCysGluLysIleL 220
Db      599 TTATCCCGCAAGTCTCATTTCTCGGTGTGTGTGAATGACAGCTTTTGTGAAAAATTT 658
Qy      220 euPProTLeuAspLysSerValAspPheIleGluLysValLysValAspAsnGlyCysV 240
Db      659 TGGCGGTGTGGACAAATCATGTAGATTTCATTAGAAAGCAAAAGCTCCATGATGATG 718
Qy      240 alleuValHisCysLeuAlaGlyLysSerArgSerLathrIleAlaIleAlaTyrIleM 260
Db      719 TTCTAGTGCACCTGTAGCTGGGATCTCCGCGTCCGCCACATCGCTATCGCTATCATCA 778
Qy      260 eLlyAspArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLysArgProt 280
Db      779 TGAAGAGATGACATGCTTTAGATGAAGCTTACAGATTGTGAAAGAAAAAGACCTTA 838
Qy      280 hrlLeSerProAsnPheAsnPheLeuGlyGluLeuLeuAspTyrGluLysLysIleLysA 300
Db      839 CTATATCTCCAACTTCAATTTTCTGGGCCACTCTTGAGCTATGAAAGAAATTTAA 898
Qy      300 sngLInThrGlyAlaSerGlyProLysSerLysLeuLysLeuLysLeuLysProA 320
Db      899 ACCAGACTGGAGCATCAGGGCCAAAGAGAACTCAAGCTGTGACCTGGAGAAACCA 958
Qy      320 sngLInProValProAlaValSerGluGlyGlyGluLysSerGluThrProLeuSerProp 340
Db      959 ATGAACCTGTCTCTGTCTCTCAGAGGGTGACAGAAAGCGAGAGCCCTTCACGTCCAC 1018
Qy      340 rOCyAlaIAspSerLathrSerGluAlaAlaGlyGluThrProValHisProAlaSerV 360
Db      1019 CCTGTGCCACTCTGTCTACTCAGAGCGCAGAGCAAAAGCCCGTGACCTCCGCCACG 1078
Qy      360 aLProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAlaL 380
Db      1079 TGGCCAGCGTGGCCAGCGTGCAGCCGCTGTTAAGAGACAGCCGCTGTATCAGGGCC 1138
Qy      380 euSerGlyLeuHisLeuSerLAspArgLeuGluAspSerAsnLysLeuLysValArgSerP 400
Db      1139 TCAGTGGCGTGCACCTGTCTCGCAGACAGCGCTGGAAACAGCAATAGCTTCACAGCGTCTCT 1198
Qy      400 heSerLeuAspLysSerValSerTyrSerLAspSerLAspSerLAspSerLAspSerL 420
Db      1199 TCTCTGTGATCAATCATCATGTTATCATTCAGCCAGCATGGAGATCTTATCATGAGCT 1258
Qy      420 heSerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAspGlyThrA 440
Db      1259 TCTCCATCATGAAGATGCTTGGATTACTACAAACCTTCCACTACTCGATGGAGACA 1318
Qy      440 snuLysLeuCyGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerP 460
Db      1319 ACAAGCTAGTCCAGTCTCCCGCTGTTACAGAACTATCGAGAGAGACTCCCGAAACAGATC 1378
Qy      460 roAspLysGluGluLysSerLLeProLysLysLeuGlnThrLAspArgProSerAspSerG 480
Db      1379 CTGATTAAGAGAGAGCAGCATCTCCAAAGAGTGAAGACCGCAGGCTTACAGACAGCC 1438
Qy      480 InSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuL 500
Db      1439 AAGAGCAGAGATTCGATTCGGTTCAGAACAGCAGCAGTGGACCGCCAGAGGTCCCTTT 1498
Qy      500 euSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheG 520
Db      1499 TATCTCATCTGCATCGAAGTGGAGCGTGAAGAGCAATTAACACACCACTTCTCTTTCG 1558
Qy      520 LysLeuSerThrSerGlnHisLeuThrLysSerLAspGlyLeuGlyLysLeuLysGlyThrH 540
Db      1559 GCTTTTCCACAGCCAGCAGCAGCCTACAGAACTCTGAGCTGAGGCTTTAAGAGGCTGAG 1618
Qy      540 IAspSerLLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheA 560

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Db      1619 ACTGGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACAGCAGCTGTATTTTG 1678
Qy      560 laThrGluSerSerHisPheTyrSerLAspSerAlaIleTyrGlyLysSerLAspSerTyrS 580
Db      1679 CCACAGAGCTTCACACCTTATCTGCTCAGCCATCTACGAGAGCAGTGCAGTACT 1738
Qy      580 eAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgA 600
Db      1739 CTGCTTACAGCTGCAGCAGCAGCTGCCACTTGGGAGAGCAAAATCTATTTCTGTGGCAGGC 1798
Qy      600 rGGLNysProSerAspArgAlaAspSerArgSerTyrHisGluGluSerProPheG 620
Db      1799 GGCAGAGCAAGTACAGAGCTGACTCGCGCGAGCTGCATGAGAGAGACCCCTTTG 1858
Qy      620 LysLeuGluPheLysArgArgSerCysGlnMetGluPheGlyGluSerLLeuMetSerGluA 640
Db      1859 AAAACAGATTAAAGCAGAACTGCCTCAATGAAATTTGAGAGAGCATCATGTCAAGAA 1918
Qy      640 sArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetG 660
Db      1919 ACAGGTCAAGGAGAGAGCTGGGGAAGTGGCAGTCAGTCTAGCTTTTGGGACAGCATG 1978
Qy      660 LysLeuIleGluValSer 665
Db      1979 AAATCATGAGGTCTCC 1995

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RESULT 4

US-10-094-749-673
Sequence 673, Application US/10094749

Publication No. US20030219741A1
GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOZARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 673
LENGTH: 2102
TYPER: DNA
ORGANISM: Homo sapiens
US-10-094-749-673

Alignment Scores:

Pred. No.:	0	Length:	2102
Score:	472.00	Matches:	662
Percent Similarity:	99.10%	Conservative:	0
Best Local Similarity:	99.10%	Mismatches:	3
Query Match:	70.98%	Indels:	6
DB:	17	Gaps:	0

US-10-029-345A-109 (1-665) x US-10-094-749-673 (1-2102)

QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluValAlaLeuLeuGlu 20
 Db ATGGCCCATGAGATGATGGAACTCAATGTGTAAGAGAGGTGGGTGGCTGCTGCGAA 115
 QY 21 SerGlyThrGluValLeuLeuIleAspSerArgProPheValGluValThrSer 40
 Db AGTGAACGGAAGAAAGTGGCTGATGATGATGATGATGATGATGATGATGATGATG 175
 QY 41 HisIleLeuGluValIleAlaLeuIleAspSerArgLeuMetLeuValArgLeuGln 60
 Db CACATTTGGAGGACATTAATCACTGCTCCAACTTATGAGAGGAAAGGTGGCAACG 235
 QY 61 AspValLeuIleThrGluLeuIleGlnHisSerAlaValHisValAspIleAsp 80
 Db GACAAAGTGTATTAACAGAGCTCACTCCAGCATTCAGCGAAACATTAAGGTGACATGAT 295
 QY 81 CysSerGlnValValValValValValValValValValValValValValValVal 355
 Db TGCAGTCAGAGGTTGATGATTAACATCAAGCTCCCAAGATGTTGCTCTCTCTTCA 355
 QY 101 AspCysPheLeuThrValLeuLeuGlyValLeuGlyValSerPheAsnSerValHisLeu 120
 Db GACTGTTTCTCACTGATCTTCTGGGTAACTGGAGAAAGCTTCACTGTTCACTG 415
 QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuGlyGluGlySer 140
 Db CTTCAGAGGTGGTGGTGGAGTTCTCTGTTGTTTCCCTGGCTCTGTGAAGAAATCC 475
 QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
 Db ACTTAGTCCCTCACTGATCTTCTGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 535
 QY 161 Arg-IleLeuProAsnLeuValLeuGlyCysGlnArgAspValLeuAsnValGluLeu 180
 Db CT-AATTTCTCCCATCTTATCTTGGCTGCAGAGATGCTCTCAAGAGAGCTGAT 594
 QY 180 e-GlnGlnAsnGlyIleGlyValValLeuAsnIleAspTyr-ThrCysProLysProAsp 199
 Db -GCAGAGAAATGGATGGTGTATGTATGTAATGCAAGCA-TACCTGTCCAAAGCTGAC 652
 QY 200 PheIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIle 219
 Db TTTATCCCTCCAGTCTCACTTCTGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 712
 QY 220 LeuProTrpLeuAspLysSerValAspPheIleGluValAlaValAsnValGlyCys 239
 Db TTGCCGTGTGGACAAATCAATGATGATTCATTTGAGAAAGCAAAAGCCCTCAATGATGT 772
 QY 240 ValLeuValHisCysLeuValGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIle 259
 Db GTTCTAGTGCATGTTAGCTGGGATCTCCCGCTCCGCAACATGCTGATGCTCAATC 832
 QY 260 MetLysArgMetSerPheSerLeuAspGluAlaValArgPheValValGlyValArgPro 279
 Db ATAAAGAGATGACATGCTTATGATGAAGCTTCAAGATTTGTAAGAAAGAAAGAAAGCT 892
 QY 280 ThrIleSerProAsnPheAsnPheLeuGlyGlnLeuAspValValGlyValValValVal 299
 Db ACTATATCTCCAAACTTCAATTTCTGGGCAACTCTGAGCTTATGAGAAAGAAATTAAG 952
 QY 300 AsnGlnThrGlyAlaSerGlyProLysSerLysLeuValLeuValIleValValValVal 319
 Db AACGAGACTGGAGCATCGAGGCAAAAGCAAACTCAAGCTGCTGCACTGGAGAAAGCCA 1012
 QY 320 AsnGluProValProAlaValSerGluValGlyGlnLysSerGluThrProLeuSerPro 339
 Db 1013 AATGAACCTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1072
 QY 340 ProCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSer 359
 Db 1073 CCTGTGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1132

QY 360 ValProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAla 379
 Db GTGGCCAGCTGGCCCGAGCGTGCAGCGCTGCTGTTAGAGAGAGAGCCCGCTGATAGCGG 1192
 QY 380 LeuSerGlyLeuValIleLeuSerAlaAspArgLeuGluAspSerAsnValLeuLysArgSer 399
 Db CTGAGTGGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1252
 QY 400 PheSerLeuAspIleLysSerValSerTyrSerAlaSerMetAlaIleSerLeuHisGly 419
 Db TTCTCTGATGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1312
 QY 420 PheSerSerSerGluAspAlaLeuGluTyrTyrLysProSerThrThrLeuAspGlyThr 439
 Db 1313 TTCTCTGATGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1372
 QY 440 AsnLysLeuCysGlnPheSerProValGlnIleLeuSerGluGlnThrProGluThrSer 459
 Db 1373 AACAAAGTATGCAATGCTTCCCTGTTCAAGAACTATCGAGCACTCCGAAACCAAGT 1432
 QY 460 ProAspLysGluGluAlaSerIleProLysValLeuGlnThrAlaArgProSerAspSer 479
 Db 1433 CTTGATTAAG 1492
 QY 480 GlnSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnAspSerLeu 499
 Db 1493 CAGAGCAAGCGATGCAATGGCTGATGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1552
 QY 500 LeuSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPhe 519
 Db 1553 TTATCTCACTGATCAATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1612
 QY 520 GlyLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuLysGlyTyr 539
 Db 1613 GGCCTTCCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1672
 QY 540 HisSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTrpTyrPhe 559
 Db 1673 CACTGGATATCTTGGCCCCCAGACCTTACCTTCCCTGCTGACAGAGCGTGGATTTT 1732
 QY 560 AlaThrGlnSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyr 579
 Db 1733 GCCAGAGAGCTGCACTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1792
 QY 580 SerAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArg 599
 Db 1793 TCGCTTACAGCTGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1852
 QY 600 ArgGlnLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSerProPhe 619
 Db 1853 CCGCAGAGCCCAAGTGAAG 1912
 QY 620 GluValGlnPheLysArgArgSerCysGlnMetGluPheGlyGlnSerIleMetSerGlu 639
 Db 1913 GAAAGAGAGTTTAAACGCAAGAGCTGCCAAATTTGAGAGAGAGAGAGAGAGAGAGAGAG 1972
 QY 640 AsnArgSerArgGluGluLeuGlyValValGlySerGlnSerSerPheSerGlySerMet 659
 Db 1973 AACAGGTCAACGGGAAG 2032
 QY 660 GluIleIleGluValSer 665
 Db 2033 GAAATCAATGAGGTCTCC 2050

RESULT 5

US-10-168-506-2
 ; Sequence 2, Application US/10168506
 ; Publication No. US20040053229A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FLOMMAN, GREGORY D.
 ; APPLICANT: MARTINEZ, RICARDO
 ; APPLICANT: WHYTE, DAVID

Db 2276 CTGCCTACAGCTGCAGCAGCTGCCACTTGGGGAACCAAGTCTATTCTGTGCGCAGGC 2335
Qy 600 rgglllyrsProSerAapAaglaAapSerAargSerTphlsglulgluSerProphag 620
Db 2336 GGGAGAGGCCAATGACAGAGCTGACTCCGGCGAGCTGGCATGAAGAGCCCTTTG 2395
Qy 620 luluysglInPheylsAargSerCyagGlnMetGluPheGlygluSerllleMetSerGluA 640
Db 2396 AAAAGCAGTTTAAACCAAGAGCTGCCAATGAAATTGGAGAGACATCATGTCCAGAGA 2455
Qy 640 snhAargSerAglulgluLeuGlylyrValGlySerGlnSerSerPheSerGlySerMetG 660
Db 2456 AAGGgtCACAGGAGAGGCTGGGGAAGTGGGCAgTCAGTCTATTTCGGGCAgCATGG 2515
Qy 660 luilellegluValSer 665
Db 2516 AATCATTTGAGGCTCTCC 2532

RESULT 6
US-10-296-115-520
/ Sequence 520, Application US/10296115
/ Publication No. US20040053248A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq Inc
/ TITLE OR INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
/ FILE REFERENCE: 784PCT
/ CURRENT APPLICATION NUMBER: US/10/296.115
/ CURRENT FILING DATE: 2002-11-18
/ PRIOR APPLICATION NUMBER: US09/488,725
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: US09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ NUMBER OF SEQ ID NOS: 1478
/ SEQ ID NO 520
/ LENGTH: 2966
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(2966)
/ OTHER INFORMATION: n = a,t,c,g or g
US-10-296-115-520

Alignment Scores:
Pred. No.: 0
Score: 472.00 Length: 2966
Percent Similarity: 99.39% Matches: 648
Best Local Similarity: 99.39% Conservative: 0
Query Match: 70.98% Mismatches: 2
Indels: 4
Gaps: 0

US-10-029-345a-109 (1-665) x US-10-296-115-520 (1-2966)

Qy 16 ValAlaleuLeuGluSerGlyThrgluysValleuLeuileAapSerAargProphVal 35
Db 68 GTGGCTCTCTGGAAGTGAACGGAAGAAAGCTGCTATTATGATGACCGGCAATTTGTG 127
Qy 36 GluTyAaThrSerSerIleleuGluAlaleuAnlleAaSerSerIleuMetIys 55
Db 128 GAATCAAAATACATCCCACTTTTGAAGCCATTATATCACTGCTCCAACTTATGAG 187
Qy 56 ArgAargLeuGlnGluAapIysValleuIleThrgluLeuileGlnIleSerSerIleHis 75
Db 188 CCAAGGTTGCAACAGCAAAAGTGTATTAATACAGGCTCATCCAGCATTCAGCAAAACAT 247
Qy 76 lvsValAapIleAapCyasSerGluysValValValIlyrAapGlnSerSerGlnAapVal 95
Db 248 AAGGTGACATTGATGACGTCAAGAGGTGTGATTACATCAAAAGCTCCCAAGATGTT 307
Qy 96 AlaSerleuSerSerAapCyasPheleuThrValleuLeuGlylyrleuGluysSerPhe 115
Db 308 GCGTCTCTCTTCAGACTGTTTCTCACTGTACTTCTGGGTAAACTGGAAGAGCTTC 367

Qy 116 AapSerValIleIleuLeuAlaGlyGlyPheAlaGluPheSerAargCyasPheProGlyLeu 135
Db 368 AACTCTGTTTCACTGCTTCCAGGTGGGTTTGTGAGTTCTCTCGTTGTTTCCCTGGCTTC 427
Qy 136 CyasGluGlylyrSerThreValProThrCyasIleSerGlnProCyasLeuProValAla 155
Db 428 TGTGAAGGAATAATCCACTTACTTCCCTACCTTCATTTCTCAGCTTTCCTTACCTGTTCC 487
Qy 156 AapIleGlyProThrAargIleuProAanleuTyIleuGlyCyasGlnAargAapValleu 175
Db 488 AACATTGGGCAACCCGAATCTTCCCAATCTTTATCTTGGCTGCGACAGAGATGCTTC 547
Qy 176 AapIysGluLeuIle-GlnGlnAasGlyIleGlyTyrrValleuAanIleAserTyrr-Thrc 195
Db 548 AACCAAGAGCTGAT--CGACGAGAATGGGATGGTTATGTATGTAATGCGACAA--TACCT 605
Qy 195 yspProIysPheAapPheIleProGluSerHisPheLeuAargValProValAanAapSerP 215
Db 606 GTTCCAAAGCCTGACTTTATCCCGAGTCTCAATTCCTGCGTGTGCTGTGAATGACAGCT 665
Qy 215 heCyasGluIysIleuProThrleuAapIysSerValAapPheIleGluysAlaIysA 235
Db 666 TTTGTGAGAAATTTTGGCTGCTGTTGGCAAAATGATGATTCATTGAGAAAGCAAAAG 725
Qy 235 lAserAasGlyCyasValleuValHisCyasleuAlaGlyIleSerAargSerAlaThrIleA 255
Db 726 CTTCCAAATGAGATGTCTTACTAGTGCATGTTAGTGGGATCTCCGCTCCGCAACATCG 785
Qy 255 laileAlaTyrlleMetIysAargMetAapMetSerleuAapGluAlaTyrrAargPheVal 275
Db 786 CTATGCGCTTACATATGAAAGAGATGGACATGCTTTGATGAAGCTTACAGATTGTGTA 845
Qy 275 ysgIuysAargProThrIleSerProAanPheAanPheleuGlyGlnleuLeuAasTyrg 295
Db 846 AAGAAAAAGCCTACTATATCTCCAAACTTCAATTTTCGGGCCAACTCTGACTTAAG 905
Qy 295 luluysIysIleIysAasGlnThrglyAlaSerGlyProIysSerIysleuIysleuLeu 315
Db 906 AGAAGAAAGATTAAAGAACCAACATGAGCAATCAGAGGCGCAAAAGCAAACTCAAGCTCTGC 965
Qy 315 lAseuGluysProAasGluProValProAlaValSerGluGlyGlyGlnIysSerGlu 335
Db 966 ACCTGAGAGAGCCAAATGAACCTGCTCTGCTCTCTCAAGGGTGAAGAAAAGCGACA 1025
Qy 335 hrProleuSerProProCyasAlaAapSerAlaThrsSerGluAlaIaGlyGlnAargProV 355
Db 1026 CGCCCTCACTCAACCCCTGCGCACTGCTTACCTCAAGAGCAGACGAAAGAGCCCG 1085
Qy 355 alHisProAlaSerValProSerValProSerValGlnProSerleuLeuGluAapSerP 375
Db 1086 TGCATCCCGCGACGCTGCCCAAGGCTGCCAGGCGTGAAGCCGTGCTGTGAAGAGCAAC 1145
Qy 375 roleuValGlnAlaIeuserGlyleuHisIleuserAlaAapAargLeuGluAapSerAanl 395
Db 1146 CGCTGTATACAGGGCTCAATGGGCTGACCTGTCCGAGACAGCGCTGAAGAACAGCATTA 1205
Qy 395 yIleuIysAargSerPheSerleuAapIleIysSerValSerTyrrSerAlaSerMetAla 415
Db 1206 AGCTCAAGGCTTCTTCTCTGGAATTCATCAATCATGTTTATATTCAGCCGACGTGGCAG 1265
Qy 415 lAserleuHisIleIysPheSerSerGluAapAlaIeugIleTyrrTyrrAapSerThr 435
Db 1266 CATCTTACATGGCTTCTTCCCTCATAGAAATGCTTTGGAATATCTCAAACTTCCACTA 1325
Qy 435 hrleuAapGlyThrAanIysleuCyasGlnPheSerProValGlnGluLeuSerGlu 455
Db 1326 CTCTGATGGAGCAACAAAGCTATGCTCCCTGCTCCCTGTTCAAGAACTATCGAGCAGA 1385
Qy 455 hrProGluThrsSerProAapIysGluGluAlaSerIleProIysIysleuGlnThrAla 475
Db 1386 CTCCGGAAGACAGTCTCTATAGAGAGAGAGACCAATCCCAAGAACTCAGACCGCCA 1445
Qy 475 rgProSerAapSerGlnSerIysAargleuHisSerValAargThrsSerSerGlyThra 495


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Db      1446 GGCCTTCAGACAGCAGCAGCAGCAGTTCGATTCGGTCAGAACACAGAGAGTGGACCG 1505
QY      495 laelnaargserleuenserProleuHiAArgserglyserValgluaaprryHt 515
Db      1506 CCAGAGGCTCCCTTTATCTCCACTGCATCGAAGTGGAGCCGTGGAGCAATTACCA 1565
QY      515 hyserPheleupheglyleuSerThrsSerInglInHsleuThrylsSerlaGllyeng 535
Db      1566 CCGCTTCCTTTCCGCTTTCCACAGCCAGCAGCACTTCACGAAAGTCTGCTGGCTGG 1625
QY      535 lyleuylserglytrpHiserAspIleleuAlaProglInHrsThrsProserleuThrs 555
Db      1626 GCTTAAGGCTGGCACTCGGATATCTTGGCCCCCAGACCTTACCCCTCCAGCA 1685
QY      555 etserTrpYrPheAlaThrGluSerSerHisPheYrYserAlaSerlaGllyeng 575
Db      1686 GCAGCTGGATTTGGCACAGAGTCTTCACACTTCTACTGCTCAGCCATCTACGGAG 1745
QY      575 lYserAlaSerTrYserAlaTrYserCyserSerGlnleuProThrCyserGlyAspGlnValT 595
Db      1746 GCGATCCCACTTACTGCTTACAGCTGACGCAAGCTGCCACTTGGGAGACCAAGTCT 1805
QY      595 yserValaArgArgGlnlyrProserAspArgAlaAspSerArgArgSerTrpHisG 615
Db      1806 ATTCTGGGCGACGCGGAGAACCAAGTACAGAGCTGACTGCGCGGAGCTGGCAGT 1865
QY      615 lgluSerProPheGlnlyrGlnPheYrArgArgSerCyserGlnMetGluPheGlyGlu 635
Db      1866 AAGAGAGCCCTTTGAAGACAGTTTAAACGAGAACTGCGCAATTTGGAGAGA 1925
QY      635 erleuSerGluAuaArgSerArgGlnGluGlnleuGlyYrValglYserGlnSerSerP 655
Db      1926 GCATCATGTCAAGAACAGGTCAAGGAAAGCTGAGGAAAGTGGCAGTCTAGCT 1985
QY      655 hserglyserMetGluIleleuGlyValser 665
Db      1986 TTTCCGCGACGACGATGAAATCATTTGAGTCTCC 2017

RESULT 7
US-10-257-026-1
; Sequence 1, Application US/10257026
; Publication No. US20040086859A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; TITLE OF INVENTION: New dual specificity phosphatase
; FILE REFERENCE: DUSP10XDMs
; CURRENT APPLICATION NUMBER: US/10/257,026
; CURRENT FILING DATE: 2003-11-07
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3059
; TYPE: DNA
; ORGANISM: Homo sapiens
; PEPTIDE:
; NAME/KEY: CDS
; LOCATION: (127)..(2121)
US-10-257-026-1

Alignment Scores:
Pred. No.: 0 Length: 3059
Score: 472.00 Matches: 663
Percent Similarity: 99.40% Conservative: 0
Best Local Similarity: 99.40% Mismatches: 2
Query Match: 70.98% Indels: 4
DB: 17 Gaps: 0

US-10-029-345A-109 (1-665) x US-10-257-026-1 (1-3059)
QY      1 MetAlaHsGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGln 20
Db      127 ATGGCCCATGAGATGATGGAACTCAATTTGTTACTGAGAGGTGTGTGCTGCTGGAA 186

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QY      21 serglyThrGluValleuLeuIleAspSerArgProPheValGluTrpAsnThrSer 40
Db      187 AGTGAACGGAAAGAGTGGCTTAATGATACCGGCACTTGTGGAAATACATATACCTC 246
QY      41 HsileleuGluAlaIleAsnIleAsnCyserIleuMetIleYrArgArgLeuGln 60
Db      247 CACATTTTGGAGCCATTAATATCAATGCTCCAGCTTATGAGGAAAGTTGGCAACG 306
QY      61 AspyValleuIleThrGluLeuIleGlnHsSerAlaIleYrHisIleYrValleuP 80
Db      307 GACAAAGTGTATTAACAGAGCTCAATCCAGCTTACGCCAAACATTAAGTTGACATTGAT 366
QY      81 CyserGlnlyValValValTrpAspGlnSerSerGlnAspValAlaSerleuSerSer 100
Db      367 TCGATCAGAAAGTTGATTAACATCAAGCTCCCAAGAGTTGGCTCTCTCTCTTCA 426
QY      101 AspCyPheleuThrValleuLeuGlyYrleuGlnlyrSerPheAsnSerValHisleu 120
Db      427 GACTGTTTTCTACGTACTTCTGGGTAAACTGGAGAAAGCTTCAACTCTGTCACTG 486
QY      121 leuAlaGlylyPheAlaGluPheSerArgCyPheProGlyLeuCyserGluGlyYrSer 140
Db      487 CTGGCAGGTGGGTTGCTGATGTTCTCTGTTTCCCTGGCCTGTGAAAGAAATCC 546
QY      141 ThrleuValProThrCyserleuSerGlnProCyserleuProValAlaAsnIleGlyProThr 160
Db      547 ACTCATGCTCCATCCGACATTTCTAGCTTCTTACCTGTGCAACATTTGGCCCAACC 606
QY      161 ArgIleleuProAsnleuTrleuGlyCyserGlnArgAspValleuAsnlyrGluLeuIle 180
Db      607 CGAATTTCTCCAACTTTATTTATTTGGCTGCCAGAGATGCTCTCAACAGAGAGCTGAT- 665
QY      181 -GlnGlnenglyIleGlyTrValleuAsnAlaSerTrp-ThrCyserProlyAspAsp 200
Db      666 GCAGCAGATGGAGTGTATGTATGTTAATCCAGCAA-TACCTGTCCAAAGCCGTGACT 724
QY      200 HeIleProGlnSerHisPheleuArgValProValAsnAspSerPheCyserGlnlyrIle 220
Db      725 TTATCCCGAGTCTCAATTTCTGCGGTGCTGTGATATACAGCTTTGTGAAAAATTT 784
QY      220 euProTrleuAspIleYserValAspPheIleGluValAlaYrAsleAsnGlyCyAsv 240
Db      785 TGCCGTGTGGACAAATAGATGATTTCAATTGAAAGCAAAAGCTTCATGATGATG 844
QY      240 AlIleuValHisCyserleuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTrpIle 260
Db      845 TTCTAGTGCACTGTTAGCTGGGATCTCCGCTCCGCCACATCGCTATCGCTACATCA 904
QY      260 eLYrArgMetAspMetSerleuAspGluAlaTrpArgPheValYrGluYrAspProT 280
Db      905 TGAAAGAGATGGACATGCTTTAGATGAAGCTTACAGATTTGTGAAGAAAAAGACTTA 964
QY      280 hrIleSerProAsnPheAsnPheleuGlyGlnleuLeuAspTrpGlnlyrIleYrAs 300
Db      965 CTAATATCTCCAACTTCAATTTTCTGGGCCAACTCTGGACTTAAGAAAGAAATTAA 1024
QY      300 engInThrGlyAlaSerGlyProlyrSerlyrleuYrleuLeuLeuHsleuGlnlyrPro 320
Db      1025 ACCAGACTGAGCATCAGGCGCAAGCAAACTCAAGCTGTGCACTCGAGAAAGCCAA 1084
QY      320 engInProValProAlaValAspGlnlyrGlyGlnlyrSerGlnThrProleuSerProp 340
Db      1085 ATGAACCTGTCTCTGTCTGAGAGGGTGAACAAGAAAGCAAGCGCCCTCACTCCAC 1144
QY      340 roCyAlaAspSerAlaThrSerGlnAlaAlaGlyIleArgProValHisProAlaServ 360
Db      1145 CCTGTGCCGACTCTCTACTACAGGAGCAGAGCAAGAGCCCTGTGATCCCGCAGGG 1204
QY      360 alProSerValProSerValGlnProSerleuLeuGlnAspSerProleuValGlnAla 380
Db      1205 TCCCCAGCGTGGCCAGCGAGCGCTGCTGTGAAGACAGCCGCTGTGACAGGCGC 1264

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DB      1817 GCCAGGCTTCACAGACAGCAGACGATGCTGATCGGTGAGAACAGCAGCAGTGGC 1876
QY      494 ThrAlaGlnArgSerLeuSerProLeuHisArgSerGlySerValGlnAparAntYr 513
DB      1877 ACCGCCACAGAGGTCCTTTATATCTCCATCGATCGAAGTGGAGCGGTGGAGCAATTAC 1936
QY      514 HisThrSerPheLeuPheGlyLeuSerThrSerGlnHisLeuThrHisLeuSerValGly 533
DB      1937 CACACACAGCTTCCTTTTCGGCTTCCTCCACAGCAGCAGCAGCAGCAGTCTGCTGGC 1996
QY      534 LeuGlyLeuValGlyTyrHisSerAspIleLeuAlaProGlnThrSerThrProSerLeu 553
DB      1997 CTGGGCTTAAAGGCTGGCAGCTCGAATATCTGGCCCCCAGACCTTACCCCTTCCCG 2056
QY      554 ThrSerSerTrpTyrPheAlaThrGlnSerSerHisPheTyrSerAlaSerAlaIleYr 573
DB      2057 ACCAGACAGCTGTGATTTTGGCAGAGTCTCTCACACTTCTACTCTGCTCAGCCATCTAC 2116
QY      574 GlnGlySerAlaSerAlaTyrSerAlaTyrSerCysSerGlnLeuProThrCysGlyAapGln 593
DB      2117 GAGGAGAGTCCAGCTTACTTGGCTTACAGCTGCAAGCTGCGCCTTGGCGAGACCA 2176
QY      594 ValTyrSerValArgArgArgGlnYrProSerAspArgAlaAparSerArgArgSerTrp 613
DB      2177 GTCTATCTGTGGCAGAGCGCGGAGAACGACAGAGCTGACTCGGCGCGGAGCTGG 2236
QY      614 HisGlnGlnSerProPheGlnGlyValGlnPheValArgArgSerCysGlnMetGlnPheGly 633
DB      2237 CATTGAAGAGAGCCCTTTGAAAGCAGTTTAAACGAGAGCTGCCAAATTGGAATTGGAA 2296
QY      634 GluSerIleMetSerGlnAsnArgSerArgGlnGlnLeuGlyValGlySerGlnSer 653
DB      2297 GAGAGCATCTGTCAGAGAACAGCTCAGCGGAAAGCTGGGGAAGTGGGAGCTCAGTCT 2356
QY      654 SerPheSerGlySerMetGlnIleIleGlnValSer 665
DB      2357 AGCTTTTCGGGAGCAGCATGGAATCATTTAGGTCTCC 2392

RESULT 9
US-09-964-277-1
; Sequence 1, Application US/0964277
; Patent No. US20020137170A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; TITLE OF INVENTION: DSP-16 DUAL-SPECIFICITY PHOSPHATASE
; FILE REFERENCE: 200125.434
; CURRENT APPLICATION NUMBER: US/09/964,277
; CURRENT FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-277-1

Alignment Scores:
Pred. No.: 0 Length: 3496
Score: 472.00 Matches: 663
Percent Similarity: 99.40% Conservative: 0
Best Local Similarity: 99.40% Mismatches: 2
Query Match: 70.98% Indels: 4
DB: 9 Gaps: 0

US-10-029-345a-109 (1-665) x US-09-964-277-1 (1-3496)
QY      1 MetAlaHisGlnMetIleGlyThrGlnIleValThrGlnArgLeuValAlaLeuLeuGln 20
DB      562 ATGGCCCATGATGATGATTGGAATCTCAAAATTGTACTGAGAGTGTGGTCTGCTGGAGAA 621
QY      21 SerGlyThrGlnValLeuLeuIleAparSerArgProPheValGlnTyrAenThrSer 40

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DB      622 AGTGAACGGAAGAAAGTGTCTTAATTGATCCCGGCACTTTGTGAATATACATATCC 681
QY      41 HisIleLeuGlnAlaIleSerIleLeuPheCysSerIleLeuMetIleArgTrpLeuGlnGln 60
DB      682 CACATTTTGAAGCCATTATATATCAATGCTCCAAAGCTTATGAAGGAGGTGGCAACAG 741
QY      61 AspIleValLeuIleThrGlnLeuIleGlnHisSerAlaLeuHisIleValAspIleApar 80
DB      742 GACAAAGTTTATTTACAGAGCTCATCGACATTCAAGCAAACTTAAAGTTGACATTGAT 801
QY      81 CysSerGlnIleValValValTyrAapGlnSerSerGlnAparValAlaSerLeuSerSer 100
DB      802 TCGAGTCAGAGGTTGATGATTACATCAAAAGCTCCAAAGTGGTCCCTCTCTCTTCA 861
QY      101 AapCysPheLeuThrValLeuLeuGlyValLeuGlnValSerPheAparSerValHisLeu 120
DB      862 GACTGTTTCTCATCTGATCTTCTGGGTAAACGAGAGAGGCTTCAACTCTGTTCACCTG 921
QY      121 LeuAlaGlyGlyPheAlaGlnPheSerArgCysPheProGlyLeuGlyGlnGlySer 140
DB      922 CTTCAGAGTGGGTTTGTAGTCTCTCTGTTTCTTGGCTCTGTAAAGGAATTC 981
QY      141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAparIleGlyProThr 160
DB      982 ACTCTAGTCCCTACCTGATTTCTCAGCCTTGCTTAACGTGGCAACATTGGGCAACC 1041
QY      161 ArgIleLeuProAsnLeuTyrIleGlyCysGlnArgAspValLeuAsnIleGlnLeuIle 180
DB      1042 CCAATTTCTCCAAATCTTATCTTGGCTGCCAGCGAGTGTCTCAACAGAGCTGAGT- 1100
QY      181 -GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyr-ThrCysProIleProApar 200
DB      1101 GCAAGCAATGGGATTTGTTATGTTTAAATGCAAGCA-THCCTGTCCAAAGCTTGACT 1159
QY      200 HisIleProGlnSerHisPheLeuArgValProValAsnAparSerPheCysGlnIleLeu 220
DB      1160 TTATCCCGAGCTCATTTCCGCGTGTGCTGTGAATGACAGCTTTGTGAAGAAATTT 1219
QY      220 EupProTrpLeuAparIleValAparPheIleGlnValAlaValAsnAsnGlyCysVal 240
DB      1220 TCCCGTGTGTGAACAATCAGTATGATTTCAATGAGAAAGCAAGCTCCCAATGGATG 1279
QY      240 AlLeuValHisCysValLeuIleGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIle 260
DB      1280 TTTCTAGTGCATGTTAGTGTGAGATCTCCGCTCCGCAACATCGCTATCGCTTACATCA 1339
QY      260 eLysArgMetAspMetSerLeuAparGlnAlaTyrArgPheValIleGlyValArgProT 280
DB      1340 TGAAGAGATGACATGCTTTTATGATGAAAGCTTACAGATTGTGAAGAGAGAGAGAGCTTA 1399
QY      280 HisIleSerProAparPheAparPheLeuGlyGlnLeuLeuAparTyrGlnValValIle 300
DB      1400 CTATATCTCCAAATCTTCAATTTTCTGGGCCCACTCCTGGAATATGAGAAAGATTAA 1459
QY      300 SerGlnThrGlyAlaSerGlyProIleSerIleLeuIleLeuIleLeuGlnValValProA 320
DB      1460 ACCAGACTGAGACATCAAGGCGCAAGAGCAAACTCAAGTGTGCACTCGAGAGAGCCAA 1519
QY      320 SerGlnProValProAlaValSerGlnGlyGlyIleValSerGlnThrProLeuSerProP 340
DB      1520 ATGAACCTCTCCCTGCTGTCTCAGAGGAGGAGCAAGAGAGAGAGAGAGAGAGAGAGAG 1579
QY      340 roCysAlaAparSerAlaThrSerGlnAlaIleGlyGlnArgProValHisProAlaSerV 360
DB      1580 CCTGTGCCACTCTGCTACTCAGAGGCGAGGAGCAAGAGGCGCGGTGATCCCGGCAAGG 1639
QY      360 AlProSerValProSerValGlnProSerLeuLeuGlnAparSerProLeuValGlnAlaL 380
DB      1640 TCCCAAGCTGCGCAGCGGAGCGGCTGCTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1699
QY      380 euSerGlyLeuHisLeuSerAlaAparArgLeuGlnAparSerValValLeuValArgSerP 400

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Db      1700 TCAATGGGCTGCACTGTCCGACAGAGCTGGAGACAGCAATTAAGCTCAAGCCTTCT 1759
Qy      heserleuaspilyleuSERVALserTYrSERalaserneclalaserleuHISglYp 420
Db      1760 TCTCTCGATATCAATATCATGTTTCATATTCAGCCAGAGCTGACAGATCTTACATGAGCT 1819
Qy      heserSerSerSerGluAapAlaleuGluTYrTYrleuPProSerThrThreuAapGlyThra 440
Db      1820 TCTCTCATCAAGAGATGCTTGGAAATACAAACCTTCCACTCTCGATGGAGACA 1879
Qy      smlyseuCYsginPheSerProVALingluLeuSerGluGlnThrProGluThrSerP 460
Db      1880 ACAAGCTTATGCCAGTCTCCCTGTTCAAGAACTATCGAGAGAGACTCCCAAAACAGTTC 1939
Qy      roAsplysgluGluAaserileProLYsleuGlnThraAargProSerApsSerG 480
Db      1940 CTGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1999
Qy      lnseryAargleuHISerVALargThrSerSerSerGlyThraAaglnaSerleuL 500
Db      2000 AAGAGAGAGAGATTCGATTCGATTCAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2059
Qy      euserProleuHISargSerGlySerVALgluAapserTYrHISerPheleuPheG 520
Db      2060 TATCTCCACTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2119
Qy      lYleuSerThrSerGlnGlnHISleuThrLYsSerAagLYleuGlyleuLYsGlyThraP 540
Db      2120 GCTTTCACACAGCAGCAGCAGCAGCAGCAGAGAGTCTGCTGGCTGGCTTAAAGAGCTGGC 2179
Qy      lsserAapilaleuAalProGlnThrSerThrPProSerleuThrSerSerTYrPhea 560
Db      2180 ACTCGAATATCTGGCCCCCAGAGACTCTTACCCCTTCAGACAGAGAGAGAGAGAGAGAG 2239
Qy      larnGluSerSerHISpHeTYrSerAlaserAlaileuLYsGlySerAlaserTYrS 580
Db      2240 CCAAGAGAGCTCTCACTTACTCTGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2299
Qy      eraIaTYrSerCYserGlnleuPProThrCYsglyAapGlnVALTYrSerVALargA 600
Db      2300 CTGCTTACAGCTGAGCAGCAGCTGCGCACTTGGAGAGCAGCAAGCTTATTCGTCGAGAG 2359
Qy      rGlnLYsProSerAapAargAlaapSerAargAargSerTYrPheGlnGluSerProPheG 620
Db      2360 GGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2419
Qy      lulyseGlnPheLYsAargAargSerCYsglnMetGlnPheGlyGlnSerileMetSerGluA 640
Db      2420 AAAAGCAGTTTAAACGAGAGAGAGCTGCCAATGGAAATTTGAGAGAGAGAGAGAGAGAG 2479
Qy      smArSerAargGluGluLeuGlyLYsVALglYserGlnSerSerPheSerGlySerMetG 660
Db      2480 ACAAGCTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2539
Qy      luleileuGluVALser 665
Db      2540 AAATCATTTGAGGTCTCC 2556

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; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO: 261
; LENGTH: 3521
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-370-715B-261

Alignment Scores:
Pred. No.: 0
Score: 472.00
Percent Similarity: 99.40%
Best Local Similarity: 99.40%
Query Match: 70.98%
DB: 18 Gaps: 0

US-10-029-345A-109 (1-665) x US-10-370-715B-261 (1-3521)

Qy      1 MetAlaHISgluMetileGlyThrGlnleValThrGluAargleuVALaleuLeuGlu 20
Db      564 ATGGCCATGAGAGATGATGGAACTCAATTTTACTAGAGAGTGGCTGGCGGAA 623
Qy      21 SerGlyThrGluLYsVALleuLeuIleAapSerAargProPheVALgluTYrAanThrSer 40
Db      624 AGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 663
Qy      HISileuGluAlaileuAlaenIleAapCYserLYsleuMetLYsAargAargleuGln 60
Db      684 CCAATTTTGAAGCATTATATCACTGCTCCAGAGTTTGAAGAGAGAGAGAGAGAGAGAGAG 743
Qy      AapLYsVALleuIleThrGluLeuIleGlnHISerAlaLYsHISerLYsVALAapIleAap 80
Db      744 GACAAAGGTAAATTACAGAGCTCATCAGCATTACAGCAGAAATTAAGTTGACATTGAT 803
Qy      81 CYserGlnLYsVALleuVALTYrAapGlnSerSerGlnAapVALaserleuSerSer 100
Db      804 TCGAGTCAAGAGAGTGTAGTTTACAGTCAAGAGCTCCCAAGATGTTCCCTCTCTCTCA 863
Qy      101 AapCYsPheleuThrVALleuLeuGlyLYsleuGluLYsSerPheAanSerVALHISleu 120
Db      864 GACTGTTTCTCACTGATCTTGGGTAACTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 923
Qy      121 leuAlaGlyLYsPheAlaGluPheSerAargCYsPheProGlyleuCYsgluGlyLYsSer 140
Db      924 CTGGAGAGTGGGTTTCTGAGTCTCTCGTGTGTTCCCTGGCCTCTGTGAAGAGAAATCC 983
Qy      141 ThrleuVALProThrCYsIleSerGlnProCYsleuProVALAlaenIleGlyProThr 160
Db      984 ACTCTAGTCCCTTACCTGCACTTCTCAAGCTTCTTACCTGTTCACCAACATTTGGGCAAC 1043
Qy      161 ArgIleleuProAanleuTYrleuGlyCYsGlnAargAapVALleuAanLYsGluLeuIle 180
Db      1044 CGAATTCCTCCCAATCTTATCTTGGCTGCGAGAGAGATGCTCAAGAAGAGCTGAT- 1102
Qy      181 -GlnGlnAenGlyIleGlyTYrVALleuAanAlaserTYr-ThrCYsProLYsProAap 200
Db      1103 GACGAGAAATGGAGATGTATGTGTAAATGCCAGCA- TACCTGTCCAAGAGCTGACT 1161
Qy      200 heIleProGluSerHISpHeleuAargVALProVALAanAapSerPheCYsgluLYsIleL 220
Db      1162 TATATCCCGAGTCTATTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1221
Qy      220 euProTYrleuAapLYsSerVALAapPheIleGluLYsAlaLYsAserAanGlyCYsV 240
Db      1222 TCCCGTGTGGCAAAATCAGATGATTCATTGAGAAAGCAAAAGCCCTCCAGATGAGATG 1281
Qy      240 alleuVALHISCYseuAlaGlyIleSerAargSerAlaThrIleAlaIleAlaTYrIleM 260
Db      1282 TTCTAGTCACTGTTTACTGAGATCTCCGCTCGGCAACCATGCTATGCGCTCATCA 1341

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RESULT 10
US-10-370-715B-261
; Sequence 261, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILARY
; APPLICANT: BRIDGEL, HONTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune

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QY	260	elYvArGMeAAspMetSerLeuAaPgiUnaIaYArGPhaYalYgGluYbYsArGProT	280
Db	1342	TGAAGAGATGACATGTCCTTTAGATGAAGCTTACAGATTTGTGAAGAAAGAAAGACCTTA	1401
QY	280	hrlLeSerProAaPnPhaAaPnPhaLeuGluGlnLeuLeuAaSPtyGluYbYbYsIleYbA	300
Db	1402	CTATATCTCCAAACCTTCAATTTTCTGGGCAACTCTGGACTATGAAAGAAAGATTAAAG	1461
QY	300	engInThrGlyAlaSerGlyProLYsSerLYbLeuLYbLeuLhIbLeuGluYbProA	320
Db	1462	ACCGAGCTGGAGCATCAGGCGCAAGAACCAACTCAAGCTGTGCACCTGGAGAAAGCCAA	1521
QY	320	engInProValProhAlaValSerGluYbGlyYbGlnLYsSerGluThrProLeuSerProP	340
Db	1522	ATGAACCTGTCCCTGTCTCTCAGAGGGTGGACAAAGAAACGAGACGCCCTCACTCAAC	1581
QY	340	roCYbAlaAaPSeArLaThrSerGluUnaIaGlyAlaArgProValhIaSProAlaSerV	360
Db	1582	CCTGTGGCGGACTCTGTACTCTCAGAGGACAGACAAAGGCCCTGTGATCCCGCCACGG	1641
QY	360	aIProSeValProSeValGlnProSerLeuLeuGluAaPSeProLeuValGlnAlaL	380
Db	1642	TGCCAGAGGTGCCAGCGTGACCGGTGCTGTAGAGACAGCCGCGTGGAACAGCGCG	1701
QY	380	eUsErGlyLeuLhIbLeuSerhIaAaPArgLeuGluAaPSeRbnuLYbLeuLYbArGSeP	400
Db	1702	TCAGTGGGCTCACTGTCTCCGACACAGGCTGGAGAAACAGCAATTAAGCTCAAGCCTTCT	1761
QY	400	heSeRLeuAaPILeLYsSerValSerTYrSerAlaSeMeAlaIaSerLeuLhIbGlyP	420
Db	1762	TCTCTCTGATATCAATTCAGTTTCAATTCATTCAGCCAGATGGACACTCTTACATGACT	1821
QY	420	heSeRSeSerGluAaPAlaLeuGluTYrTYrLYbProSeThrThirLeuAaPgiLYThRA	440
Db	1822	TCTCTCATCAGAAAGATGCTTTGGAAATCTAACAACTTCCACTACTCTGATGGAGCA	1881
QY	440	enLYbLeuCYgGlnPhaSeRProValGlnGluLeuSerGluGlnThrProGluThrSeP	460
Db	1882	ACAAGCTATGGCAGATTCCTCCCTGTTCAGGAACATTCGAGAGAGACTCCCAACACACTC	1941
QY	460	roAaPlybGluGluAaSerLlePProLYbLYbLeuGlnThrAlaArgProSeArbSeRg	480
Db	1942	CTGATTAAGAGAAACCGACATCCCCAAGAAAGCTGCAAGCGCACGACCTTTCAGACACC	2001
QY	480	InSerLYbArgLeuLhIaSerValArgThrSeRSeSerGlyThzLaGlnArgSerLeuL	500
Db	2002	AGAGCAACGATTCGATTCGGTCAGAACACAGACAGAGTGGCACGCCCAAGAGTCCCTT	2061
QY	500	eUsErProLeuLhIaRgSerGlySerValGluAaPArTYrThIbThrSeRPhaLeuPhg	520
Db	2062	TATCTCCACTGCATCGAAGTGGAGCGTGGAGAACAAATTACACACAGCTTCTCTTTCG	2121
QY	520	LYLeuSeRThrSerGlnGlnLhIaLeuThrybSeRAlaGlyLYeGluLYeulysGlyTYrPh	540
Db	2122	GCCTTTCACACAGCCAGACGACCTTCAGAAAGTCTGTGGCCTTGAGCTTAAAGGCTGCG	2181
QY	540	IaSeRAsPILeLnuLlaProGlnThrSeRThnProSeRLeuThrSeSerTYrPha	560
Db	2182	ACTGGGAATCTTGGCCCCCAGACCTTACCCCTTCCCTACACGACGCTGGATTTTG	2241
QY	560	IaThnGluSeRserhIaPherYrSerAlaSerAlaIeTYrGlyLYeSerAlaSerTYrS	580
Db	2242	CCACAGAGTCTCCACACTTACTCTGTGCTCAGCCATCTACGGAAGGAGTGCCAGATTACT	2301
QY	580	erAlaTYrSeRCySeSerGlnLeuProThnCYbGlyAaPgiUnaLYrSeRValaArga	600
Db	2302	CTGCTTAAGCTGCAGCGACGCTGCCACTTGGGAGACCAAGTCAATTCGTGGCCAGG	2361
QY	600	rgGlnLYbProSeSerArPArgAlaAaPSeRArgArGSeRThpIbGluGluSeRProPhg	620
Db	2362	GCGCAAGACCAAGTACAGAGCTGACTGCGCGCGAGAGCTGGCAATAAAGAGACCCCTTTG	2421
QY	620	IuLYbGlnPhelybArgArGSeRCyGlnMeGluPhneGlyGluSerLleWetSeRgIua	640

Accession	Protein	Position	Sequence	Position
Db		2422	AAAGCAGTTTAAACGCAGAGCTGCCAATGGAATTTGGAGAGAGCATCATGTCCAGCA	2488
Qy	bnarGseraRgJnGluleuGlYrVaIysrGlnSerPheSerGlySerMetG	640		660
Db		2482	ACAGTCACGGGAGAGACTGGGGAAAGTGGCGATCTACGCTTTTGGGGCAGCATGG	2541
Qy	IuIleIleGluValSer	660		665
Db		2542	AAATCATTTGAGCTTCC	2558

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RESULT 11
US-09-816-494-1
: Sequence 1, Application US/09816494
: Patent No. US20020034807A1
: GENERAL INFORMATION:
: APPLICANT: Meyers, Rachel A.
: TITLE OF INVENTION: 38692 AND 21117, NOVEL DUAL SPECIFICITY
: TITLE OF INVENTION: PHOSPHATASE MOLECULES AND USES THEREFOR
: FILE REFERENCE: 10448-030002
: CURRENT APPLICATION NUMBER: US/09/816,494
: PRIOR APPLICATION NUMBER: 2001-03-23
: PRIOR FILING DATE: 2000-03-24
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 3544
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (589)...(2583)
US-09-816-494-1

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Alignment Scores:	
Pred. No.:	0
Score:	472.00
Percent Similarity:	99.408
Best Local Similarity:	99.408
Query Match:	70.984
DB:	9
Length:	3544
Matches:	663
Conservative:	0
Mismatch:	2
Indels:	4
Gaps:	0

US-10-029-345A-109 (1-665) x US-09-816-494-1 (1-3544)

Qy	1	MerLhHsgIuWctIeGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGln	20
Db	589	ATGGCCCATGATGATGGATGGAACTCAAAATTGTACTGAGAGCTGGTGGCTCTGGTGA	648
Qy	21	SerGlyThrGlnIuValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer	40
Db	649	AGTGGAAACGAAAAAGCTGCTCTTAATTGATGACCGGCATTGTGGAAATCAATACATCC	708
Qy	41	HisIleLeuGlnIuAlaIleAsnIleAsnCysSerIysLeuMetIyValArgLeuGlnGln	60
Db	709	CACATTTTGGAGCCATTAAATATCAACTGCTCCAGCTTATGAAACGGAAGCTTCCACAG	768
Qy	61	AspIyValLeuIleIleThrGlnLeuIleGlnHisSerIleAlaValHisIlyValAspIleArg	80
Db	769	GACAAAGCTTAAATTACAGAGCTCATCAGACTTCACGAAACATTAAGTTGACATTCAT	828
Qy	81	CysSerGlnIyValIleValIleTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer	100
Db	829	TGCAGTCAGAAAGCTTGATGTTTACGATCAAAAGCTCCCAAGATGTGCTCTCTCTTCA	888
Qy	101	AspCysPheLeuThrValLeuLeuGlnIlyIysLeuGlnIlySerPheAsnSerValHisIleu	120
Db	889	GACTGTTTTCACACTGACTTCTGGGTAACTGGAGAAAGAGCTTCAACTGTGTACACTG	948
Qy	121	LeuAlaIyGlyPheAlaGluPheSerArgCysPheProGluIleuCysGlnIlyIySer	140
Db	949	CTTGACAGTGGTGTGCTGAGTCTCTCTGTTGTTCCCTGTGCTCTGTGAAGAAATCC	1008


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: PRIOR APPLICATION NUMBER: US 09/815,419
: PRIOR FILING DATE: 2001-03-22
: Remaining Prior Application data removed - See File Wrapper or PALM
: NUMBER OF SEQ ID NOS: 114
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 25
: LENGTH: 3544
: TYPE: DNA
: ORGANISM: Homo Sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (589)...(2586)
: US-10-377-072-25

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Alignment Scores:

Pred. No.:	0	Length:	3544
Score:	472.00	Matches:	663
Percent Similarity:	99.40%	Conservative:	0
Best Local Similarity:	99.40%	Mismatches:	2
Query Match:	70.98%	Indels:	4
GB:	17	Gaps:	0

US-10-029-345A-109 (1-665) X US-10-377-072-25 (1-3544)

QY	MetAlHiegluwerlleglYhrGlnlieValThrgluAqgleuValAlaleuLeuGlu 20
Db	589 ATGGCCCAAGAGATGATGTGAACCTCAATTGTACTGAGAGCTTGCGCTGCGAA 648
QY	21 SerGlyThrgluuysValleuLeuulleaSpSerAgrpProheValgluYrAsnThrSer 40
Db	649 AGTGGAAACGGAAABAAGTGTGCTGAATTGATACCGCGCAATTGTGGAAATCAATACATCC 708
QY	41 HislleLeuGlualalleaenilleaenCySerlySleuwtelyPaqAqgleuGln 60
Db	709 CACATTTTGGAGCCCAATTATATCAACGCTCCCAAGCTTAAAGAACCAAGGTGGCAAG 768
QY	61 AspIysValleuulleThrgluLeuulleGlnHisserAlaYrSHsluYValAspIleAsp 80
Db	769 GACAAAGTGTAAATTCAGAGCTCAATCCAGCACTTAGGAAACATAAAGTTGACATTTGAT 828
QY	81 CySerGlnlyeValValValYrAspGlnSerSerGlnAspValAlaserLeuSerSer 100
Db	829 TGCAGTCAGAGGTTTACTTTTACATCAAACTCCCAAGATGTGCTCTCTCTTCA 888
QY	101 AspCyPheleuThrValleuLeuGlyLysleuGluYsSerPheAsnSerValHisleu 120
Db	889 GACTGTTTCTCACTACTACTCTCGGGTAACTGGAGAGAGACTTCAACTCGTTCACTG 948
QY	121 LeuAlaGlyValPheAlaGluPheSerAqPhePProglYleuCyGluGlyLysSer 140
Db	949 CTTCGACAGGCGGTTTCTGAGTTCCTCGTTGTTTCCCTGCGCTCTGTGAAGGAAATCC 1000
QY	141 ThrIleuValProthrCysAlleSerGlnProCysleuProValAlaAsnilleglYProthr 160
Db	1009 ACTCTAGTCCCTACCTGCATTTCTCAAGCTTGCTTAACTGTGGCAACATTTGGGCCAAC 106
QY	161 ArgIleleuProAsnleuThyrleuGlyCysGlnAqAspValleuAsnlySguLeuIle 180
Db	1069 CGAATCTTCCCAATCTTTATCTTGCGCGCCAGCAGATGTCCTCAACAAGAGGCTGAT- 112
QY	181 -GlnGlnAsnGlyIleGlyYrValleuAsnAlaserYr-ThrCyProlYsProAsp 200
Db	1128 GCAGCAGAAATGGAGTGGTATGTGTAAATCCCGCA- TACTCTGCCAAAGCTGCAGT 118
QY	200 helIeProgluSerHisPheleuAqValProValAsnAspSerPheCyGluLysIleIle 220
Db	1187 TTATCCCCAGATCTCATTTCTCGCGTGCGCTGTAAAGCAAGCTTTTGTGAGAAATTT 124
QY	220 euProTrleuAspLysSerValAspPheillegluLysAlaLysAlaserAsnGlyCysv 240
Db	1247 TGGCGTGCGTTGGCAACAATCAGTANATTCATTGAGAAAGCAAAAGCCCTCCATGAGATG 130
QY	240 alleuValHisCySleuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaYrIleu 260

Db	1307	TTCTTAGTGCATGTTTAGCTGGAGTCTCCGCGCTCCGACCATGCGCTATCCGCTACATCA	1366
Oy	260	etlybargmeUasPmcseserleuabpGluAlaTyraArgPheVallysglybargProt	280
Db	1367	TGAAGAGGATGGACATGCTTTAATATGAAAGCTTACAGATTGTGTGMAAAGAAAAAGACCTTA	1420
Oy	280	hrlieserProaAnPheAanPheleuGlyglnleuLeuAaPTGlylylyserlyelybA	300
Db	1427	CTAATATCCCAAACTTCATATTCTTGCGGCCAACTCCGGACTATAGAAAGAAATTAAGA	1486
Oy	300	snGlnThrGlyAlAserGlyProlySerleuBleuLyLeuLeuHihleuGlnlybProA	320
Db	1487	ACCAAGACTGGAGCATCAGGGCCAAAGCAAACTCAAGCTGTGCACCTGGAGAAAGCCA	1544
Oy	320	snGlnProValProAlaValserGlnGlyglnlybSerGlyuThrProleuSerProp	340
Db	1547	ATGAACCTGTCCTGCTGTCTCAGAGGGGTGACAGAAAGAGAGACGCCCTCACTGCAC	1606
Oy	340	roCyValaIaAserSerAlaThrserGlnAlaIaGlyglnArgProValHihProAlaSerV	360
Db	1607	CCGTGGCCGACTCGCTACCTCAAGAGGACAGAGCAAAAGCCCGCTGATCCCGCACGG	1666
Oy	360	aIProserValProSerValGlnProserleuLeuGlnAaPseSerProleuValGlnAlaL	380
Db	1667	TGCCAGCGTCCCAAGCGTCGACCGCTGCTGTTAGAGACAGCCCGCTGTACAGGGCC	1722
Oy	380	euserGlyLeuHihleuSerAlaAaPArgleuGlnAaPseSerAaBlyleuLybAargSerP	400
Db	1727	TCAGTGGGCTGCACCTGTCCGACAGAGGCTGGAAGACAGCAATACCTCAAGGCTTCT	1786
Oy	400	heserleuAaPrlleuLyserValserTyrsSerAlaSerMetAlaAlaSerleuHihGlyP	420
Db	1787	TCTCTCTGGAATCAAAATCAGTTTCATATTCAGCAGCAGATGGCAGCATCTTACATGCT	1846
Oy	420	heserSerSerGlnAaPrlaleuGlnTyTyTybProserThThreleuAaPrlTybA	440
Db	1847	TCTCTCTCAACAAAGATGCTTTGGAAATCTACAAACCTTCCACTACTGTGAATGGACCA	1906
Oy	440	snLybLeuCyGlnPheSerProValGlnGlnleuSerGlnGlnThrProGlnThrSerP	460
Db	1907	ACAAGCTATGCGACGTTCTCCCTGTTCAGAACTATGAGACAGACCTCCGAAACACAGTC	1966
Oy	460	roAaPlybGlnGlnAlaSerleuLeuProLybLybLeuGlnThrAlaArgProserAaPseRg	480
Db	1967	CTGATTAAGAAAGAACCCAGCATCCCCAAAGAAAGCTGCAGAACCGCCAGGCTTCAAGCACCC	2022
Oy	480	InserybArgLeuHihSerValArgThrserserSerGlyThhAlaGlnArgSerleuL	500
Db	2027	AGACCAAGCGATTCATTCGGTGCAGAACACACAGACAGAGGACCGCCCAAGAGTCCCTTT	2086
Oy	500	euserProleuHihAargserGlySerValGlnAaPseTybHihThrsSerPheleuPheG	520
Db	2087	TAATCTCACTGCATCGAAGTGGAGCGGTGAGAGCAATTCACACACAGCTTCTTTTCG	2144
Oy	520	lyLeuSerThrsGlnGlnHihleuThryLysserAlaGlyLeuGlyLeuLybGlyTybH	540
Db	2147	GCTTTTCCACAGACAGACAGACCTTCACAAAGTGTGCTGGCTGGGCTTAAAGGGCTGGC	2206
Oy	540	IaSerAaPrlleuAlaAaProGlnHihserThhProserleuLeuThrsSerThhTybPheA	560
Db	2207	ACTGGAAATTTGACCCCCCAAGCTTTCACCTCCCTCCCTACCAAGCAGCTGATTTTGG	2266
Oy	560	IaThnGlySerSerHihPheTySerAlaSerAlaIleTyGlyGlySerAlaSerTybS	580
Db	2267	CCACAGAGTCTCACTTACCTGTGCTCAGCATTACAGAGGACAGTCCAGTTACT	2322
Oy	580	erAlaTySerCySerGlnleuAaProThCybGlyAaPrlAlaTybSerValArgArgA	600
Db	2327	CTGCTTACAGCTGCAGCAGCTGCCCACTTCCGAGACCAAGTGTATTTCTGTGGCAGGC	2386
Oy	600	rgGlnlybProserAaPrlAlaAaPseArgAaPseTybHihGlnGlnleuSerProPheG	620

Db 2387 GGCAGAGCAAGTACAGACTGACTCGCGCGAGCTGCAATGAAGAGCCCTTTG 2446
Qy 620 LulvGlnPheIyehArgSerCyseGlnMetGluPheGluSerIleMetSerGluu 640
Db 2447 AAAGCAGTTTAAACGCGAGAGCTGCAATGGAATTGAGAGAGCATCATCTCAGAGA 2506
Qy 640 snAtgSerArgIuGluIuLeuGluYlyeValGlySerGlnSerSerPheSerGlySerMetG 660
Db ACAGCTCACGGGAGAGACTGGGAAAGTGGGACAGTCAGCTTTTCGGGAGCATGG 2566
Qy 660 LulleIleGluValSer 665
Db 2567 AAATCATTTAGAGTCTCC 2583

RESULT 13
US-10-377-072-25

/ Sequence 25, Application US/10377072
/ Publication No. US20040157221A9
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals Inc.
/ APPLICANT: Curtis, Kory A.J.
/ APPLICANT: Logan, Thomas Joseph
/ APPLICANT: Glucksmann, Maria A.
/ APPLICANT: Meyers, Rachel E.
/ APPLICANT: Williamson, Mark J.
/ APPLICANT: Rudolph-Owen, Laura A.
/ APPLICANT: Chun, Miyoung
/ APPLICANT: Tsai, Feng-Ying
/ TITLE OF INVENTION: NOVEL 25869, 25934, 26335, 50365, 21117,
/ TITLE OF INVENTION: 38692, 46508, 16816, 16839, 49937, 49931 AND 49933 MOLECULES
/ FILE REFERENCE: MP103-0180NM1M
/ CURRENT APPLICATION NUMBER: US/10/377,072
/ PRIOR FILING DATE: 2003-02-27
/ PRIOR APPLICATION NUMBER: US 09/895,860
/ PRIOR FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: US 60/215,370
/ PRIOR FILING DATE: 2000-06-29
/ PRIOR APPLICATION NUMBER: US 09/723,806
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 60/187,455
/ PRIOR FILING DATE: 2000-03-07
/ PRIOR APPLICATION NUMBER: US 09/843,297
/ PRIOR FILING DATE: 2001-04-25
/ PRIOR APPLICATION NUMBER: US 60/199,801
/ PRIOR FILING DATE: 2000-04-26
/ PRIOR APPLICATION NUMBER: US 09/861,801
/ PRIOR FILING DATE: 2001-05-21
/ PRIOR APPLICATION NUMBER: US 60/205,508
/ PRIOR FILING DATE: 2000-05-19
/ PRIOR APPLICATION NUMBER: US 09/816,494
/ PRIOR FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: US 09/815,419
/ PRIOR FILING DATE: 2001-03-22
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PasteSeq for Windows Version 4.0
/ SEQ ID NO 25
/ LENGTH: 3544
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (589)...(2586)
US-10-377-072-25

Alignment Scores:

Pred. No.: 0 Length: 3544
Score: 472.00 Matches: 663
Percent Similarity: 99.40% Conservative: 0
Best Local Similarity: 99.40% Mismatches: 2
Query Match: 70.98% Indels: 4
DB: 18 Gaps: 0

US-10-029-345a-109 (1-665) x US-10-377-072-25 (1-3544)

Qy 1 MetAlahIsgIuMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
Db 589 ATGGCCCATAGATGATTTGAACTCAAAATTGTACTGAAAGGTGGTGGCTCTCGGAA 648
Qy 21 SerGlyThrGluIuValLeuLeuIleApsSerArgProPheValGluTyrAsnThrSer 40
Db 649 AGTGAACCGGAAAGAGTGGCTCAATTGATACCGGCATTTGTGAAATACATACATCC 708
Qy 41 HieIleLeuGluAlaIleAsnIleAsnCyseSerIySleMetIyArgArgLeuGln 60
Db 709 CACATTTTGGAGCCATTATATCACTGCTCCAGCTTAAGAGCGAAGGTTGCACAG 768
Qy 61 AppIyValLeuIleThrGluLeuIleGlnIleSerAlaIySHIlyeValAapIleAap 80
Db 769 GACAAAGTGTAAATACAGAGCTCATCCAGATTCAAGAAACATTAAGTTGACATTGAT 828
Qy 81 CySerGlnIyValValIyValTyrAapGlnSerSerGlnAapValAlaSerLeuSerSer 100
Db 829 TCCAGTCAAGAGCTTGTATGATCAATCAAGCTCCCAAGATGTGGCTCTCTCTTCA 888
Qy 101 AapCysePheLeuThrValLeuLeuGluYlyeLeuGluIuYseSerPheAsnSerValIleu 120
Db 889 GACTGTTTTCTCAGTGTACTTCTGGTAACTGGAGAAAGCTTCACTGTTCACCTG 948
Qy 121 LeuAlaGlyIyPheAlaGluPheSerArgCysePheProGlyLeuCyseGluGlyIySer 140
Db 949 CTTCAGAGTGGGTTTGTGAGGTTCTCGTGTTCCTCGGCTCTGTGAAGGAAATCC 1008
Qy 141 ThrLeuValProThrCyseIleSerGlnProCyseLeuProValAlaAsnIleGlyProThr 160
Db 1009 ACTCTAGTCCCTACCTCATTTCTCAGCCTGTGTTACTCTTGCCCAACATGGCCCAACC 1068
Qy 161 ArgIleLeuProAsnLeuTyrLeuGluYCyseGlnAapValLeuAsnIyGluLeuIle 180
Db 1069 CGAATTTCTCCCAATCTTATCTTGTGGCTCCAGCGAGATGCTCAACAAAGAGCTGAT- 1127
Qy 181 -GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyr-ThrCyseProIyPheAap 200
Db 1128 GCAGCAGAAATGGATGTGTTATGTGTAAATCCAGCA-TRCTGTGCAAAAGCTGACT 1186
Qy 200 heIleProGluSerHisPheLeuArgValProValAsnApsSerPheCyseGluIySle 220
Db 1187 TTTATCCCAAGTCTCTATTCCTGCGTGGCTGTGAAGAGAGCTCCCAATGATGATGTG 1306
Qy 220 eubProIleuAspIySerValAapPheIleGluIyValAlaIySerAsnIyCyseV 240
Db 1247 TGGCGGTGTGACAAATCAATCAATGATTTCAATTGAGAAAGAGCCCTCCAAATGATGTG 1306
Qy 240 AlIeuValHisCyseLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleu 260
Db 1307 TTTCTAGTCACTGTTTACTGCGATCTCCGCTCCGCAACCATGCTATGCGCTACATCA 1366
Qy 260 eIlyeArgMetApsPheSerLeuAspGluIaTyrAapPheValIyGluIyArgProT 280
Db 1367 TGAAGAGATGAGCAATGCTTTAGTAAAGCTTACAAATTTGTGAAGAAAGAAAGACTTA 1426
Qy 280 hrIleSerProAsnPheAsnPheLeuGluIyLeuLeuAapTyrGluIyValIleIyArg 300
Db 1427 CTATATCTCCAAATTTCAATTTCTGGGCCAACCTCGACTGATGAGAAAGATTTAA 1486
Qy 300 snGlnThrGlyAlaSerGlyProIySerSerIySleLeuLeuHisIleuGluIyArgPro 320
Db 1487 ACCAGACTGAGAGCATTCAGGCGCAAGCAAACTCAAGCTGCTGCACTCGGAGAGCCAA 1546
Qy 320 snGluProValProAlaValSerGluGlyGlyGlnIySerSerGluThrProIySerProp 340
Db 1547 ATGAACCTGTGCTGCTGTCTCAGAGGTGAGCAAGAAAGCAAGAGCCCTCAAGTCAAC 1606
Qy 340 roCyseAlaApsSerAlaThrSerGluAlaGlyGlnArgProValHisProAlaSerV 360


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Db      1607 CCTGTCGCCGACTGCTGACTCAGAGCAGAGCAAGAACCCGCTGATCCCGCCAGCG 1666
Qy      360 aIProSerValProSerValGlnProSerLeuLeuGlnAapSerProLeuValGlnAla 380
Db      1667 TGCCACGCGCGCCACGTCGACACCCCTGCTGTTAAGAGCAGACCCGCTGGTACAGAGCC 1726
Qy      380 euserGlyLeuHsLeuSerAlaAapArgLeuGlnAapSerAenLysLeuLysArgSer 400
Db      1727 TCGATGGGCTGCACCTCTCCGACAGACGCTGGAAAGACATTAAGCTTCAAGCTTCTCT 1786
Qy      400 heSerLeuAapLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHsGlyP 420
Db      1787 TCTCTCTGATATCAATCAATCAGTTTCAATTCACGACGATGACGATCCTTCAATGCT 1846
Qy      420 heSerSerSerGlnAapAlaLeuGlnTyrTyrTyrProSerThrThrThrLeuAapGlyThra 440
Db      1847 TCTCTCATCAGAAAGATGCTTGGAAATCACTAACACCTTCACTACTCTGGATGGAGCA 1906
Qy      440 snLysLeuCySgInPheSerProValGlnGlnLeuSerGlnGlnThrProGlnThrSerP 460
Db      1907 ACAAGCTATGCCAGTTCTCCCTCTTCAAGAACTATCGAGAGCACTCCGGAACCAAGTC 1966
Qy      460 roAapLysGlnGlnAaSerLysLeuLysLeuGlnThrAlaArgProSerAapSerG 480
Db      1967 CTGATTAAGAGGAGAGCAGCATCCCAAGAAAGCTGGACAGCCGCGCAGGCTTACAGACAGCC 2026
Qy      480 InSerLysArgLeuHsSerValArgThrSerSerSerGlyThraAlaGlnArgSerLeu 500
Db      2027 AGAGCAGAGCATTTGCAATTCGCTCAGAACCCAGCAGCAGCTGGCAGCCGACAGAGCTCCCTTT 2086
Qy      500 euserProLeuHsArgSerGlySerValGlnAapAenTyrHsThrSerPheLeuPheG 520
Db      2087 TATCTCACTGATTCGAGTGGAGGCTGGAGAGCAATTAACCAACAGCTTCTTTCTTG 2146
Qy      520 LysSerThrSerGlnGlnHsLeuThrLysSerAlaGlyLeuGlyLeuYTrpH 540
Db      2147 GCCTTTCACCAACGACGACGACACTCAGCAAGTCTGCTGGCTGGGCTTAAAGGCTGGC 2206
Qy      540 IseSerAapLysLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheA 560
Db      2207 ACTCGATATCTTGGCCCCCAAGACCTTAACCTTCCCTGACACAGCAGCTGATTTTG 2266
Qy      560 IathrGlnSerSerHsPheTyrSerAlaSerAlaLysTyrGlyLysSerAlaSerTyrS 580
Db      2267 CCAAGAGTCTCACTTACTTCTGCTTCACTCACTCACTCACTCACTCACTCACTCACT 2326
Qy      580 exaLysTyrSerCySserGlnLeuProThrCySgIysAapGlnValTyrSerValArgArg 600
Db      2327 CTGCTTACAGCTCAGCAGCTGCCCACTTGGGGAAGCAAGCTATTTCTGTCGCAAGGC 2386
Qy      600 rGlnLysProSerAapArgAlaAapSerArgArgSerTyrHsGlnGlnLysSerProPheG 620
Db      2387 GGCAGAGAGCCAAAGTGCAGAGCTGACTCGCGCGGAGCTGGCATGAAGAGAGCCCTTTG 2446
Qy      620 LysLeuGlnPheLysArgArgSerCySgInMetGlnPheGlyLysSerAlaMetSerGln 640
Db      2447 AAAAGCAATTAAACGAGAAAGCTGCCAAATGGAATTTGAGAGAGCATATCTCAGAG 2506
Qy      640 snArgSerArgGlnGlnLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetC 660
Db      2507 ACAAGTCAACGGAAGAGCTGGGGAAGTGGGCACTACGTTCTTTCGGGCAAGATGG 2566
Qy      660 LysLeuLeuGlnValSer 665
Db      2567 AAATCATTTGAGTCTCC 2583

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RESULT 14

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US-10-425-114-26234
; Sequence 26234, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua

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; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack B
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26234
; LENGTH: 3625
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4119-028-H6_FLI
US-10-425-114-26234

Alignment Scores:
Pred. No.: 0
Score: 472.00
Percent Similarity: 99.408
Best Local Similarity: 99.408
Query Match: 70.988
DB: 17
Gaps: 0

US-10-029-345a-109 (1-665) x US-10-425-114-26234 (1-3625)

Qy      1 MetAlaHsGlnMetLeuGlyThrGlnLeuValThrGlnArgLeuValAlaLeuLeuGln 20
Db      692 ATGGCCCATGAGATGATGTGAATCTCAATTTGTTACTGAGAGGTGGTGCTCTGCTGAA 751
Qy      21 SerGlyThrGlnLysValLeuLeuLeuLeuAapSerArgProPheValGlnTyrAenThrSer 40
Db      752 AGTGAACCGAAAAAGTGTGCTAATGTATACCCGCAATTTGTGAATACATATCATCC 811
Qy      41 HsLeuGlnAlaIleAenIleAenCySserLysLeuMetLysArgArgLeuGlnGln 60
Db      812 CACATTTTGAAGCCATTATATCAATGCTCTCAAGCTTATAGAGGAAGTTGCAACAG 871
Qy      61 AapLysValLeuLeuLeuThrGlnLeuLeuGlnHsSerAlaLysHsLysValAapLysAap 80
Db      872 GACAAAGTGTATATTAACAGAGCTCATCCAGATTCCAGCAACATTAAGTTGACATTGAT 931
Qy      81 CySserGlnLysValValValTyrArgPheGlnSerSerGlnAapValAlaSerLeuSerSer 100
Db      932 TCACGTCAAGAGGTGTATGATTAAGATCAAACTCCCAAGATGTGCTCTCTCTTCA 991
Qy      101 AapCySphLeuThrValLeuLeuGlyLysLeuGlnLysSerPheAenSerValHsLeu 120
Db      992 GACTGTTTCTCACTGATCTTCTGGGTAACTGGAGAGAGCTTCAACTCTGTCACCTG 1051
Qy      121 LeuAlaGlyGlyPheAlaGlnPheSerArgCySphProGlyLeuCySgInGlyLysSer 140
Db      1052 CTTGACAGGTGGGTTGCTGATGCTCTGCTGTTCCCTGCTGCTGTAAGGAAATATCC 1111
Qy      141 ThrLeuValProThrCySgIleSerGlnProCySgLeuProValAlaAenIleGlyProThr 160
Db      1112 ACTCTAGTCCCTTACCTGCACTTCTCAAGCTTCTTCACTGTTGCCAACTTGGGCCAAC 1171
Qy      161 ArgGlyLeuProAenLeuTyrLeuGlyCySgInArgAapValLeuAenLysGlnLeuIle 180
Db      1172 CGAATTCCTCCCAATCTTATCTTGGCTGCCAGCGAGATGCTCTCAACAGAGCTGAT- 1230
Qy      181 -GlnGlnAenGlyIleGlyTyrValLeuAenAlaSerTyr-ThrCySProLysProAapP 200
Db      1231 GCAGCAGATGGGATGGTTGTTATGTGTTAATCCAGCAAA-TACTGTCCAAAGCTGACT 1289
Qy      200 heLysProGlnSerHsPheLeuAaGValProValAenAapSerPheCySgInLysIle 220
Db      1290 TTATCCCGCAGCTCATTTCTCGCGTGCCTGTGATACAGCTTTTGTGAAATATTT 1349
Qy      220 euProThrLeuAapLysSerValAapPheIleGlnLysAlaLysAenGlyCySgV 240

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Db      2430 CTGGCTACAGCTGACCCAGCTGCCCACTTGTGGGAGACCAAGTCTATTCTGTGCGCAGGC 2489
QY      600 TGTGTLNYPProSerAaPaAgaIaaPserAgaYgSerTTPHlglUglUserProPhg 620
Db      2490 GGCGAAGACCAAGTGCACAGAGCTGACTCGCGCGGAGCTGCAGTCAAGAGAGGCCCTTTG 2549
QY      620 TLTySgInPheYsAgaYgSerCySgImetGluPheglYglUserTlleMeSerGlUA 640
Db      2550 AAAAGCACTTTAAACCCAGAAAGCTCCCAATGAAATTTGGAGAGAGATCATGTCTCAGAGA 2609
QY      640 enAgsErAgtglUglUserglYlySValglYserGlnSerSerPheSerGlySerMeGc 660
Db      2610 ACAGGTCCAGCGGGAAGAGCTGGGGAAAGTGGCAGTCAGTCTTGTGGGACAGATGG 2669
QY      660 LTLTlleglUglUser 665
Db      2670 AATTCATTGAGGTCTCC 2686

RESULT 15
US-10-343-357-17
; Sequence 17, Application US/10343357
; Publication No. US20040058341A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y.Tom
; APPLICANT: ELIOTT, Vicki S.; RAMKUMAR, Jayalaxmi
; APPLICANT: YAO, Monique G.; BURFORD, Neil
; APPLICANT: WANG, Yumei E.; STEWART, Elizabeth A.
; APPLICANT: GANDHI, Ameena R.; ARVIZU, Chandra S.
; APPLICANT: LEE, Ernestine A.; HAPFLIZ, April J.A.
; APPLICANT: LU, Dying Alina M.; TRIBOUHEY, Catherine M.
; APPLICANT: GRIFFIN, Jennifer A.; BAUGHN, Mariah R.
; APPLICANT: YUE, Henry; WARREN, Bridget A.
; APPLICANT: NEUTEN, Danielle B.; CHAMLA, Narinder K.
; APPLICANT: KEARNEY, Liam
; TITLE OF INVENTION: PROTEIN PHOSPHATASES
; FILE REFERENCE: PI-0173 PCT
; CURRENT APPLICATION NUMBER: US/10/343,357
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: PCT/US01/23716
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 60/221,679
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/223,272
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/224,309
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 60/226,728
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/229,254
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: US 60/231,366
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 3766
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040058341A1 7480570CBI
US-10-343-357-17

Alignment Scores:
Pred. No.:      0      Length:      3766
Score:          472.00  Matches:      663
Percent Similarity: 99.40%  Conserved: 0
Best Local Similarity: 99.40%  Mismatches: 2
Query Match:      70.98%  Indels: 4
DB:              17      Gaps: 0

US-10-029-345A-109 (1-665) x US-10-343-357-17 (1-3766)

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/ CURRENT APPLICATION NUMBER: US/10/648,593
/ CURRENT FILING DATE: 2003-08-26
/ PRIOR APPLICATION NUMBER: 60/406,385
/ PRIOR FILING DATE: 2002-08-27
/ NUMBER OF SEQ ID NOS: 557
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO: 115
/ LENGTH: 4790
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-648-593-115

Alignment Scores:
Pred. No.: 0          Length: 4790
Score: 472.00        Matches: 663
Percent Similarity: 99.40%      Conservative: 0
Best Local Similarity: 99.40%    Mismatches: 2
Query Match: 70.98%             Indels: 4
DB: 18                         Gaps: 0

US-10-029-345A-109 (1-665) x US-10-648-593-115 (1-4790)

QY      1 MetAlHisglumetiIeglyThrglnileValthrgluargLeuValAlaleuLeuGlu 20
Db      184 ATGCCCATAGATGATGATGGAATCTAAATTGTTACTGAGAGGTGGTCTCTGCGAA 243
QY      21 SerGlyThrgluValleuLeuileAapSerArqProPheValGluTyraSerThSer 40
Db      244 AGTGAAGCAAGAAAGTGTCTGCTAAATTGATAGCCGCGCATTTGGTGAATCAATACATCC 303
QY      41 HisIleLeuGluAlaIleAsnIleAanCyseSerIyLeuMetIyBahghLeuGln 60
Db      304 CACATTTTGAAGCCATTATATCACTGCTCCAGCTTAAGAACCAAGTTGCAACAG 363
QY      61 AapIyValleuIleThrgluLeuileGlnHisSerIaIyShisIyValAapIleAap 80
Db      364 GACAAAGGTATTAATACAGAGCTCATCCAGCATTCAGCAAAACATAAGTTGACATTTGAT 423
QY      81 CyseSerGlnIyValIaIyValIyAspGlnSerSerGlnAapValAaserIeAapSer 100
Db      424 TGCATGTCAGAAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483
QY      101 AapCysePheLeuThrgluValleuLeuGluIyValleuGluIySerPheAanSerValHisIleu 120
Db      484 GACGTGTTCTCATCTGATGATCTTCTGCGTAACTGGAAGAGAGCTTCAACTCTGTTCACTG 543
QY      121 LeuAlaGlyGlyPheAlaGluPheSerArqCysePheProGlyLeuCyseGluGlySer 140
Db      544 CTTCAGGTGGGTTTGTCTGAGTTCTCTCGTTGTTCTCTGCGCTCTGTGAAAGAAATCC 603
QY      141 ThreValProThrCyseIleSerGlnProCyseLeuProValAlaAsnIleGlyProThr 160
Db      604 ACTCTAGTCTCCCTACCTGATTTCTCAGCCCTTGCTTACCTGTTCCCAACCTTGGCAACCC 663
QY      161 ArgIleLeuProAanLeuTyreLeuGlyCyseGlnAapSerValleuAanIySerGlnIle 180
Db      664 CGAATCTTCCCAATCTTATCTTGTGCTGCCAGCAAGTCTCTCAAAAGAGAGCTGAT- 722
QY      181 -GlnGlnAanGlyIleGlyTyraValleuAanIaSerTyra-ThrCyseProIyProAap 200
Db      723 GCGCAAGAAATGGGATGTTATGTTAAATGCCAGCAA-THCCTGTCCAAAGCTTAACT 781
QY      200 heIleProGlnSerHisPheLeuArgValProValAanAapSerPheCyseGluIySerIle 220
Db      782 TTAATCCCGAGTCTCATTTCTGCGTGGCCGTGAATGAGACAGCTTTGTGAGAAATTT 841
QY      220 euProIyPheAapIySerValAapPheIleGluIyValAalIySerAanGlyCyay 240
Db      842 TCCCGTGTGGCAAAATCAGTATTTCAATTGAGAAAGCAAAAGCTTCAATGAGAGTGG 901
QY      240 aIleuValHisCyseIleuAlaGlyIleSerArqSerAlaThrIleAlaIleAlaTyriIle 260
Db      902 TTCTAGTCACTGTTTACTGGAGATCTCCCGCTCCGCAACATCGCTATCGCTAATCA 961
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QY      260 eIlyBahgMetAapMetSerIleuAapGluAlaTyraPheValIyysGluIyArqProT 280
Db      962 TGAAGAGATGACATGCTTTAGATGAGCTTACAGATTGTGAAAGAAAGAAAGCTTA 1021
QY      280 hrIleSerProAanPheAanPheLeuGlyGlnleuLeuAapTyrgluIyIySerIleIyBa 300
Db      1022 CTATATCTCCAACTTCAATTTTCTGGGCCAACTCCGTGACTATGAGAAAGATTAAGA 1081
QY      300 enGlnThrgluAlaSerGlyProIySerIyLeuIySerLeuIySerLeuIySerLeuIySer 320
Db      1082 ACCAGACTGGAGCATCAGGCGCAAGAGCAAACTCAACTGCTGCACTGGAGAGGCCAA 1141
QY      320 enGluProValProAlaValSerGluGluGlyGlnIySerGluThrProLeuSerProp 340
Db      1142 ATGAACCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1201
QY      340 roCyseAlaAapSerAlaThrSerGluAlaIleGlyGlnArgProValHisProAlaSerV 360
Db      1202 CCTGTGCCGACTCTGCTACTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1261
QY      360 aIProSerValProSerValGlnProSerLeuLeuGluAapSerProLeuValGlnAla 380
Db      1262 TCCCAAGGATGCCAGCGGTGAGCGCTGCTGTTAAGAGCAAGCCGCTGTTACAGGCCG 1321
QY      380 euSerGlyLeuHisIleuSerAlaAapArgLeuGluAapSerAanIySerIyAapSer 400
Db      1322 TCAGTGGGCTCAGCTCGTCCGCAAGAGCTGAGAACCAATAGCTTCAAGCTTCTCT 1381
QY      400 heSerLeuAapIleIySerValSerTyserIaSerMetAlaIaaserIleuIleGlyP 420
Db      1382 TCTCTGAGATATAAATCAAGTTTCATATACACCGAGATGAGAGCATCTTAACATGGCT 1441
QY      420 heSerSerSerGluAapAlaLeuGluIyTyriTyserProSerThrThreAapArgIyThra 440
Db      1442 TCTCTCATCAGAAAGATCTTGGATATCTCAAACTTCTCACTATCTGATGGAGCA 1501
QY      440 snIySerCyseGlnPheSerProValGlnGluLeuSerGlnIyThrProGluThrSerP 460
Db      1502 ACAAGCTATCCAGATCTCTCCCTGTTCAAGAACTATCGGAGAGCATCCGAAACCATTC 1561
QY      460 roAapIyGluGluAlaSerIleProIyLeuLeuGlnThrAlaArgProSerAapSerG 480
Db      1562 CTGATAGAGGAGGAGGAGGAGGATCCCAAGAGCTGAGAGCGCCAGGCTTCAAGAGCC 1621
QY      480 InsertyaArgLeuHisSerValaArgThrSerSerSerGlyThraIleGlnArgSerIleu 500
Db      1622 AGAGCAAGGATTTGATTCGTCAGAACCAAGCAGCAGTGGACCGCCAGAGTCCCTTT 1681
QY      500 euSerProLeuHisAArgSerGlySerValGluAapAanTyriThrSerPheLeuPheG 520
Db      1682 TATCTCACTGATGAGATGGAGCGTGGAGAGCAATTAACCAACAGCTTCTCTTTTTC 1741
QY      520 IyLeuSerThrSerGlnGlnHisLeuThryIySerAlaGlyLeuGlyIyLeuGlyTyriP 540
Db      1742 GCCTTTCAACCAAGCAGAGGAGCACTCAAGAGTCTGCTGGCTGGGCTTAAAGGCTGGC 1801
QY      540 IaserAapIleuAlaProGlnThrSerThrProSerLeuThrSerSerTyriTyPheA 560
Db      1802 ACTGGATATCTTGGCCCCCAAGACTCTACCTCTTCCGAGCAAGAGCTGATTTTTC 1861
QY      560 IathGlnSerSerHisPheTyserAlaSerAlaIleTyrglyGlySerAlaSerTyS 580
Db      1862 CCAGAGATCTCAGACTTCACTGCTCAGAGCATTAAGAGGAGGAGGAGGAGGAGGAGG 1921
QY      580 eAlaTyserCyseSerGlnleuProThrCyseGlyAapGlnValIySerValaArgArg 600
Db      1922 CTGCTTACAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1981
QY      600 rGlnIyPProSerAapArgAlaAapSerArgArgSerTrpHisGluGluSerProPheG 620
Db      1982 GGCAGAAAGCAAGTGAAGAGTGACTCGCGGGGAGGCTGGCATGAAGAGAGGAGGAGGAGG 2041
```


QY 420 heserSerg1uasp1aleuG1uYrTyrTyrPserThrThrLeuaspG1YThra 440
Db 1847 TCTCTCATCAAGAGAGCTTTGGAAATACCAACCTTCACTACCTGAGTGGAGCA 1906
QY 440 snlybLeuCyegInPheSerProValGlnGluLeuSerg1uGlnThrProGlnThSerP 460
Db 1907 ACAAGCTATGCAAGTCTCCCTGTTCAAGAACTATCGAGAGAGACTCCCGAAACCACTC 1966
QY 460 roaApLySGluGlnAlaSer1leProLyLeuGlnThrAlaArgProSerAaspSerg 480
Db 1967 CTGATTAAG 2026
QY 480 lnserybArgLeuHisSerValArgThrSerSerg1Yhrh1aGlnaGserLeuL 500
Db 2027 AGAGCAAGCATTTGATTCGTGATGAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2086
QY 500 euserProLeuHisArgSerg1YserValGlnaAspAntYrHisThrSerPheLeuPheG 520
Db 2087 TATCTCACTGCAATCAAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2146
QY 520 lYleuSerThrSerg1GlnHisLeuThrLySerAlaG1YleuG1YleuLySG1YrPh 540
Db 2147 GCCTTTCACACGAG 2206
QY 540 iSerAsp1leuAlaProGlnThrSerThrProSerLeuThrSerTriPyrPhea 560
Db 2207 ACTCGAATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACAGAGAGAGAGAGAGAG 2266
QY 560 lathrGluSerSerHisPheTyrSerAlaSerAla1leTyrG1YleuLySerAlaSerTyrS 580
Db 2267 CCACAGAGCTCACTCACTTCTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCA 2326
QY 580 eR1a1YserCySerg1uLeuProThrCySG1YaspGlnValYrSerValArgArg 600
Db 2327 CTGCTTACAGCTGACGAG 2386
QY 600 rGlnLyPProSerAspArg1aAspSerArgaGserTTPH1eGlnG1uSerProPheG 620
Db 2387 GCGAG 2446
QY 620 lulyGlnPheLyArgArgSergCySg1InetGlnPheG1YglnSer1leMetSerg1uA 640
Db 2447 AAAAGAGATTAAACGAG 2506
QY 640 snatGserArgGlnGlnLeuG1YySvalG1YserGlnSerSergPheSerg1YserMetG 660
Db 2507 ACAAGTACCGAG 2566
QY 660 lulle1leGlnu1Ser 665
Db 2567 AAATCATTTGAGTCTCC 2583

RESULT 18
US-10-357-930-20969
/ Sequence 20969, Application US/10357930
/ Publication No. US20040259086A1
/ GENERAL INFORMATION:
/ APPLICANT: Schlegel, Robert
/ APPLICANT: Endege, Willem
/ APPLICANT: Monahan, John
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
/ TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
/ FILE REFERENCE: HUMAN PROSTATE CANCER
/ CURRENT APPLICATION NUMBER: US/10/357,930
/ PRIOR FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: 09/785,276
/ PRIOR FILING DATE: 2003-02-16
/ PRIOR APPLICATION NUMBER: 60/183,319
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: 60/189,862
/ PRIOR FILING DATE: 2000-03-16
/ PRIOR APPLICATION NUMBER: 60/207,454

QY 420 heserSerg1uasp1aleuG1uYrTyrTyrPserThrThrLeuaspG1YThra 440
Db 1847 TCTCTCATCAAGAGAGCTTTGGAAATACCAACCTTCACTACCTGAGTGGAGCA 1906
QY 440 snlybLeuCyegInPheSerProValGlnGluLeuSerg1uGlnThrProGlnThSerP 460
Db 1907 ACAAGCTATGCAAGTCTCCCTGTTCAAGAACTATCGAGAGAGACTCCCGAAACCACTC 1966
QY 460 roaApLySGluGlnAlaSer1leProLyLeuGlnThrAlaArgProSerAaspSerg 480
Db 1967 CTGATTAAG 2026
QY 480 lnserybArgLeuHisSerValArgThrSerSerg1Yhrh1aGlnaGserLeuL 500
Db 2027 AGAGCAAGCATTTGATTCGTGATGAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2086
QY 500 euserProLeuHisArgSerg1YserValGlnaAspAntYrHisThrSerPheLeuPheG 520
Db 2087 TATCTCACTGCAATCAAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2146
QY 520 lYleuSerThrSerg1GlnHisLeuThrLySerAlaG1YleuG1YleuLySG1YrPh 540
Db 2147 GCCTTTCACACGAG 2206
QY 540 iSerAsp1leuAlaProGlnThrSerThrProSerLeuThrSerTriPyrPhea 560
Db 2207 ACTCGAATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACAGAGAGAGAGAGAGAG 2266
QY 560 lathrGluSerSerHisPheTyrSerAlaSerAla1leTyrG1YleuLySerAlaSerTyrS 580
Db 2267 CCACAGAGCTCACTCACTTCTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCA 2326
QY 580 eR1a1YserCySerg1uLeuProThrCySG1YaspGlnValYrSerValArgArg 600
Db 2327 CTGCTTACAGCTGACGAG 2386
QY 600 rGlnLyPProSerAspArg1aAspSerArgaGserTTPH1eGlnG1uSerProPheG 620
Db 2387 GCGAG 2446
QY 620 lulyGlnPheLyArgArgSergCySg1InetGlnPheG1YglnSer1leMetSerg1uA 640
Db 2447 AAAAGAGATTAAACGAG 2506
QY 640 snatGserArgGlnGlnLeuG1YySvalG1YserGlnSerSergPheSerg1YserMetG 660
Db 2507 ACAAGTACCGAG 2566
QY 660 lulle1leGlnu1Ser 665
Db 2567 AAATCATTTGAGTCTCC 2583

US-10-029-345A-109 (1-665) x US-10-357-930-20969 (1-5145)
QY 1 Met1aHsGluMet1leG1YThrGln1leValThrGluArgLeuVal1a1euleuGln 20
Db 589 ATGGCCATGAG 648
QY 21 SerG1YThrGluLySValleuLeu1leAaspSerArgProPheValG1uYrAsnThrSer 40
Db 649 AGTGAG 708
QY 41 His1leuGlnAla1leAen1leAncySeryLyLeuMetLybArgArgLeuGln 60
Db 709 CACATTTTGGAG 768
QY 61 AspLyValleu1leThrGlnLeu1leGlnHisSerAlaYbHisLyVal1a1leasp 80
Db 769 GACAAAGTATTATTCAG 828
QY 81 CySerg1uLySVal1a1leVal1YrAspGlnSerSerg1aAspVal1a1leSerLeuSer 100
Db 829 TGCAATGAG 108
QY 101 AspCyPheLeuThrValleuLeuG1YySvalG1YserPheAaspSerVal1a1leu 120
Db 889 GACTGTTTCTCACTGAG 948
QY 121 leu1aG1YyPheAlaGlnPheSerArgCyPheProG1YleuCySG1uG1YySer 140
Db 949 CTTCAG 1008
QY 141 ThrLeuValProThrCyHisSerGlnProCyLeuProVal1a1aen1leG1YProThr 160
Db 1009 ACTTAG 1068
QY 161 Arg1leuProAsnLeu1YrLeuG1YCyGlnArgAspVal1leuAsn1ySG1uG1Yleu 180
Db 1069 CGAATTTCTCCCAATCTTATCTTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1127
QY 181 -GlnGlnAsn1Y1leG1YrVal1leuAsn1a1SerTyr-ThrCySProLyPProasp 200
Db 1128 GAG 1186
QY 200 he1leProGluSerHisPheLeuArgVal1ProValaAspSerPheCySG1uYy1leu 220
Db 1187 TTATCCCGAGAGTCACTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1246

QY 220 euProTIPLeuAspLysSerValAspPheIleGluValAlaValAspAsnGlyCysV 240
 Db 1247 TGCGCTGGTGGACAAATTCAGTATTCATTGAGAAAGCAAAAGCCTCCAAATGAGATG 1306
 QY 240 alleuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleM 260
 Db 1307 TTTCAATGCGACTGTTTGTAGCTGGGATCTCCGCTCCGACCATGCTATGCGCTACAC 1366
 QY 260 eLysValGlyMetAspMetSerLeuAsnAspGluAlaTyrArgPheValIleGluValArgPro 280
 Db 1367 TGAAGAGATGAGATGCTTTAGATAGAGCTTACAAATTTTGAAAAAGAAAGACCTTA 1426
 QY 280 hrIleSerProAsnPheAsnPheLeuGlyIleLeuLeuAspTyrGlyIleValIleVal 300
 Db 1427 CTAAATCTCCAAATTCATATTTTCTGGGCCAACTCCGAGCTATGAGAAAGAGTTTAA 1486
 QY 300 enGlnThrGlyValAspGlyProLysSerLysLeuValLeuLeuHisLeuGluValPro 320
 Db 1487 ACCAGACTGGAGCATCAGGCGCAAAAGCAAACTCAAGCTGCTGCACTGGAGAGACCA 1546
 QY 320 enGluProValProAlaValSerGluGlyIleGlyIleValSerGluThrProLeuSerPro 340
 Db 1547 ATGAACCTGTCCTGCTGCTCAGAGGAGTGGACGAAAGGAGAGACGCGCTCAGTCCAC 1606
 QY 340 roCysAlaAspSerAlaThrSerGluAlaAlaGlyIleArgProValHisProAlaSerV 360
 Db 1607 CCGTGGCGACTGCTGCTACCTCAGAGGACAGAGCAAAAGCCGCTGCTACCTCCGCGCAG 1666
 QY 360 alProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAla 380
 Db 1667 TGCCCAACGTCGCCAGAGGTGACAGCGCTGCTGTTAGAGAGACAGCCGCTGATACAGGCG 1726
 QY 380 euSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAlaValLeuValArgSerP 400
 Db 1727 TCGAGTGGCTGCACCTTCCGACAGACGCTGGAAAGCACCAATTAACCTCAAGGTTCTC 1786
 QY 400 heSerLeuAspIleLeuSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyP 420
 Db 1787 TCTCTCGGATTCAAATTCAGTTTCATATTCAGCCAGCATGCGAGCATCTTACATGGCT 1846
 QY 420 heSerSerSerGluAspAlaLeuGluTyrTyrIleValProSerThrThrLeuAspGlyTh 440
 Db 1847 TCTCCTCATCAGAAAGATGCTTTGGAAATACAAACCTTCACATCTGATGGAGCA 1906
 QY 440 enLysLeuValGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerP 460
 Db 1907 ACAAGCTATGCGCAATCTCTCCCTGTTAGAGAACTATGAGAGCACTCCGAAACCCAGTC 1966
 QY 460 roAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSerG 480
 Db 1967 CTGATTAAGAGAGAGCCAGCATCCCAAGAGGCTGCAAGCCGCGCATCTTCAGACAGCC 2026
 QY 480 InSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500
 Db 2027 AGAGCAAGCGATTCGATTCGATTCGAGAACGAGCACTGAGCAACGCGCCAGAGGCTCTT 2086
 QY 500 euSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheG 520
 Db 2087 TATCTCCACTGCATCGAAGTGGAGCTGAGAGCAATTCACACACAGCTTCCTTTTCG 2146
 QY 520 LysLeuSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLeuValGlyTyrP 540
 Db 2147 GCGCTTTCACACGACGACGACGACCTTCAGAAAGTTCGCTGGCTCGGAGCTTTAAGGCTGGC 2206
 QY 540 LysSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrTyrPhe 560
 Db 2207 ACTCGATATCTTGGCCCCCAGACCTTACCCCTTCCTGACAGAGAGCTGGATTTTGG 2266
 QY 560 LanthRgUserSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrS 580
 Db 2267 CCAGAGAGTCTCTCACCTTCTACCTGCTCAGGCACTCAGGAGGAGGAGGAGGAGGAGTACT 2326
 QY 580 eraLathRgUserCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArg 600

Db 2327 CTCCTACAGCTGCACGACGATGCCCATTCGCGAGACCAAGCTATTCTGTGCGGAGCG 2386
 QY 600 rglInLysProSerAspAlaValAlaAspSerArgArgSerThrPHisGluGluSerProPheG 620
 Db 2387 GGCAGAGCGCAAGTGTGACAGAGCTGACTCCGCGGAGCTGGCAATGAAAGAGAGCCCTTTG 2446
 QY 620 LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMetSerGluVal 640
 Db 2447 AAAAGCATTTTAAACCCAGAGCTGCCAAATGAAATTTGGAGAGACATCATTCAGAGA 2506
 QY 640 snArgSerArgGluGluLeuGlyValGlySerGlnSerPheSerGlySerMetG 660
 Db 2507 ACAGGTACCGGAGAGAGCTGGGAGAAAGTGGAGAGTCAAGTCTACTTTTGGCGCAGCATGG 2566
 QY 660 LulleIleGluValSer 665
 Db 2567 AAATCATTTGAGGTCTCC 2583

RESULT 19

US-10-357-930-21071
 ; Sequence 21071, Application US/10357930
 ; Publication No. US20040259086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Endege, Wilton
 ; APPLICANT: Monahan, John
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 ; FILE REFERENCE: MRI-0078CN
 ; CURRENT APPLICATION NUMBER: US/10/357,930
 ; CURRENT FILING DATE: 2003-02-04
 ; PRIOR APPLICATION NUMBER: 09/785,276
 ; PRIOR FILING DATE: 2003-02-16
 ; PRIOR APPLICATION NUMBER: 60/183,319
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: 60/189,862
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/207,454
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/211,314
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: 60/219,007
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: 60/255,281
 ; PRIOR FILING DATE: 2000-12-13
 ; NUMBER OF SEQ ID NOS: 62232
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 21071
 ; LENGTH: 5145
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1, 5144, 5145
 ; OTHER INFORMATION: n = A, T, C or G
 ; US-10-357-930-21071

Alignment Scores:

Pred. No.: 0 Length: 5145
 Score: 472.00 Matches: 663
 Percent Similarity: 99.408 Conservative: 0
 Best Local Similarity: 99.408 Mismatches: 2
 Query Match: 70.984 Indels: 4
 DB: 18 Gaps: 0

US-10-029-345A-109 (1-665) x US-10-357-930-21071 (1-5145)

QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
 Db 589 ATGGCCCATGAGATGATGTAATTCGAACTCAAAATTTGATGAGAGGATGCTGCTGCGAA 648

QY 21 SerGIYThrGluValLeuLeuIleIleAspSerArgProPheValGluTYraThrSer 40
DB 649 AGTGAACGGAAAAAGTCTCTTAATGATGACCGGCGCATTTGGGAATACATATACATCC 708
QY 41 HisIleLeuGluValIleAsnIleAsnCYseSerIysLeuMetLysArgGlyLeuGln 60
DB 709 CACATTGGAAGGCATTAATATCACTGCTCCAAAGCTTATGAAGCGAAGTTGCAACAG 768
QY 61 AspLysValLeuIleThrGluLeuIleGlnHisSerLysAlaYshIstLysValAspIleAsp 80
DB 769 GACAAAGTTAATTAACAGACTCATCCAGATTCACGCAAAACATAGGTGACATGAT 828
QY 81 CysSerGlnLysValValValTYraAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
DB 829 TGCAGTCAGAAAGTTGATGTTTACGATCAAAAGCTCCCAAGATTTCTCTCTCTCA 888
QY 101 AspCysPheLeuThrValIleLeuGluLysLysLeuGluLysSerPheAsnSerValHisLeu 120
DB 889 GACTGTTTCTCACTGACTTCTGGGGTAACTGGAGAAAGCTTCAACTCTGTCACCTG 948
QY 121 LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGlyLeuGluGlyLysSer 140
DB 949 CTTCGAGGTGGTTTCTGAGTTCTCTCGTTGTTCCCTGAGCTCTGTGAAGAAAATCC 1008
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
DB 1009 ACTCTAGTCCCTAAGCTGATTCAGACCTGCTTACCTGTTGCCAATTTGGGCCAAC 1068
QY 161 ArgIleLeuProAsnLeuTYrLeuGlyCysGlnArgAspValIleAsnLysGlnLeuIle 180
DB 1069 CGAATTCCTCCCAATCTTATCTTGTGCTGCCAGCAAGATGTCCTCAACAGAGACTAT 1127
QY 181 -GlnGlnAsnGlyIleGlyTYrValLeuAsnAlaSerTYr-ThrCysProLysProAsp 200
DB 1128 GAGCAGAAATGGAGATGGTATGTTAAATGCCAGCA-TACCTGTCCAAGCTGACT 1186
QY 200 HeIleProGlnSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIle 220
DB 1187 TTATCCCCGAGCTCATTTCCGTGGTGGCTGCGAATGACAGCTTTTGTGAAGAAAATTT 1246
QY 220 euProThrLeuAspLysSerValAspPheIleGluValAlaYshIleAsnGlyCysVal 240
DB 1247 TGCCGTGTGGACAATCAATCAATGATTCATTTGGAAGCAAAAGCTCCAAATGATG 1306
QY 240 AlLeuValHisCysLeuAlaGlyIleSerArgSerLysAlaThrIleAlaIleAlaTYrIle 260
DB 1307 TTCTAGTGCACCTTTAGCTGGATCTCCGCTCCGACCATGCTATCGCTCATCA 1366
QY 260 eLysArgMetAspMetSerLeuAspGluAlaTYraArgPheValLysGluLysArgPro 280
DB 1367 TGAAGAGATGACATGCTTTAGATGAGCTTACAGATTTGTGAAGAAAAGCAACTTA 1426
QY 280 hrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTYrGluLysValIleLys 300
DB 1427 CTATATCTCCAAATCTCAATTTCTGGGCCAACTCTGAGCATATGAGAAAGATTAGA 1486
QY 300 snGlnThrGlyValAserGlyProLysSerLysLeuLysLeuLeuHisLeuGluLysPro 320
DB 1487 ACCAGACTGAGCATCAGGCGCAAGAGCAAACTCAAGCTGTGCACTTGAGAAACCA 1546
QY 320 snGluProValProAlaValSerGluGlyGlyLysSerGluThrProLeuSerPro 340
DB 1547 ATGAACCTGCTCTGCTGCTCAAGAGGTGACAAAGAGCAAGCGCCCTCAGTCAC 1606
QY 340 roCYaAlaAspSerAlaThrSerGluAlaAlaGlyLysArgProValHisProLysArg 360
DB 1607 CCTGTGCTCACTCTCACTCAAGAGCAGCAGCAAGCCCTGCTGATCCGCCAGCG 1666
QY 360 alProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAla 380
DB 1667 TGCCCAAGGTGCCAGCTGCAAGCGCTGCTTAAAGAGCAAGCCCTGCTGTAAGCGCG 1726
QY 380 euSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnLysLeuLysArgSer 400

DB 1727 TCAATGGAGCTGACCTGCTCCGACAGAGGCTGGAAAGACAAATAGCTCAAGCTTCT 1786
QY 400 heSerLeuAspIleLysSerValSerTYrSerAlaSerMetAlaAlaSerLeuHisGlyP 420
DB 1787 TCTCTGTGATATCAATATCAATGATGTTTCAATATTCACCGACAGCATGAGATCTTAATGCT 1846
QY 420 heSerSerSerGluAspAlaLeuGluTYrTYrLysProSerThrThrLeuAspGlyThra 440
DB 1847 TCTTCATCAGAAAGATGCTTGGAAATCTACAAACTTCCACTCTGATGGAGCA 1906
QY 440 snLysLeuCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerP 460
DB 1907 ACAAGCTAAGCCAGTTCTCCCTCTGTCAGAACTATCGAGACAGATCCCGAAACCAAGTC 1966
QY 460 roAspLysGluGluAlaSerIleProLysLysLeuGlnThrAlaArgProSerAspSer 480
DB 1967 CTGATTAAGAGAGAACCCAGCATCCCAAGAGCTGACAGCCGCAAGGCTTCAGACAGCC 2026
QY 480 InSerLysArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500
DB 2027 AGAGCAGAGCATGTCATTCGCTCAGAACCAAGCAGATGGACCGCCAGAGGCTCTT 2086
QY 500 euSerProLeuHisArgSerGlySerValGluAspAsnTYrHisThrSerPheLeuPhe 520
DB 2087 TATCTCACTGATCAAGTGGAGCGTGGAGGCAATTCACACACAGCTTCTTTTG 2146
QY 520 LysSerThrSerGlnGlnHisLeuThrLysSerAlaGlyLeuGlyLysValTYrPH 540
DB 2147 GCCTTTCACACAGCAGACAGACACTCAAGAACTGTGCTGGCCCTTAAAGGCTGGC 2206
QY 540 IAspSerIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTYrPhe 560
DB 2207 ACTGGATCTTGGCCCCCAGACCTTACCTCCCTCCAGACCACTGATTTTG 2266
QY 560 IaThrGlnSerSerHisPheTYrSerAlaSerAlaIleTYrGlyLysSerAlaSerTYrS 580
DB 2267 CCACAGAGCTCTCACTTCTACTCTGCTCAGCCATTCACGAGGAGCTGCACATCT 2326
QY 580 eAlaTYrSerCysSerGlnLeuProThrCysGlyAspGlnValTYrSerValArgArg 600
DB 2327 CTGCTACAGCTCAGACAGCTGCCCATTTGGAGAGCCAAATCTTATTTCTGTCAGAGC 2386
QY 600 rGlnLysProSerAspArgAlaAspSerArgArgSerTYrHisGluLysSerProPhe 620
DB 2387 GCGAAGAGCAATGACAGAGCTGACTCGCGGAGGCTGGCATGAAAGAGAGCCCTTG 2446
QY 620 LysGlnPheLysArgArgSerCysGlnMetGluPheGlyGluSerIleMetSerGlu 640
DB 2447 AAAAGCAGTTTAAACGCAAGAGCTCCAAATGGAATTTGGAGAGCATATGTCAGAGA 2506
QY 640 snArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetG 660
DB 2507 ACAGTTCAGGGAAAGCTGGGGAAAGTGGCAGTCACTTTCGGGAGCATGG 2566
QY 660 LysIleIleGlyValSer 665
DB 2567 AAATCATTGAAGTCTCC 2583

RESULT 20
US-10-357-930-21083
Publication 21083, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endesig, William
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FIDELITY REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04


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PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,119
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,114
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 21083
LENGTH: 5145
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 1, 5144, 5145
OTHER INFORMATION: n = A,T,C or G
US-10-357-930-21083

Alignment Scores:
Pred. No.: 0 Length: 5145
Score: 472.00 Matches: 663
Percent Similarity: 99.40% Conservative: 0
Best Local Similarity: 99.40% Mismatches: 2
Query Match: 70.98% Indels: 0
DB: 18 Gaps: 0

US-10-029-345a-109 (1-665) x US-10-357-930-21083 (1-5145)
QY 1 MetAlhIeGluNecIleGlyThrGlnIleValThrGluArgLeuValAlaLeuGlu 20
DB 589 ATGGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 648
QY 21 SerGlyThrGluValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
DB 649 AGTGAACGGAAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 708
QY 41 HisIleLeuGluAlaIleAlaIleAlaIleAlaIleAlaIleAlaIleAlaIle 60
DB 709 CACATTTTGGACCCATTAATATCACTGCTCCAGGCTTATGAGGAGGATGCAACG 768
QY 61 AspIleValLeuIleThrGluLeuIleGlnHisSerAlaIleHisIleValAspIle 80
DB 769 GACAAAGTGTTAATACAGAGCTCATTCACGATTCACGAAACATAGGTTGACATGAT 828
QY 81 CysSerGlnIleValValValValValValValValValValValValValValVal 100
DB 829 TGCAGTCAGAGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 888
QY 101 AspCysPheLeuThrValIleLeuLeuGlyValLeuGluValSerPheAlaIleLeu 120
DB 889 GACTGTTTCTCACTGACTTCTGGGTAACTGAGAGAGAGCTTCAACTGTTCACTG 948
QY 121 LeuAlaGlyValPheAlaGluPheSerArgCysPheProGlyLeuCysGluGlySer 140
DB 949 CTTCGAGGTGGGTGTGCTGAGTCTCTGTTGTTTCCCTGCTGCTGAGAGAGAGAT 1008
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAlaIleGlyProThr 160
DB 1009 ACTCTAGTCCCTACCTGCACTTCTCAGCCTTGCTTACCTGTTGCAACATGGGCAAC 1068
QY 161 ArgIleLeuProAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 180
DB 1069 CGAATCTTCCCAATCTTATCTTGTGCTGACGAGATGCTCTCAACAGAGAGCTGAT- 1127
QY 181 -GlnGlnAengIylIeGlyTyValLeuAlaIleSerTyr-ThrCysProIleProAsp 200

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DB 1128 GCAGCAGATGGGATGGTATGTTATGATGCAACA-TACCTGTCGAACCTGACT 1186
QY 200 heIleProGluSerHisPheLeuArgValProValaIleAspSerPheCysGluValIle 220
DB 1187 TTAATCCCAAGTCTCAATTCCTGCGGTGCTGTGATGATCAACCTTTTGGAAAAATTT 1246
QY 220 euProTrpLeuAspIleSerValAspPheIleGluValAlaValAspArgGlyCysV 240
DB 1247 TGCCGTGTTGCAAAATCATGATGATTTCTGAGGAGAGAGAGAGAGAGAGAGAGAG 1306
QY 240 alleuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIle 260
DB 1307 TTCTATGCACTGTTTATGCTGGGATCTCCGCTCGGCAACATCGGTATGCTTACATCA 1366
QY 260 eLlyAsArgMetAspMetSerLeuAspGluAlaTyrArgPheValIleGluValArgPro 280
DB 1367 TGAAAGAGATGACATGCTTTAGATGAAGCTTACGATTTTGGAAAAAGAAAGCTTA 1426
QY 280 hrIleSerProAlaPheAlaPheLeuGlyGluLeuAlaIleValIleValIleVal 300
DB 1427 CTATATCTCAAACTTCAATTTCTGAGCCAACTCTGAGCTATGAGAGAGATTTAAGA 1486
QY 300 engIleThrGlyAlaSerGlyProIleSerIleValIleLeuAlaIleValIlePro 320
DB 1487 ACCAGACTGAGATCAGAGGCGCAAGAGCAACTCAAGCTGCTGCACTGGAGAGCCAA 1546
QY 320 engIleProValProAlaValSerGluGlyGluIleValSerGluThrProLeuSerPro 340
DB 1547 ATGAACTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1606
QY 340 rocValaIleAspSerAlaThrSerGluAlaAlaGlyValIleProValaIleProVala 360
DB 1607 CCGTGCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1666
QY 360 alProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuValGlnAla 380
DB 1667 TGCCAGCGCTGCCAGCGCGAGCGCGCTGTTAAGAGACAGCGCGCTGTTAAGAGCG 1726
QY 380 euSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAlaIleValIleValIle 400
DB 1727 TCAGTGGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1786
QY 400 heSerLeuAspIleValSerValSerTyrSerAlaSerSerAlaIleSerLeuHisGly 420
DB 1787 TCTCTGATATCAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1846
QY 420 heSerSerSerGluAspAlaLeuGluTyrTyrIleAspSerThrThrLeuAspGlyThr 440
DB 1847 TCTCTCATCAAGATGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1906
QY 440 snIleLeuCysGlnPheSerProValGlnIleLeuSerGluGlnThrProGluThrSer 460
DB 1907 ACAAGCTATGCAAGTCTCCCTGTTCAAGAACTATCGAGAGAGATCTCCGAAACAG 1966
QY 460 roAspIleGluGluAlaSerIleProValIleLeuGlnThrAlaAspProSerAspSer 480
DB 1967 CTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2026
QY 480 IleSerValArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500
DB 2027 AGAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2086
QY 500 euSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPhe 520
DB 2087 TATCTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2146
QY 520 IlyLeuSerThrSerGlnGlnHisLeuThrIleSerAlaGlyIleLeuValGlyTyrHis 540
DB 2147 GCTTTTCCACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2206
QY 540 IeSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPhe 560

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Db 2207 ACTGGATATCTGGCCCCCAGACTCTACCCCTTCCTGACCAGAGCTGGTATTTG 2266
 QY 560 laThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrS 580
 Db 2267 CCAAGAGTCTCTCAACACTTCTACTCTCTCAAGCATTCTAGAGGAGGAGCCAGTTACT 2326
 QY 580 eraIaTyrSerCysSerGlnLeuProThrCysGlyIleAspGlnValTyrSerValArgAla 600
 Db 2327 CTGCTTACAGCTGACGACCACTGCTCCCACTTGCAGAGCCAAAGTCTATTCTGTGGCAGGC 2386
 QY 600 rGgInLysProSerAspArgAlaAspSerArgArgSerTrpHisGluGluSerProPheG 620
 Db 2387 GGCAGAACCCAGAGAGAGAGAGTGAAGTCTCGCGGAGGCTGGCATGAGAGAGACCCCTTTG 2446
 QY 620 luYsgInPheLysArgArgSerCysGlnMetGlnPheGlyGluSerIleMetSerGluAla 640
 Db 2447 AAAAGCAGTTTAAACGCAAGAGCTGCGCAATGGAATTTGAGAGAGCATCATGTCAGAGA 2506
 QY 640 snArgSerArgGluGluLeuGlyLysValGlySerGlnSerSerPheSerGlySerMetG 660
 Db 2507 ACAGGTCACCGGAAAGAGTGGGGAAGTGGGAGTCACTTTCGGGCGAGCATGG 2566
 QY 660 luIleIleGluValSer 665
 Db 2567 AATCATTTAGGCTCTCC 2583

RESULT 21

US-10-357-930-21303
 / Sequence 21303, Application US/10357930
 / Publication No. US20040259086A1
 / GENERAL INFORMATION:
 / APPLICANT: Schlegel, Robert
 / APPLICANT: Monahan, John
 / TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 / TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 / FILE REFERENCE: MRI-007BCN
 / CURRENT APPLICATION NUMBER: US/10/357,930
 / PRIOR FILING DATE: 2003-02-04
 / PRIOR APPLICATION NUMBER: 09/785,276
 / PRIOR FILING DATE: 2003-02-16
 / PRIOR APPLICATION NUMBER: 60/183,319
 / PRIOR FILING DATE: 2000-02-17
 / PRIOR APPLICATION NUMBER: 60/189,862
 / PRIOR FILING DATE: 2000-03-16
 / PRIOR APPLICATION NUMBER: 60/207,454
 / PRIOR FILING DATE: 2000-05-25
 / PRIOR APPLICATION NUMBER: 60/211,314
 / PRIOR FILING DATE: 2000-06-09
 / PRIOR APPLICATION NUMBER: 60/219,007
 / PRIOR FILING DATE: 2000-07-18
 / PRIOR APPLICATION NUMBER: 60/255,281
 / NUMBER OF SEQ ID NOS: 12-13
 / SOFTWARE: PaSeq for Windows Version 4.0
 / SEQ ID NO 21303
 / LENGTH: 5145
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: misc feature
 / LOCATION: 1, 5144, 5145
 / OTHER INFORMATION: n = A,T,C or G
 US-10-357-930-21303

Alignment Scores:

Pred. No.: 0
 Score: 472.00
 Percent Similarity: 99.40%
 Best Local Similarity: 99.40%
 Query Match: 70.98%
 Db: 18

Length: 5145
 Matches: 663
 Conservative: 0
 Mismatches: 2
 Indels: 4
 Gaps: 0

US-10-029-345a-109 (1-665) x US-10-357-930-21303 (1-5145)
 QY 1 MecAlaHisGluMetIleGlyThrGlnIleValIleThrGlnArgLeuValAlaLeuLeuGlu 20
 Db 589 ATGGCCCATGAGATGATTTGAACTCAAAATTTGTAAGAGAGGTGGTGGCTGGAGAA 648
 QY 21 SerGlyThrGlnLysValLeuLeuIleAspSerArgProPheValGluTyrAsnThrSer 40
 Db 649 AGTGAACCGGAAAGAGTGGCTGAATTTGATACCGGCACTTTGTGAATACATCATCC 708
 QY 41 HisIleLeuGlnAlaIleAsnIleAsnCysSerLysIleMetLysArgArgLeuGlnGln 60
 Db 709 CACATTTTGGAGCCATTATATTCATCTGCTCAAGCTTAATGAGCGGAAGGTTCAACAG 768
 QY 61 AspLysValLeuIleThrGlnLeuIleGlnHisSerAlaLysHisLysValAspIleAsp 80
 Db 769 GACAAAGTGTATTAATACAGAGCTCATCCAGCATTCAGCGAAACATTAAGTTGACATTGAT 828
 QY 81 CysSerGlnLysValValValIleTyrAspGlnSerSerGlnAspValAlaSerLeuSer 100
 Db 829 TGCAGTCAGAGAGTTGTAGTTTACGATCAAGCTCCAAAGATGTTGCTCTCTCTTCA 888
 QY 101 AspCysPheLeuThrValLeuLeuGlyLysLeuGluLysSerPheAsnSerValHisLeu 120
 Db 889 GACTGTTTTCTCAGTGTACTTCTGGGTAACATGGAAGAGCTTCATCTGTTCACCTG 948
 QY 121 LeuAlaGlyLysPheAlaGluPheSerArgCysPheProGlyLeuCysGluGlyLysSer 140
 Db 949 CTTCAGAGTGGTTTCTGCTGAGATCTCTCGTGTGTTCCCTGGCTCTGTGAAGGAAATCC 1008
 QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
 Db 1009 ACTTAGCCCTTACCTCACTTCTCAGCTTGTCTTACCTTCTCCAACTTGGGCCAACCC 1068
 QY 161 ArgIleLeuProAsnLeuTyrLeuGlyCysGlnArgAspValLeuAsnLysGluLeuIle 180
 Db 1069 CGAATTTCTCCCAATCTTATCTTGGCTGCCAGCGAGATGCTCTCAACAAGAGGCTGAT - 1127
 QY 181 -GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyr-ThrCysProLysProAsp 200
 Db 1128 GCAGCAAGATGGGATGGTTATGTGTTAATGCGAGCA-TCCTGTCCAAAGCCGTGACT 1186
 QY 200 helLeuProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluLysIle 220
 Db 1187 TTATCCCGAGTCTCATTTCTCGCGTCCCTGTAATACAGCTTTGTGAGAAATTT 1246
 QY 220 euProTyrLeuAspLysSerValAspPheIleGlnLysAlaLysAlaSerAsnGlyCysV 240
 Db 1247 TGCCTGTGTTGAGCAAAATCAGTACGATTTCAATTAAGAAAGCAAAAGCCCTCAATGATGTG 1306
 QY 240 alleuValHisCysIleuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleM 260
 Db 1307 TTTTATGTGACGTGTTAGCTGGAGATCTCCGCTCGGCAACCATGCTATGCTCATACNTA 1366
 QY 260 euLysArgMetAspMetSerLeuAspGluAlaTyrArgPheValLysGluLysArgProT 280
 Db 1367 TGAAGAGATGACATGCTTTAGTGAAGCTTACAGATTGTGAAAAAGAAAAAGAACTTA 1426
 QY 280 hrIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGlnLysLysIleLysA 300
 Db 1427 CTATATCTCCAAACTTCAATTTTCTGGGCCAACTCTGGAAGCTATGAGAAAGATTAGA 1486
 QY 300 enGlnThrGlyAlaSerGlyProLysSerLysLeuLysLeuHisLeuGlnLysProA 320
 Db 1487 ACCAAGCTGAGACATCAGGCGCCAAAGAGCAAACTCAAGCTGTGCACTTGGAGAAAGCCAA 1546
 QY 320 enGluProValProAlaValSerGluGlyGlnLysSerGluThrProLeuSerProP 340
 Db 1547 ATGAACCTGTCTCCGTGTCTCAAGAGGTGAGCAAGAAACGAGAGCCCTTCAATGCCAC 1606
 QY 340 roCysAlaAspSerAlaThrSerGlnAlaAlaGlyGlnArgProValHisProAlaSerV 360

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Db      1607  CCGTGGCCGACCTCTGCTACTCTACAGAGGACAGACAAAGGCCGTGATCCCGCAGCG  1666
Qy      360  aIProSeVaIProSeVaIgiNProSeLeuLeuGiuaPSeProLeuVaIgiNaIaI  380
Db      1667  TGCCACAGCGTGCACCGCGTGCAGCGCGTGCCTGTTAGAGAGACGCCCGCTGTGAACGGCGC  1726
Qy      380  euSeRgiLyeuNhiISeuSeRiLaPaRgLeuGiuaPSeRSeAsuLySeuLySaRgSeR  400
Db      1727  TCAGTGGGCTGCACTGTTCGGCAGACAGCTGGAGAGACAGCAATAGCTCAAGCGTTCTT  1786
Qy      400  heSeRLeuApRiLeuSeRSeVaISeRTrSeRiLaSeRMeLaIaIaSeRLeuNhiIgiLyP  420
Db      1787  TCTGCTCGATATCAATCAATCAATTCATATTCAGCCAGCATGGAGCATCTTACATGCT  1846
Qy      420  heSeRSeRSeRgiLuePaRiLaLeuGiUuTYTrLyLPProSeRThThRiLeuApRgiLYThRa  440
Db      1847  TCTCCTCATCAGAAATGCTCTTGGAAATCTCAAACTTCCATCTCGATGGAGCA  1906
Qy      440  anLySeuCyGgiLPhSeRProVaIgiNgiuSeRgiuNgiLThPProgiLunThSeR  460
Db      1907  ACAAGCTATGCGAGTGTCTCCCTGTTCAGAACTATCGAGACAGCTCCGAACCGATC  1966
Qy      460  roApRySeGiUuIaIaSeRiLePProLyLyLSeuGiNThRaIaRgProSeRAsPSeRg  480
Db      1967  CTGATPAAGAGAGAACCGACATCTCCCAAGAACTGCAACCCGACGCTTCAAGACCC  2026
Qy      480  InSeRyPaRgiLeuNhiISeRValaRgThRSeRSeRgiLYThRaIaIaRgSeRLeu  500
Db      2027  AGAGCAAGCGATTGCATTCGGTTCAGAACCAACAGACAGAGGACCGCCAGAGTCCCTTT  2086
Qy      500  euSeRProLeuNhiIaRgSeRgiLySeRValgiuPaRiThThiStHeSeRheLeuPheg  520
Db      2087  TATCTCCACTCATCGAAGTGGAGCGTGGAGAGAAATPACACACCGACTCTCTTTGCG  2146
Qy      520  lyLeuSeRThSeRgiNgiNhiISeuThRyLySeRiLaIeLygiLySeuLygiLyTrPh  540
Db      2147  GCTTTTCAACCAAGCAGACACACTCAAGAACTGCTGCGCTGGGCTTAAAGGCTGCG  2206
Qy      540  IsSeRAsPileuNaIaProgiNThRSeRThProSeRLeuThSeRSeRTrPyRhea  560
Db      2207  ACTCGGATATCTTGCCCCCAGACCTTACCCCTTCCCTGACAGCAGCTGATATTTTG  2266
Qy      560  IaThRgiuSeRThiIaPheRySeRiLaSeRiLaIeLygiLygiLySeRiLaSeRTrys  580
Db      2267  CCACAGAGTCTCAACTCTACTCTGCTCAGCCATCTAGGAGGACAGTCCAGTTACT  2326
Qy      580  eRaIaTySeRSeRgiNgiuPProThCyGgiLAsPgiLvaITrSeRValaRgRga  600
Db      2327  CTGCTTACAGCTGCAGCCAGCTGCCACTTTCGGAGACCAAGCTATTTCTGTGCGAGGC  2386
Qy      600  rGiNgiuPProSeRAsPaRgaIaPSeRiLaRgRSeRTrPhIaIgiuNgiuSeRProPheg  620
Db      2387  GCGAGAAACCAAGTACAGAGCTGACTCGCGCGGAGCTGGCAGTGAAGAGAGCCCTTTG  2446
Qy      620  luLygiNPhelYeRgRgSeRcyGgiNMeGiuphegiLygiuSeRiLeMeSeRgiua  640
Db      2447  AAAAGCAATTTAAACGCAAGAGCTGCCAAATGGAAATTTGGAGAGCATCTGTCAGAGA  2506
Qy      640  anPArSeRgiGgiuNgiuLeuGiLyLyVaIgiLySeRgiNSeRSeRPhSeRgiLySeRMeG  660
Db      2507  ACAAGTCCCGGGAAAGACTGGGGAAAGTGGGCACTGACTTACTTTTTCGGGACAGATGG  2566
Qy      660  luIeIaIeGiLvaISeR  665
Db      2567  AAATCATTTGAGGTCTCC  2583

RESULT 22
US-10-357-930-21307
; Sequence 21307, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Bndege, Wilborn

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APPLICANT Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21307
LENGTH: 5145
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 1, 5144, 5145
OTHER INFORMATION: n = A,T,C or G
US-10-357-930-21307

Alignment Scores:
Pred. NO.: 0 Length: 5145
Score: 472.00 Matches: 663
Percent Similarity: 99.40% Conservative: 2
Best Local Similarity: 99.40% Mismatches: 2
Query Match: 70.98% Indels: 4
DB: 18 Gaps: 0

US-10-029-345A-109 (1-665) x US-10-357-930-21307 (1-5145)
QY 1 MetLAHsgUwcttIegLYthGlnlIeValThrgUwgleuValAlaleuLeuGln 20
DB 589 ATGGCCCATGAGATGATGGAACTCAATGTTACTGAGAGTGGCTGCTCTGTGAA 648
QY 21 SerGlyThrgUwysValleuLeuIleAspSerArpPropheValGluTyraAsnThSer 40
DB 649 AGTGAACGGGAAAGGCTGCTAATGATGACCGGCCCATTTGGGAATACATACATCC 708
QY 41 HisIleuGlnAlaIleAsnIleAsnCysSerIysleuWctLYsArGArgLeuGlnGln 60
DB 709 CACATTTTGGAGAGCATTAATATCACTGCTCCAGCTTAAGAAAGCGAAGTTGCACAG 768
QY 61 AspIysValleuIleThrgUleuIleGlnHisSerAlaIysHisIysValAspIleAsp 80
DB 769 GACCAAGTGTTAATTAACAGAGCTCATCAGCATTCAGCGAAACATTAAGTTGACATTGAT 828
QY 81 CysSerGlnIysValIleValIleTyraAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
DB 829 TGCAGTCAGAAAGGTGGATTTACAGATCAAGCTCCCAAGATGTGGCTCTCTCTTCA 888
QY 101 AspSpysPheLeuThrValleuLeuGlyIysleuGlnIysSerPheAsnSerValHisleu 120
DB 889 GACGTGTTTCTCACTGATTAATCTTCGGGTAATCGAAGAAAGCTTCAACTCTGTTCACTG 948
QY 121 LeuAlaGlyIyPheAlaGlnPheSerArGysPheProGlyIeuCyrgIuGlyIysSer 140
DB 949 CTTGCAAGTGGGTGTGCTGAGTTCTCTCGTGTGTTCCCTGCGCTCTGTGAAGGAAATCC 1008
QY 141 ThrIeuValProThrCysIleSerGlnProCysleuProValAlaAsnIleGlyProThr 160

```

Db 1009 ACTGATGCTTACCTGATTTCTCAGCGTTCTTACCTTGTGCAACATTTGGGCCAAC 1068
Qy 161 ArgilleuProantleuTyrrleuGlyCyeglnArgapValleuanslysgluleuile 180
Db 1069 CGAATTTCTTCCCAATCTTTATCTTGGCTGCAGAGATGTCTTCAACAAGAGGCTGAT- 1127
Qy 181 -GlnGlnasnglylTleGlyTyrrValleuAenAlasertYr-ThrCysProlyspProasp 200
Db 1128 GCAGCAAGATGGAGTTGGTTATGTATGCTTAATGCCACCA-7ACCTGTCCAAAGCCGTGACT 1186
Qy 200 heileProGlyuserHisPheleuArgValProValasnapserPheCysglusilel 220
Db 1187 TTTATCCCGAGTCTCAATTTCTTCCGCTGTGTGATGACAGCTTTGTGAGAAATTT 1246
Qy 220 eufProTlPleuAspLysSerValaAppheleGlnlyValaValasleuArglyCysv 240
Db 1247 TGCCGTTGGTTGCAACATAGTAGATTTCATTTGAGAAACAAACCTTCCATGTGATGTG 1306
Qy 240 alleuValHsCyelValaGlylTleSerArgSerAlaThrTleAlaTleAlaTyrTle 260
Db 1307 TTTCTAGTGCACGTGTTTACCTGGGATCTCCGCTCCGCCACCATGTGCTATCCCTACATCA 1366
Qy 260 eelYsArgMetAspMetSerleuAspGlnAlaTyrArgPheVallysglnlyArgProt 280
Db 1367 TGAAGAGATGACATGTCTTTAGATGAAGCTTACAGATTGTGAAGAAAGAAAGACCTTA 1426
Qy 280 hrlTleSerProAsnPhaenPheleuGlyGlnleuLeuAspTyrGlnlyValylTleYsA 300
Db 1427 CTATATCTCCAACTTCAATTTCTTGGGCCAACTCTTGAGCTTATGAGAAAGATTAGA 1486
Qy 300 snglTnHrGlyAlaSerGlyProlysserlyleuYsleuLeuHsleuGlnlyspPro 320
Db 1487 ACCAAGCTGAGACATCAGGGCCAAAGACAACTCAAGCTGTGCACCTGAGACAGCA 1546
Qy 320 snglUProValProAlaValserGlyGlyGlnlyYsSerGlyTnHrProleuSerPro 340
Db 1547 ATGAACCTGCTCCCTGTGTCTCAGAGGGTGGACAGAAACGAGACGCCCTTAGTCTCAC 1606
Qy 340 roCyAlaAspSerAlaThrSerGlnAlaAlaGlyGlnArgProValHsProAlaSerY 360
Db 1607 CTTGTGCCGACTGTGCTTACCTCAGAGGACAGACAGACAAAGCCCGTGCATCCGCCAGCG 1666
Qy 360 alProSerValProSerValGlnProserleuGlnUasPserProleuValGlnAla 380
Db 1667 TGCCACAGTGGCCAGCGTGCAGCGTCTGTTAGAGACACCCGCTGTGACAGCGCC 1726
Qy 380 euserGlyleuHsleuSerAlaAspArgleuGlnUasPserAnlyleuYsArgSerP 400
Db 1727 TCACTGGGCTGCACCTGTCCGACAGACAGCTGAGAAACAGCAATAGCTCAAGCCTTCT 1786
Qy 400 heserleuAspLyleYsSerValSerTyrSerAlaSerMetAlaAlaSerleuHsGlyP 420
Db 1787 TCTCTCGATATCAATCATGTTCTTCAATTCAGCAGCATGGCAGATCTTAACTGCT 1846
Qy 420 heserSerSerGlnUasPAlaUeGlyTyrTyrlyspProserThrThrleuAspGlyThra 440
Db 1847 TCTCTCATAGAAAGATGCTTGGATATCTAACAACCTTCACTCATCTGTGATGGAGCA 1906
Qy 440 snlyleuCyGlnPheSerProValGlnUleuSerGlnUlnHrProGlnThrSerP 460
Db 1907 ACAAGCTAGCCAGTCTTCCCTCTTCCAGAACTATCGAGACAGATCTCCCAAAACAGTC 1966
Qy 460 roAspLyGlnUalaserlTleProlylyleuGlnThrAlaArgProserAspserg 480
Db 1967 CTGATTAAGAGAGACAGCATCCCAAGAGCTGCAACCGCAGGCTTCAAGACGCC 2026
Qy 480 InserlyArgleuHsSerValaArgThrSerSerSerGlyThrAlGlnArgSerleu 500
Db 2027 AAGAGCAAGCATTTGATTCGGTCAGAACACACACAGTGGCAGCCGACAGAGTCCCTTT 2086
Qy 500 euserProleuHsArgSerGlySerValGlnUasPAnlyThraThrSerPheleuPheg 520
Db 2087 TATCTCCATCTGATGAGTGGAGCGTGGAGGACATTTACACACAGCTTCTTTTGG 2146

Qy 520 lyleuSerThrSerGlnGlnHsleuThrlySerAlaGlyleuGlyleuYsGlyTTPH 540
Db 2147 GCTTTTCACACACAGCAGACACTTCAAGATGTGTGCTGTGGCCCTTAAAGGCTGGC 2206
Qy 540 liserAspLileuAlaProGlnThrSerThrProSerleuThrSerSerTTPYrPhea 560
Db 2207 ACTCGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGTAGCCAGCAGCTGTGATTTTG 2266
Qy 560 lathrGlySerSerHsPheTyrSerAlaSerAlaTleTyrGlyGlySerAlaSerTyrS 580
Db 2267 CCAAGAGTCCACACATTTCTACTGTGCTGCTGAGCATCTAAGAGGAGGAGTCCAGTTACT 2326
Qy 580 exAlaTyrSerCyserGlnleuProThrCysGlyAspGlnValTyrSerValArgArg 600
Db 2327 CTGCCACAGCTGCAGCCAGCTGTCCACTTGCAGAGACAAAGTATATCTGTGGCAGGC 2386
Qy 600 rGlnlyspProSerAspArgAlaAspSerArgSerTTPHleGlnUleuSerProPheg 620
Db 2387 GGCAGAGCCAGTGAAGAGCTGACTGCGCGGAGCTGGCATGAAGAGAGCCCTTTG 2446
Qy 620 lUlyGlnPheYsArgArgSerCyGlnMetGlnUeGlyGlyUserTleMetSerGlnUa 640
Db 2447 AAAAGCATTTTAAAGCAGAAAGCTGCCAAATGGAAATTTGAGAGAGCATCATGCAGAG 2506
Qy 640 snArgSerArgGlnUleuGlyYsValGlySerGlnSerSerPheSerGlySerMetG 660
Db 2507 ACAGGTCAAGGAGAGCTGGGGAAGTGGGCACTGACTTACTTCTTCTGGGAGCATGG 2566
Qy 660 lUlleGlnUalSer 665
Db 2567 AAATCATTAAGTCTCC 2583

RESULT 23
US-10-357-930-22820
Sequence 22820, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
FILE REFERENCE: MRI-0078CN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22820
LENGTH: 5145
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 1, 5145
OTHER INFORMATION: n = A,T,C or G
US-10-357-930-22820

Alignment Scores:

Pred. No.: 0
 Score: 472.00
 Percent Similarity: 99.408
 Best Local Similarity: 99.408
 Query Match: 70.988
 DB: 18

Length: 5145
 Matches: 663
 Conservative: 0
 Mismatches: 2
 Indels: 4
 Gaps: 0

US-10-029-345a-109 (1-665) x US-10-357-930-22820 (1-5145)

QY 1 MetAlHIGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGln 20
 DB ATGGCCCATGAGATGATTGGAATCAATGTTACTGAGAGGTGGTGGCTCTGCTGAA 648
 QY 21 SerGlyThrGlnIleValLeuLeuIleAspSerArgProPheValGlnIleThrSer 40
 DB AGTGAACGCAAAAGATGCTGCTAATGTAAGCCGCCAATTTGTGAAATACAAATACATCC 708
 QY 41 HisIleLeuGlnIleAlaIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIle 60
 DB CACATTTTGGAGCCATTATATATCACTGCTCCAGCTTATGAAAGCGAGTTGGCAACAG 768
 QY 61 AspIleValLeuIleThrGluLeuIleGlnIleSerIleAlaIleValIleAspIleAsp 80
 DB GACAAAGTGTATTAACAGAGCTCATCCAGCATTCAGCGAAACATTAAGGTGACATTGAT 828
 QY 81 CysSerGlnIleValIleValIleValIleValIleValIleValIleValIleValIle 100
 DB TCGAGTCAGAAAGGTGTAGTTACGATCAAAAGCTCCCAAGATGTTCTCTCTCTTCA 888
 QY 101 AspCysPheLeuThrValLeuLeuGlyIleValLeuGlyIleValLeuIleValIle 120
 DB GACTGTTTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 948
 DB 949 CTGACAGTGGGTTTCTGAGTCTCTCGTTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1008
 QY 141 ThrIleValIleProThrCysIleSerGlnIleProCysIleProValIleAsnIleGlyProThr 160
 DB 1009 ACTCTGATCTCCATCCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1068
 QY 161 ArgIleLeuProAsnLeuIleGlyIleValIleValIleValIleValIleValIle 180
 DB 1069 CGAATCTTCCCAATCTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1127
 QY 181 -GlnIleAsnGlyIleGlyIleValIleValIleValIleValIleValIleValIle 200
 DB 1128 GAGCAGAGATGGGATGGTATGTTATGTTAATGCCAGCA-TACCTGTCAGAAAGCTGACT 1186
 QY 200 IleIleProGluSerHisPheLeuArgValIleProValIleAsnAspSerPheCysGlyIleValIle 220
 DB 1187 TTAATCCCAAGTCTCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1246
 QY 220 AspProIleLeuAspIleValIleValIleValIleValIleValIleValIleValIleValIle 240
 DB 1247 TGGCGGTGGTGGCAATCAATGATTTCAATGAAAGCAAAAGCTCCCAATGAGATGG 1306
 QY 240 AlIleValIleCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaIleAlaIleAla 260
 DB 1307 TTCTATGACCTGTTAGCTGGGATCTCCCGCTCCCGCAACATCGTATGCGCTATACATA 1366
 QY 260 eLysArgMetAspMetSerLeuAspGlnAlaIleValIleValIleValIleValIleValIle 280
 DB 1367 TGAAGGATGAGCATGCTCTTATGATGAAGCTTACAGATTTGTGAAGAAAGAAAGCTCA 1426
 QY 280 hrlIleSerProAsnPheAsnPheLeuGlyIleLeuLeuAspIleValIleValIleValIleValIle 300
 DB 1427 CTAATATCTCCAACTCAATTTCTGGGCACTCTCGACTATGAGAAAGAAATTAAGA 1486
 QY 300 snGlnThrGlyIleSerGlyProIleSerIleValIleValIleValIleValIleValIleValIle 320
 DB 1487 ACCAGCTGGAGCATGAGGCGCAAAAGCAAACTCAAGCTGCTGCACTGGAGAAAGCA 1546

QY 320 snGlnProValIleProAlaValIleSerGlnGlyIleValIleValIleValIleValIleValIleValIle 340
 DB 1547 ATGAACCTGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1606
 QY 340 roCysAlaAspSerAlaThrSerGlnIleAlaIleGlyIleValIleValIleValIleValIleValIle 360
 DB 1607 CCTGTGCGGACTCTGCTACCTGAGGCGCAGCAAAAGGCGCGGTGATCCCGCAGCG 1666
 QY 360 AlProSerValIleProSerValIleProSerLeuLeuGlnIleAspSerProLeuValIleGlnAla 380
 DB 1667 TCCCAAGCTGCGCCAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1726
 QY 380 SerSerGlyLeuHisIleSerAlaAspArgLeuGlnIleAspSerAlaValIleValIleValIleValIle 400
 DB 1727 TCAAGGCTGCACTGCTGCGCAAGAGCTGAGAGCAAGCAATAGCTCAAGCTTCCCT 1786
 QY 400 hSerLeuAspIleIleValIleValIleValIleValIleValIleValIleValIleValIleValIle 420
 DB 1787 TCTCTGGAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1846
 QY 420 hSerSerSerGlnIleValIleValIleValIleValIleValIleValIleValIleValIleValIle 440
 DB 1847 TCTCTCATCAAGAAAGTCTTGAATCTACAAACCTTCCACTCTGATGGAGCA 1906
 QY 440 snIleValIleGlnIleProValIleGlnIleValIleValIleValIleValIleValIleValIleValIle 460
 DB 1907 ACAAGCTAGCCAGATCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1966
 QY 460 roAspIleGlnIleValIleValIleValIleValIleValIleValIleValIleValIleValIleValIle 480
 DB 1967 CTGATTAAGAGGAGAACCCAGCATCCCAAGAACTGCAAGCCGAGGCTTCAAGACGC 2026
 QY 480 IAsnIleValIleValIleValIleValIleValIleValIleValIleValIleValIleValIleValIle 500
 DB 2027 AGAGCAAGGATGATTCGTCAGAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2086
 QY 500 snSerProLeuHisArgSerGlyIleValIleValIleValIleValIleValIleValIleValIleValIle 520
 DB 2087 TATCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2146
 QY 520 ILeuSerThrSerGlnIleHisIleValIleValIleValIleValIleValIleValIleValIleValIle 540
 DB 2147 GCTTTTCCACGAGCAGAGACGACCTTCAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2206
 QY 540 IAspSerIleLeuAlaProGlnIleThrSerThrProSerLeuThrSerSerThrIlePheAla 560
 DB 2207 ACTCGAATATCTGAGCCCGCCAGACCTCAACCTTCCCTGACAGAGCTGTGATTTTG 2266
 QY 560 IaThrGluSerSerHisPheThrSerAlaSerAlaIleThrGlyIleSerAlaSerIleValIleValIle 580
 DB 2267 CCACAGAGCTCCACACATTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2326
 QY 580 eAlaIleThrSerCysSerGlnIleProThrCysGlyAspGlnIleValIleValIleValIleValIleValIle 600
 DB 2327 CTGCTTACAGCTGACGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2386
 QY 600 IrgIleValIleProSerAlaIleValIleValIleValIleValIleValIleValIleValIleValIleValIle 620
 DB 2387 GGCAGAGGCAAGTACAGAGCTGACTCGCGGAGAGCTGAGCATGAGAGAGAGAGAGAGAGAGAGAGAG 2446
 QY 620 IuIleGlnIlePheIleValIleValIleValIleValIleValIleValIleValIleValIleValIleValIle 640
 DB 2447 AAAGCAGATTAAAGCAGAAAGCTCCCAATGAAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2506
 QY 640 snArgSerArgIleValIleValIleValIleValIleValIleValIleValIleValIleValIleValIleValIle 660
 DB 2507 ACAAGTCAAGGAGAAAGCTGGGAGAAAGTGGAGATCAATCAATCTTTCGGGACAGATGG 2566
 QY 660 IuIleIleGlnIleValIleSer 665
 DB 2567 AAATCATGAGGCTCTCC 2583

RESULT 24

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US-10-357-930-26669
/ Sequence 26669, Application US/10357930
/ Publication No. US20040259086A1
/ GENERAL INFORMATION:
/ APPLICANT: Schlegel, Robert
/ APPLICANT: Endege, Wilson
/ APPLICANT: Monahan, John
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
/ TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
/ TITLE OF INVENTION: HUMAN PROSTATE CANCER
/ FILE REFERENCE: MRI-007BCN
/ CURRENT APPLICATION NUMBER: US/10/357,930
/ CURRENT FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: 09/785,276
/ PRIOR FILING DATE: 2003-02-16
/ PRIOR APPLICATION NUMBER: 60/183,319
/ PRIOR FILING DATE: 2000-02-17
/ PRIOR APPLICATION NUMBER: 60/189,862
/ PRIOR FILING DATE: 2000-03-16
/ PRIOR APPLICATION NUMBER: 60/207,454
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: 60/211,314
/ PRIOR FILING DATE: 2000-06-09
/ PRIOR APPLICATION NUMBER: 60/219,007
/ PRIOR FILING DATE: 2000-07-18
/ PRIOR APPLICATION NUMBER: 60/255,281
/ PRIOR FILING DATE: 2000-12-13
/ NUMBER OF SEQ. ID NOS: 62232
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 26669
/ LENGTH: 5145
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1, 5144, 5145
/ OTHER INFORMATION: n = A,T,C or G
/ US-10-357-930-26669

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Alignment Scores:

Pred. No.:	0	Length:	5145
Score:	472.00	Matches:	663
Percent Similarity:	99.40%	Conservative:	0
Best Local Similarity:	99.40%	Mismatches:	2
Query Match:	70.98%	Indels:	0
DB:	18	Gaps:	0

US-10-029-345A-109 (1-665) X US-10-357-930-26669 (1-5145)

QY 1 MetAlahSglumEtIegIYthGlnIleValThrgArGLeuValAlaLeuLeuGlu 20
Db 589 ATGGCCCATGAGATGATGGAGATCCAAATTGTTACTGGAAGGTTGTGCTCTGTGGAA 648
QY 21 SerGlyhrgIwlySValLeuLeuIleaspSerArgProPheValGluTYrAsnThrSer 40
Db 649 AGTGAACGGGAAAAAGGCTGCTAAATGTATAGCCGGCCATTGTGGATTAAATACATCC 708
QY 41 HisIleLeuGlnAlaIleAsnIleAsnCySerIySleMetIyArgArgLeuGln 60
Db 709 CACATTTTGGAGCCATTATATCAACTCTCCCAAGCTTATGAAAGCGAAGCTTCAACAG 768
QY 61 AspIySValLeuIleThrgIleuLeuIleGlnHisSerAlaIySHIstIyValAspIleasp 80
Db 769 GACAAATGTTAATTACAGAGCTCATCCAGCATTCAGCGAAACATAAGTTGACATTGAT 828
QY 81 CysSerGlnIySValValIyIyAspGlnSerSerGlnAspValAlaIleSerLeuSerSer 100
Db 829 TCGAGTCAGAAAGSTGTAGTTTACATCAATCAAGCTCCCAAGATGTTGCTCTCTCTTCA 888
QY 101 AspCyPheLeuThrgValLeuLeuGluIySLeuGluIySerPheAsnSerValIHisIleu 120
Db 889 GACGTGTTTCTCACTGTACTTCTTGAGTTAACTCGAAGAAAGACTTCACTCTGTTCACCTG 948

QY	121	LeuAlaGlyGlyPheAlaGluPheSerArgCysPheProGluYleuCySGluGlyIysSer	140
Db	949	CTTGCAAGGTGGGTTTGCTGAGTTCTCTCGTTGTTTCCCTGGCTCTGTAAAGAAATCC	1008
QY	141	ThrIleuValProThrCysIleSerGlnProCysIleuProValAlaAsnIleGlyProThr	160
Db	1009	ACTCTAGTCCCTACCTCAGATTTTCAGCCCTGGCTTACCTGTGGCAACATTGGGCCAAC	1068
QY	161	ArgIleLeuProAsnLeuYrLeuGlyCysGlnArgAspValLeuAsnIleGluIle	180
Db	1069	CGAATTCCTCCCAATCTTTATCTTGGCTCCAGCCAGATGTCTCAACAGAGAGTGTAT	1127
QY	181	GlnGlnAsnGlyTyrIleGlyTyrValLeuAsnAlaSerTyr-ThrCysProIysProAsp	200
Db	1128	GCACAGAAATGGGAATGGTTATGTGTAAATCCAGCAA-TACCTGTCCAAAGCTGACT	1186
QY	200	heIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluIysIle	220
Db	1187	TTATCCCGCAGCTCATTTCTCGCGTGCCCTGTAAATGACAGCTTTGTGAGAAATTT	1246
QY	220	eulProThrIleuAspIysSerValaAspPheIleGluValAlaValaSerAsnGlyCysV	240
Db	1247	TGCGGTGGTTGACAAATCATGATGATTTCAATTGAGAAAGCAAAAGCTCCAAATGAGATG	1306
QY	240	alleuValHisCysIleuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIle	260
Db	1307	TTCTAGTGAACGTTTAGCTGGAGATCTCCGCTCCGACCATCGCTATCGCTCATATCA	1366
QY	260	eIlyeArgHecAspMetSerIleuAspGluAlaTyrArgPheValIysGluValArgPro	280
Db	1367	TGAAGAGATGACATGTCTTTAGATGAAGCTTACATTTGTGAAAGAAAGAAAGCTTA	1426
QY	280	hriIleSerProAsnAspPheIleuGlyGlnIleuLeuAspTyrGluIysIleVala	300
Db	1427	CTATATCTCCAACTTCATTTTCTGGGCCAATCTCCGTGACCTVATGAGAAAGATTAA	1486
QY	300	srGlnThrGlyAlaSerGlyProIysSerIysIleuIysIleuGlnIleuValPro	320
Db	1487	ACCAAGACTGGAGCATCAAGGCCAAAGAGCAACTCAAGCTGTGCACCTGGAGAAAGCCA	1546
QY	320	hrGluProValProAlaValSerGluGlyGlyIysSerGluThrProIleuSerProp	340
Db	1547	ATGAACCTGTCTCCGTCTGTCTCAAGAGGTGGACAGAAAGCCAGACGCCCTCATGTCC	1606
QY	340	roCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnArgProValHisProAlaSer	360
Db	1607	CTGTGGCGAATCTGTACTCAGAGAGCAGACAGCAAGGCCGTGATCTCCGCAAGC	1666
QY	360	alProSerValProSerValGlnProSerIleuLeuGluAspSerProIleuValGlnAla	380
Db	1667	TGCCACAGGCCCCAGAGGTGCACCTCTCTGTAGAGACAGCCCGCTGGTACAGGCGC	1726
QY	380	eusErGlyIleuHisIleSerAlaAspArgIleuGluAspSerAsnIleuIysArgSer	400
Db	1727	TCAAGTGGCTGCACCTGTCCGACAGACAGGCTGAAGACAGCAATTAAGTCAAGGTTCT	1786
QY	400	heserIleuAspIleIysSerValSerTyrSerAlaSerMetAlaIleSerIleuHisGly	420
Db	1787	TCTCTCGAATTAACAATCATGTTTCAATATTACGACGATGCGACATCTTATATAGCT	1846
QY	420	heserSerSerGluAspAlaIleuGluTyrTyrIysProSerThrThrIleuAspGlyThr	440
Db	1847	TCCTCTCATCAAGAAATGCTTTGGAAATCTCAAACTTCCATCACTGTGAATGGACCA	1906
QY	440	snIysIleuCysGlnPheSerProValGlnIleuSerGluGlnThrProGluThrSer	460
Db	1907	ACAAAGCTAAGCAGATTCTCCCTGTTCAGAACTATGAGAGACAGCTCCGAAACCAAGTC	1966
QY	460	roAspIysGluGluIleSerIleProIysIysIleuGlnThrAlaArgProSerAspSer	480
Db	1967	CTGATTAAGAGAAAGCCAGATCTCCCAAGAGCTGCAACCGGACGCTTTCAGACGCC	2026

QY	480	InsErLyAryGLeuHIsErSeVaLaGThrSeSeSeSeG1ThzLaGInArGSeLeuL	500
Db	2027	AGAGCAAGGATTGCAATTCGCTCAGAACCAAGACAGAGAGGACCCGCAAGAGTCCCTTT	2086
QY	500	eUsErPrOleuHIsArGSeG1ySeSeVaGluAspAntYrHisrSePheLeupheG	520
Db	2087	TATTCCACTGCATGAGAGTGGAAGCGTGAAGGACAAATTACACACAGCTTCCTTTGG	2146
QY	520	lyLeuSeThSeSerGInGlnHIsLeuThrLySeSeAlGlyLeuGlyLeuYsG1yTPH	540
Db	2147	GCCTTCCACCGACGACGACGACCTCAGCAAGCTGCTGGCCTGGGCTTAAGGGCTGGC	2208
QY	540	IsErAspHIsLeuHLaProGInThrSeThrProSeLeuThrSeSeThrPyrrPheA	560
Db	2207	ACTGGATATCTTGAGCCCCCGACAGCTTACCTTCCTCGACAGAGCTGGTATTTTG	2266
QY	560	laThrG1uSeSeSeHIsPheTySeSeAlaSeSeAlaLeTyG1yG1ySeSeAlaSeTyS	580
Db	2267	CCACAGAGGCTCCACACTTCTACTCTGCTCAGCCATCTACGAGAGGAGTGCATTACT	2322
QY	600	erAlaTySeCySeSerGInLeuProThrCyG1yAspGlnValTySeSeVaLaArGaRga	600
Db	2327	CTGCTTAAGCTGCAGCAGCAGCTGCCACCTTGCGGAGACCAAGTCTATTCGTGGCGCAGGC	2386
QY	600	rGInLySeProSeSeArPaRgaLaAspSeArArGArSeThrHisGluGluSeRProPheG	620
Db	2387	GGCAAAACCCAAAGTACAGAGAGCTGACTGGCGCGAGGCTGGCGATMAAGAGGCCCTTTG	2446
QY	620	luLyG1nPhelYsArGArRgSeCyG1nMetGluPhG1yGluSeThlMetSeSerGluA	640
Db	2447	AAAGCAGTTTAAACGCAAGAGCTGCCAAATGGAATTTGGAGAGAGCATCATGTACAGGA	2506
QY	640	sArGSeArG1uGluLeuGlyLyVaGlySeGInSeSeSePheSeSerGlySeMetG	660
Db	2507	ACAGGTACGGGAAGAGCTGGGGAAAGTGGGAGTCAGTCTGCTTTGGGGACAGCATGG	2566
QY	660	luLeIlleGluValSeR	665
Db	2567	AAATCATTAAGGTCTCC	2583
RESULT 25			
US-10-357-930-26815			
Sequence 26815, Application US/10357930			
Publication No. US20040259086A1			
GENERAL INFORMATION:			
APPLICANT: Schlegel, Robert			
APPLICANT: Endege, Wilson			
APPLICANT: Monahan, John			
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR			
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF			
FILE REFERENCE: MRI-0078CN			
CURRENT APPLICATION NUMBER: US/10/357,930			
CURRENT FILING DATE: 2003-02-04			
PRIOR APPLICATION NUMBER: 09/785,276			
PRIOR FILING DATE: 2003-02-16			
PRIOR APPLICATION NUMBER: 60/183,319			
PRIOR FILING DATE: 2000-02-17			
PRIOR APPLICATION NUMBER: 60/189,862			
PRIOR FILING DATE: 2000-03-16			
PRIOR APPLICATION NUMBER: 60/207,454			
PRIOR FILING DATE: 2000-05-25			
PRIOR APPLICATION NUMBER: 60/211,314			
PRIOR FILING DATE: 2000-06-09			
PRIOR APPLICATION NUMBER: 60/219,007			
PRIOR FILING DATE: 2000-07-18			
PRIOR APPLICATION NUMBER: 60/255,281			
PRIOR FILING DATE: 2000-12-13			
NUMBER OF SEQ ID NOS: 62232			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 26815			
LENGTH: 5145			
TYPE: DNA			

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 5144, 5145
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-26815

Alignment Scores:
Pred. No.: 0 Length: 5145
Score: 472.00 Matches: 663
Percent Similarity: 99.40% Conservative: 0
Best Local Similarity: 99.40% Mismatches: 2
Query Match: 70.98% Indels: 4
DB: 18 Gaps: 0

US-10-029-345A-109 (1-665) x US-10-357-930-26815 (1-5145)
QY 1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGln 20
Db 569 ATGGCCCATGGAGATGATTTGAGACTCAATTTTCTAGAGAGGTGGTGCTCTGCTGGA 648
QY 21 SerGlyThrGluYsValLeuLeuIleAspSerArgProPheValGluYrAsnThrSer 40
Db 649 AGTGAACGGAAGAAAGCTGCTCAATGATGATGCCGGCATTTGTGGATACATATACCTC 708
QY 41 HisIleLeuGlnAlaIleAsnIleAsnCySerIysLeuMetIleArgArgLeuGlnGln 60
Db 709 CACATTTTGGAGGCATTAATATCACTGCCTCCAACTTATGAAAGCGAAGGTTCCACAG 768
QY 61 AspIysValLeuIleThrGlnLeuIleGlnHisSerAlaIysHisIleValAspIleAsp 80
Db 769 GACAAAGGTAAATTACAGACCTCATCCAGATTCAGGAAACATTAAGTTGACATTCAT 828
QY 81 CysSerGlnYsValValValYrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db 829 TGCAGTCAGAAAGTTGATGATTAGCATTAAGCTCCCAAGATGTGCTCTCTCTTCA 888
QY 101 AspCySPheLeuThrValLeuLeuGlnGlyIleLeuGlnYsSerPheAsnSerValHisLeu 120
Db 889 GACTGTTTTCACCTGACTTCTGGGTAAATCGAAGAAAGACTTCACCTGTCTCACCCTG 948
QY 121 LeuAlaGlyIlePheAlaGluPheSerArgPhePheProGlyLeuCyGlnGlyIleYsSer 140
Db 949 CTTCGAGGTGGGTTCGAGCTTCTCTGTTGTTCCCTGGCTCTGTGAAGGAAATCC 1008
QY 141 ThrIleuValProThrCySilesSerGlnProCySPheProValAlaAsnIleGlyProThr 160
Db 1009 ACTCTAGCTCCACTACTGATTTCTCAGCTTGTCTTACTGTGGCCAACTTGGGCCAAC 1068
QY 161 ArgIleLeuProAsnLeuYrLeuGlyCySPGlnArgAspValLeuAsnIleGlnLeuIle 180
Db 1069 CGAATTTCTCCCAATCTTATCTTATCTTGGCTGCAGAGAGATGTCCTCAACAAAGACTGAT - 1127
QY 181 -GlnGlnAsnGlyIleGlyYrValIleAsnAlaSerYr-ThrCySProIysProAspP 200
Db 1128 GCACACAGATGGAGTTGGTTATGTGTTAAAGCCAGCAA-TACCTGTCCAAAGGCTGACT 1186
QY 200 heIleProGlnSerHisPheLeuArgValProValAsnAspSerPheCySgluYsIleI 220
Db 1187 TTATCCCGCACTCATTTCTCGCGTGTGCTGTGAATGACACGCTTTTGTGAGAAAATTT 1246
QY 220 euProIleuAspIysSerValAspPheIleGluYsAlaIysAlaSerAsnGlyCySv 240
Db 1247 TGCCGTGGTTGGACAAATCAGTATGATTTCATTGAGAAAGCAAAGGCTCCCAATGATG 1306
QY 240 alleuValHisCyLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaYrIleM 260
Db 1307 TTTCTAGTGCATGTTTGTGCTGGATCTCCCGCTCCGACACATGCGTATGCGCTTACATCA 1366
QY 260 eLysArgMetAspMetSerLeuAspGlnAlaYrArgPheValIleGlnYsArgPProT 280
Db 1367 TGAAGAGGATGACATGTTCTTTAATTAAGCTTCAAGTTTGTGAAGAAAAAGACCTTA 1426

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QY 280 htlleSerProAsnpheAsnpheleuglyglleuLeuAspTyrGluLysLysIleLysA 300
 Db 1427 CTATATCTCCAAACTCTCAATTTTCTGGCCCAACTCCCTGAGACTATGAGAAAGATTAAAGA 1486
 QY 300 snglnThnGlyAlaSerGlyProLysSerLysLeuLysLysLeuLysLysLeuLysProA 320
 Db 1487 ACCAGACTGGAGCATCGAGGCGCAAGAGCAAACTCAAGCTGCTGCACTCGGAGAGCCCA 1546
 QY 320 snglnProValProAlValSerGluLysLysSerGluLysSerGluLysProLysSerProP 340
 Db 1547 ATGAACCTGCTCCCTGCTCTCTCAAGGGGTGAGCAAGAAAGCGAGCCCTCAGTCCAC 1606
 QY 340 roCyValaAspSerAlaThrSerGluLysLysLysLysLysLysLysLysLysLysLys 360
 Db 1507 CCGTGGCCGACTCTGCTACTCTCAGAGCGAGCAAGAGCCCGGCGATCCCGCCAGCG 1666
 QY 360 alProSerValProSerValGlnProSerLeuLeuLysLysLysLysLysLysLysLysL 380
 Db 1667 TGCCGAGCGTCCCAAGGTGAGCGCTGCTGTAGAGGACAGCCCGCTGGTAAGCGGC 1726
 QY 380 euSerGlyLeuHlsLeuSerAlaAspArgLeuGluAspSerAsnLysLysLysLysLys 400
 Db 1727 TCGATGGGCTGCACTGCTCGAGACAGGCTGGAAGACGCAATAGCTCAAGGCTTCT 1786
 QY 400 hseSerLeuAspLysSerValSerTyrSerAlaSerMetAlaAlaSerLeuHlsGlyL 420
 Db 1787 TCTCTTGGATATCAATCATGTTTCAATTCAGCCAGCATGAGCATCTTCAATAGCT 1846
 QY 420 hseSerSerSerGluAspAlaLeuGluLysTyrTyrLysProSerThrThrLeuAspGlyTh 440
 Db 1847 TCTCTCATCAAGAAATGCTTGGAAATCTACAACTTCCACTACCTGAGAGGAGCA 1906
 QY 440 snLysLeuGlyGlnhseSerProValGlnGluLeuSerGluLysLysLysLysLysLys 460
 Db 1907 ACAGACTATGCCAGTCTTCCCTGTTCAAGAACTATGAGAGCACTCCGAAACCAAGTC 1966
 QY 460 roAspLysGluGluLysSerLysLeuProLysLysLeuGlnThrAlaArgProSerAspSerG 480
 Db 1967 CTGATTAAGAGAGAGCCAGCATCCCAAGAGCTGCAAGCCGCGCCAGCTTCCAGAACCC 2026
 QY 480 lnsSerLysArgLeuHlsSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeuL 500
 Db 2027 AGAGCAAGCATTCATTCGCTGTCAGAACCAAGAGCTGAGCCGCGCCAGAGGCTCCCTT 2086
 QY 500 euSerProLeuHlsArgSerGlySerValGluAspAsnTyrHlsThrSerPheLeuPheG 520
 Db 2087 TATCTCCACCTGCATCGAAGTGGAGCGTGGAGAGCAATTAACCAACACCTTCTTTTCG 2146
 QY 520 lylLeuSerThrSerGlnGlnHlsLeuThrLysSerAlaGlyLeuGlyLysGlyLysLys 540
 Db 2147 GCTTCTCCACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2206
 QY 540 lssSerAspLysLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheA 560
 Db 2207 ACTCGGATATCTTGGCCCCCAGACCTTACCCCTTCCCTGACAGCAGCTGGTATTTTG 2266
 QY 560 lathrGluSerSerHlsPheTyrSerAlaSerAlaIleTyrGlyLysSerAlaSerTyrS 580
 Db 2267 CCAAGAGCTCTCACTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2326
 QY 580 exAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArg 600
 Db 2327 CTGCTTACAGCTGAGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2386
 QY 600 rsgLysLysProSerAspArgAlaAspSerArgArgSerTyrHlsGluGluLysSerProh 620
 Db 2387 GGCAGAGCCAAAGTACAGAGCTGACTGCGCGCGAGCTGCGCAAGAGAGAGCCCTTTG 2446
 QY 620 lylLysGlnPheLysArgArgSerCysGlnMetGluPheGlyLysSerIleMetSerGlu 640
 Db 2447 AAAAGCAAGTTTAAAGCAAGCTGCAAAATGGAAATTTGGAGAGAGCATATGTCAGAGA 2506
 QY 640 snArgSerArgGluLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 660

Db 2507 ACAAGTACCGGAAAGCTGGGGGAAAGTGGGAGTCAAGTCTTTTGGGCAAGATCG 2566
 QY 660 lyllelleGluValSer 665
 Db 2567 AAATCATTTGAGGTCTCC 2583

RESULT 26
 US-10-357-930-26912
 ; Sequence 26912, Application US/10357930
 ; Publication No. US20040259086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Bredge, Wilson
 ; APPLICANT: Monahan, John
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 ; FILE REFERENCE: MRI-007BCN
 ; CURRENT APPLICATION NUMBER: US/10/357,930
 ; PRIOR FILING DATE: 2003-02-04
 ; PRIOR APPLICATION NUMBER: 09/785,276
 ; PRIOR FILING DATE: 2003-02-16
 ; PRIOR APPLICATION NUMBER: 60/183,319
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: 60/189,862
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/207,454
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/211,314
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: 60/219,007
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: 60/255,281
 ; NUMBER OF SEQ ID NOS: 62232
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 26912
 ; LENGTH: 5145
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1, 5144, 5145
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-357-930-26912

Alignment Scores:
 Pred. No.: 0
 Score: 472.00
 Percent Similarity: 99.40%
 Best Local Similarity: 99.40%
 Query Match: 70.98%
 DB: 18
 Gaps: 0

US-10-029-345A-109 (1-665) x US-10-357-930-26912 (1-5145)

QY 1 MetAlaHlsGluMetIleGlyThrGlnIleValThrGluLysValAlaLeuLeuGlu 20
 Db 589 ATGGCCCATGAGATGATTTGAACTCAATATGTTACTGAGAGTTGGCTGCTGCTGAA 648
 QY 21 SerGlyThrGluLysValLeuLeuLysAspSerArgProPheValGluTyrAsnThrSer 40
 Db 649 AGTGGAAAGGAAAAAGTCTGCTCAATGATGATGCGGCAATTTGTGAATACATACATCC 708
 QY 41 HlsIleLeuGluAlaIleAsnIleAsnCysSerLysLeuMetLysArgArgLeuGlnGln 60
 Db 709 CACATTTTGAAGGCATTAATATCAACTGCTCCAAAGCTTAAGAGGAGTTGCAAGC 768
 QY 61 AspLysValLeuIleThrGluLeuIleGlnHlsSerAlaLysHlsLysValAspIleAsp 80
 Db 769 GACAAAGTGTATTAATTAACAGAGCTCATCCAGCATTCAGCCAAACATAGGTGATGAT 828

/ PRIOR APPLICATION NUMBER: 60/255,281
/ PRIOR FILING DATE: 2000-12-13
/ NUMBER OF SEQ. ID NOS: 62232
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ. ID NO: 26923
/ LENGTH: 5145
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 1, 5144, 5145
/ OTHER INFORMATION: n = A,T,C or G
US-10-357-930-26923

Alignment Scores:
Pred. No.: 0 Length: 5145
Score: 472.00 Matches: 663
Percent Similarity: 99.40% Conservative: 0
Best Local Similarity: 99.40% Mismatches: 2
Query Match: 70.98% Indels: 4
DB: 18 Gaps: 0

US-10-029-345A-109 (1-665) x US-10-357-930-26923 (1-5145)

QY 1 MetAlaHieGluMeTlIeGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
DB 589 ATGGCCCATGAGATGATGATGGAACCTCAAAATGTTACTGAGAGGTTGGTGCTGCTGGAA 648
QY 21 SerGlyThrGluValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
DB 649 AGTGAACGGAAGAAAGTCTGCTGATTAATTAAGCGGCATTTGGGAATACATACATCC 708
QY 41 HisIleLeuGluAlaIleAsnIleAsnCySerIleuLeuLeuLeuLeuLeuLeuLeuLeuLeu 60
DB 709 CACATTTGGAGCCATTAATATCACTGCTCCAACTTATGAAGCGAAGCTTGCACAG 768
QY 61 AspIleValLeuIleThrGluLeuIleGlnHisSerIleAlaSerIleValIleLeu 80
DB 769 GACAAAGGTTAATTAACAGAGCTCATCAAGCATTCAGCGAAGCAATTAAGTTGACATTTGAT 828
QY 81 CysSerGlnIleValIleValIleAspIleSerIleuLeuLeuLeuLeuLeuLeuLeuLeuLeu 100
DB 829 TGCAGTCAAGAGGTTGATGATTAAGATCAAAAGCTCCCAAGATGTTCCCTCTCTCTCA 888
QY 101 AspCysPheLeuThrValLeuLeuGluValLeuGluValLeuSerPheAsnSerValIleLeu 120
DB 889 GACTGTTTCTCACTGACTTCTGGGTAACGAGAGAGAGCTTCAACTCTGTTCACTG 948
QY 121 LeuAlaGlyIlePheAlaGluPheSerArgCysPheProGlyLeuGlyLeuGlyIleSer 140
DB 949 CTGCAAGTGGGTTGCTGAGTTCTCTCGTTGTTCCCTGAGCTCTGTAAGGAAATCC 1008
QY 141 ThrIleValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
DB 1009 ACTCTAGTCCCTCACTGCACTTCTCAAGCTTCTTAACCTGTTGCCAATATGGGCAACC 1068
QY 161 ArgIleLeuProAsnLeuIleuGlyCysGlnArgAspValLeuAsnIleGluLeuIle 180
DB 1069 CGAATTCCTCCCAATCTTATCTTGGCTGCCAGCAGATGCTCTTAACAGAGACTGAT- 1127
QY 181 -GlnGlnAsnGlyIleGlyTyrValLeuAsnAlaSerTyr-ThrCysProIleProAsp 200
DB 1128 GAGCAGAAATGGATTTGTTATGTGTAATGCCGCAAA-TACCTGTTCAAAAGCTGACT 1186
QY 200 HisIleProGluSerHisPheLeuArgValProValAsnAspSerPheCysGluIleLeu 220
DB 1187 TTATCCCGAGTCTCATTTCCGCTGCTGCTGATGACAGGCTTTTGGAGAAATTTT 1246
QY 220 euProThrLeuAspIleSerValAspPheIleGluValAlaIleAsnAspGlyCysArg 240
DB 1247 TGCCGTGGTGGCAAAATCAGTATTCATTTGAGAAAGCAAAAGCTCCAAATGAGATGG 1306
QY 240 alIleuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleu 260

DB 1307 TTCTAGTCACTGTTAAGCTGGGATCTCCGCTCCGCAACATCGCTATCGCTACATCA 1366
QY 260 eClysaRMeLAspMetSerLeuAspGluAlaTyrPhePheValIleGlyIleValArgProT 280
DB 1367 TGAAGAGATGAGCAGTCTTTTATGATGAAGCTTACAGATTTGTGAAGAAAAAGACCTTA 1426
QY 280 hrlIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGlyIleValIleVal 300
DB 1427 CTATATCTCCAACTTCAATTTTCTGGGCAACTCTGGACTATGAGAAAGATTAAGA 1486
QY 300 smGlnThrGlyAlaSerGlyProIleSerIleValLeuLeuIleLeuGluIleProAla 320
DB 1487 ACCAGACTGAGACATCAGGCGCCAAAGACAACTCAAGCTCTCACCCTGAGAGCA 1546
QY 320 smGluProValProAlaValSerGlyGlyGlnIleValSerGlyThrProLeuSerPro 340
DB 1547 ATGAACCTGTCCCTGCTGCTCAGAGGGTGAACAAGAGAGAGAGAGAGAGAGAGAG 1606
QY 340 roCysAlaAspSerAlaThrSerGluAlaIleGlyGlnArgProValHisProAla 360
DB 1607 CCTGTGCCGACTCTGCTCACTCAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1666
QY 360 alProSerValProSerValGlnProSerLeuLeuGluIleAspSerProLeuValGlnAla 380
DB 1667 TGCCAGAGCTGCCAGCGTGCAGCGCTCGTTTGAAGAGACAGCCGCTGTGTACAAGAGC 1726
QY 380 euSerGlyLeuHisLeuSerAlaAspArgLeuGluIleAspSerAsnIleValIleVal 400
DB 1727 TCAATGGGCTCACTCTTCCGAGAGAGGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1786
QY 400 heserLeuAspIleIleValSerValSerTyrSerAlaSerMetAlaIleAsnIleGly 420
DB 1787 TCTCTGAGATATCAATCAGTTTCATATTACAGCCAGATGCGAGATCTTACATAGGCT 1846
QY 420 heserSerSerGluAspAlaLeuGluIleTyrIleProSerThrThrLeuAspGlyThr 440
DB 1847 TCTCTATCAGAAAGATCTTGAATTAATAAACTTCACTGATGGAGCA 1906
QY 440 enIleuLeuCysGlnPheSerProValGlnIleuSerGluGlnThrProGluThrSer 460
DB 1907 ACAAGTATGCCAGTCTCCCTGTTCAAGAACTTACGAGAGAGAGAGAGAGAGAGAG 1966
QY 460 roAspIleGluGluIleAsnIleProIleValLeuGlnThrAlaArgProSerAspSer 480
DB 1967 CTATTAAG 2026
QY 480 InSerIleArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500
DB 2027 AGAGCAAGCATTTGATTCGTCAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2086
QY 500 euSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPhe 520
DB 2087 TATCTCACTGATGAAGATGGAGCGTGGAGAGCAATTAACACAGAGCTCTCTTTTCG 2146
QY 520 IYleuSerThrSerGlnGlnHisLeuThrIleValSerAlaGlyLeuGlyIleValGly 540
DB 2147 GCCTTTCACAGCAG 2206
QY 540 IAspSerAlaLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrIlePhe 560
DB 2207 ACTCGAATATTTGGCCCCCAGACCTTACCCCTTCCGACAGAGAGAGAGAGAGAGAG 2266
QY 560 IATHGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyIleSerAlaSerTyr 580
DB 2267 CCAGAGAGTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 2326
QY 580 eAlaIleTyrSerCysSerGlnLeuProThrCysGlyIleAspGlnValIleTyrSerValArg 600
DB 2327 CTGCTCAAGTGAAGCAGCTGCCCACTTGCGGAGAACAGCTATTTCTGTGCGAGAGC 2386
QY 600 rGlnIleProSerAspArgAlaAspSerArgSerTrpHisGluGluSerProPheG 620


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Db      1787 TCTCTGGAATCAATCAGTTTCATATTCAGCCAGATGGCAGCATCTTTCATGAGCT 1846
QY      heserSerSerGluAspAlaLeuGluTyrTyrIysProSerThrThrLeuAspGlyThrA 440
Db      1847 TCTCTCATCAGAAAGATGCTTTGGAAATATCAAAACCTTCACATCTCGAGTGGAGCA 1906
QY      440 snlyLeuCySgInPheSerProValGlnGluLeuSerGlnGlnThrProGlnThrSerP 460
Db      1907 ACAAGCTATGCGCAGTTCTCCCTGTTCCAGAACTATGAGAGAGACTCCCGAAACCACTC 1966
QY      460 roaApLySgInGluAlaSerIleProIylsLeuGlnThrAlaArgProSerAspSerG 480
Db      1967 CTGATTAAGAGAAAGCCAGCATCCCAAGAACTGACACCGCCAGCTTCAGACAGCC 2026
QY      480 InSerLySArgLeuHisSerValArgThrSerSerSerLyThrAlaGlnAspSerLeuL 500
Db      2027 AGAGCAAGCCATTGCAATTCGTCAGAACCAAGCAGAGCTGACCCCGCAGAGTCCCTTT 2086
QY      500 euserProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheG 520
Db      2087 TATCTCACTGCAATCCAAAGTGGAGCGCTGGAGAGCAATTACACACAGCTTCCTTTTCG 2146
QY      520 IyLeuSerThrSerGlnGlnHisLeuThrIylsSerIleGlyLeuGlyLeuIylsGlyTyrP 540
Db      2147 GCCTTTCACACCAAGCCAGCAGCACTCAGCAAGTCTGCTGGCCTTGAAGGGCTGGC 2206
QY      540 iSerAspIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerThrIylsPheA 560
Db      2207 ACTCGGATATCTTGGCCCCCAGACCTCAACCCCTTCCTCAACAGCAGCTGGATTTTG 2266
QY      560 IaThrGlySerSerHisPheTyrSerAlaSerAlaIleTyrGlyIylsSerIylsSerTyrS 580
Db      2267 CCACAGAGTCCCTCAACTTCTTCTGCTCAGCACTTACGAGAGGAGGAGGCCAGTTACT 2326
QY      580 eRHaIlySerCySgSerGlnLeuProThrCysGlyAspGlnValTyrSerValArgArgA 600
Db      2327 CTGCTCAGCTGCGCAGCAGCTGCGCCACTTCCGAGACCAAGCTATTCCTGTCGAGGC 2386
QY      600 TgGlnLyProSerAspArgAlaAspSerArgAspSerTyrPHisGlnGlyIylsSerProPheG 620
Db      2387 GGCAGAGCCAGAGTGAAGAGCTGACTGCGGCGGAGCTGGCATGAAAGAGAGCCCTTTG 2446
QY      620 IuLySgInPheLyArgArgSerCySgInMetGlnPheGlyIylsSerIleMetSerGlnVal 640
Db      2447 AAAAGCAGTTTAAACGAGAGCTGCCAATGGAATTTGAGAGAGCATCATGTCAGAGA 2506
QY      640 snArgSerArgGlnGluLeuGlyIylsValGlySerGlnSerSerPheSerGlySerMetG 660
Db      2507 ACAGCTCAGCGGAGAGCTGGGAAAGTGGGAGTCACTAGCTTTTCGGGACAGCATGG 2566
QY      660 IuIleIleGluValSer 665
Db      2567 AAATCATTTGAGTCTCC 2583

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RESULT 29

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US-10-357-930-27149
; Sequence 27149 Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: HUMAN PROSTATE CANCER
; CURRENT APPLICATION NUMBER: US/10/357,930
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862

```

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; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27149
; LENGTH: 5145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1, 5144, 5145
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-27149

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Alignment Scores:

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Pred. No.: 0 Length: 5145
Score: 472.00 Matches: 663
Percent Similarity: 99.40% Conservative: 0
Best Local Similarity: 99.40% Mismatches: 2
Query Match: 70.98% Indels: 4
DB: 18 Gaps: 0

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US-10-029-345A-109 (1-665) x US-10-357-930-27149 (1-5145)

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QY      1 MetAlaHisGluMetIleGlyThrGlnIleValThrGluArgLeuValAlaLeuLeuGlu 20
Db      589 ATGGCCCATGAGATGATTTGGAACCTCAATTGTACTGAGAGGTTGGTGGCTGCTGGAGA 648
QY      21 SerGlyThrGluIylsValLeuLeuIleAspSerArgProPheValGlnTyrAsnThrSer 40
Db      649 AGTGGAGCGAAAGAGCTGCTTAATGTATGATCCGCGCATTTGTGGAAATACATATCATCTC 708
QY      41 HisIleLeuGlnAlaIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIleAsnIle 60
Db      709 CACATTTTGGAAACCTTATATATCAACTGCTCCAGAGCTTATGAGAGAGTGGCAGACG 768
QY      61 AspLeuValLeuIleThrGluLeuIleGlnHisSerAlaIylsValValAspIleAsp 80
Db      769 GAGAAAGTGTATATACAGAGCTCATCCAGCAATTCAGGAAACATTAAGTTGACATTGAT 828
QY      81 CysSerGlnLySValValValTyrAspGlnSerSerGlnAspValAlaSerLeuSerSer 100
Db      829 TGCAGTCAGAAAGTTGTATGATTACATCAAGCTCCCAAGATGTGCTCTCTCTTCA 888
QY      101 AspCySgPheLeuThrValLeuLeuGlnIylsLeuGlnIylsSerPheAsnSerValHisLeu 120
Db      889 GACTGTGTTCTACGTACTTCTGGTAACTGAGAAAGAGCTTCAACTCTGTTCACTG 948
QY      121 IeuAlaGlyGlyPheAlaGluPheSerArgCySgPheProGlyLeuCySgInGlyIylsSer 140
Db      949 CTTCAGAGTGGTGTTCGTAATCTTCTGTTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1008
QY      141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Db      1009 ACTCAGAGCTCTACCTCATTCTCAGCTTGCAGCTTGCCTGTTGCTGCTGCTGCTGCTGCTG 1068
QY      161 ArgIleLeuProLeuLeuTyrIylsGlyCySgInArgAspValLeuAsnIylsGluLeuIle 180
Db      1069 CGAATTCCTCCCATCTTTATCTTGGCTGCGAGAGATGCTCTCAACAAGAGAGCTGAT- 1127
QY      181 -GlnGlnAsnGlyIylsGlyTyrValLeuAsnAlaSerTyr-ThrCysProLySProAsp 200
Db      1128 GCACGCAAAATGGAGATGGTATGTGTTAATGCAACA-TACCTGTCCAAAGCTGACT 1186
QY      200 helLeProGlnSerHisPheLeuArgValProValAsnAspSerPheCySgInIylsIle 220

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Db 1187 TTAACCCGAGTCTATTCTCGTGCCTGTAATGACAGCTTTTGAGAAAAATT 1246
 Qy 220 EUPROTHLEUAPLYSERVALASPHELIIEGLIULYSALALYSERHNGLYCYEV 240
 Db 1247 TSCGGGTGTGACAAATGAGATTTCAATGAGAAAGAAAGCTCCAAAGGATGTG 1306
 Qy 240 ALLEUVALHISCYBLEUALAGLYIIESEARSERVALATHRIIEALIEALITYIIEW 260
 Db 1307 TTTTATGCGACTGTTTAACTTGAAGTATCCCGCTCCGACCACTCGTATGCTTACATCA 1366
 Qy 260 EELYSARGMETASPMETSERLEUAPGLUALATYRARGPHEVALLYVEGLULYSARGPROT 280
 Db 1367 TGAAGAGATGACATGCTTTTATGATGACATTAAGATTGTGAAGAAAGAAAGACCTTA 1426
 Qy 280 HTLISEERPROANPHEANPHELEUGLYGLINEULEUAPPLYRGLULYSVLYIIELYEA 300
 Db 1427 CTATATCTCCAACTTCAATTTCTGGGCCCACTCCGACTATGAGMAAATTAAG 1486
 Qy 300 SNGINTHRGYLAISERGLYPROLYSERLYSEULYSLEULEUHLISLEUGLULYVPRO 320
 Db 1487 ACCAGACTGAGACATCAAGGCCCAAGACAAACTCAAGCTGCTGCACTGAGAGACCA 1546
 Qy 320 SNGIULYPROVALPROALVALSERGLUGLYGLINYSERGLUTHRPROLEUSERPRO 340
 Db 1547 ATGACCTGTCCCTGCTGTCTCAGAGGTGACAGAAAGCGAGAGCCCTCAGTCCAC 1606
 Qy 340 ROCYSAIAAPSERVALATHSERGLUALALAGLYINARGPROVALHISPROALISERY 360
 Db 1607 CCTGTGCGACTGTGCTACTCAGAGCAGACAGACAAAGCCCGTGCATCCGCCAGCGC 1666
 Qy 360 ALPROSERVALPROSERVALGNPROSERLEUENGLUAPSERPROLEUVALIGLUAL 380
 Db 1667 TGCCCAAGCGTCCAGAGGTGACAGCTGCTGTTAGAGACAGCCGCTGTACAGCGCC 1726
 Qy 380 EUSERGLYLEUHLISLEUSERVALASPARGLEUGLUNAPSERANLYSLEULYSARGSER 400
 Db 1727 TCAGTGGGTGCACTGTGCGAGACAGCTGGAAGACAAATTAAGCTCAAGCTTCC 1786
 Qy 400 HESERLEUAPLIELYSERVALISERTYISERVALASERMETALALASERLEUHLIGLYP 420
 Db 1787 TCTCTCTGATATCAATCATGTTTCATATTCACCCAGCATGAGACATCTTTCATGTGCT 1846
 Qy 420 HESERSERSERVALASPARALEUGLUTYRTRYLSPROSERTHRTHEUAPGLYTHRA 440
 Db 1847 TCTTCCATATGAGAGATGCTTGTGAATCTCAAACTTCCACTACTCGAATGGAGCA 1906
 Qy 440 SMLYSLEUCYSGINPHESEERPROVALGNGIULYSEARGLUGINTHRPROGLUTHSER 460
 Db 1907 ACAAGCTATCCAGTTCCTCCCTGTTCAAGAACTATTCGAGAGACATCCCGAAGACAGTC 1966
 Qy 460 ROAPLYSGIULUALASERTILEPROLYSLEULEUGINTHRAARGPROSERASPSE 480
 Db 1967 CTGATTAAGAGAAAGCAGCATCCCAAGAACTGACAGCCGACGCTTCAGACAGCC 2026
 Qy 480 INSERLYSARGLEUHLISERVALARGTHSERSESERGLYTHRAIAGINARSELEU 500
 Db 2027 AGAGCAAGCATGATTCGCTGTAAGAACAGCAGAGTGGACACCGCCCAAGAGTCCCTT 2086
 Qy 500 EUSERPROLEUHLISARGSERGLYSERVALIGLUNAPSEANTYRHLISHTSERPHELEUPHE 520
 Db 2087 TATCTCCACTGCATCGAAGTGGAGCGTGGAGCAATTCACACACAGCTTCTTTTCC 2146
 Qy 520 ILYSEUSERTHSRGNGINHLISLEUTHRILYSERVALAGLYLEUGLYLEUHYLYTPH 540
 Db 2147 GCGTTTCCACACACGACACACACTCAAGAACTGCTGCGCTTAAAGGCTGCG 2206
 Qy 540 IASERAPLILEUVALAPROGLINTHRSEERHPRROSERLEUTHRSEERTRYTYRPHA 560
 Db 2207 ACTCGGATATCTTGCCGCCAAGCCTTAACCTTCCCTGACAGAGAGTGTGATTTTG 2266
 Qy 560 IATHRGUSERSERHISPHETYSERVALASERVALLEYRGLYISERVALASERTYIS 580
 Db 2267 CCACAGAGTCTCACTTCTTACTGCTGCTCAGCAGCATTAAGAGGAGGAGGAGGAGTACT 2326

Qy 580 ERALATYSERCYSESERGLINEUPROTHR-CYGLYASPGIUNVALTYRSEVALARGA 600
 Db 2327 CTGCTTACAGCTGACACCGACCTGCCACTTGGAGAACCAAGCTTCTGTGCGAGGC 2386
 Qy 600 TGLINLYSPROSERASPARGALASERASARGSERTPHISGLUGIUSERPROHEG 620
 Db 2387 GCGAGAGCCAAAGTGCACAGAGCTGACTCGCGGCGAGCTGGCATGAAGAGGCCCTTTG 2446
 Qy 620 IULYSEGINPHELYBARGARGSERCYSGIMERCGLUPHEGLYGLIUSERIIEMETSERGLUN 640
 Db 2447 AAAAGCAGTTTAAACCAAGAGCTGCMAATGGAATTTGAGAGACCATCATGTCAAGA 2506
 Qy 640 SNAHSEERARGGLUGIULAEUGLYLYSEVALIGLYSERGINSESERPHESERGYSEMERG 660
 Db 2507 ACAGGTACGGAGAGAGCTGGGGAAAGTGGGAGTCAGTCACTTTTGGGCGACATGG 2566
 Qy 660 IULIEGLEULVALSER 665
 Db 2567 AATCATTTGAGGTCTCC 2583

RESULT 30
 US-10-357-930-28675
 ; Sequence 28675, Application US/10357930
 ; Publication No. US20040259086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Endege, Wilson
 ; APPLICANT: Monahan, John
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 ; FILE REFERENCE: MRI-007BCN
 ; CURRENT APPLICATION NUMBER: US/10/357,930
 ; CURRENT FILING DATE: 2003-02-04
 ; PRIOR APPLICATION NUMBER: 09/785,276
 ; PRIOR FILING DATE: 2003-02-16
 ; PRIOR APPLICATION NUMBER: 60/183,319
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: 60/189,862
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/207,454
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/211,314
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: 60/219,007
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: 60/255,281
 ; PRIOR FILING DATE: 2000-12-13
 ; NUMBER OF SEQ ID NOS: 62232
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 28675
 ; LENGTH: 5145
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: 1, 5144, 5145
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-357-930-28675

Alignment Scores:
 Pred. No.: 0 Length: 5145
 Score: 472.00 Matches: 663
 Percent Similarity: 99.40% Conservative: 0
 Best Local Similarity: 99.40% Mismatches: 2
 Query Match: 70.98% Indels: 4
 DB: 18 Gaps: 0

US-10-029-345A-109 (1-665) x US-10-357-930-28675 (1-5145)

Qy 1 MetAlaHleGluMetIleGlyThrGlnIleValThnGluArgLeuValAlaLeuLeuGlu 20
 |||||||

Db 589 ATGCCCATGATGATGTAACCAATTGTTACTGAGAGGTTGGCTGCTGCA 648
QY 21 SerGlyThrGlyValLeuLeuIleAspSerArgProPheValGluTyrAenThrSer 40
Db 649 AGTGAACGGAAAAAGCTGCTCTAATGATAGCCGGCATTTGTGGAAATACATACATCC 708
QY 41 HisIleLeuGluAlaIleAsnIleAsnCysSerIleuMetLeuArgArgLeuGlnGln 60
Db 709 CACATTTTGGAGCCATTAAATACACTGCTCCAGAGCTTATGAAAGGAAAGGTTGCAACAG 768
QY 61 AspIleValLeuIleThrGluLeuIleGlnHisSerAlaIleHisIleValAspIleAsp 80
Db 769 GACAAAGTTAATATACAGCTCATCCAGCATTCAGCAAACTAAGGTTGACATTCAT 828
QY 81 CysSerGlnIleValValIleTyrAspGlnSerSerGlnAspValAlaSerIleuSerSer 100
Db 829 TGCAGTCAGAAAGTTAGTTACATTCATCAAAAGCTCCCAAGAGTGGCTCTCTCTTCA 888
QY 101 AspCysPheLeuThrValLeuLeuGluIleValLeuGluIleValSerPheAsnSerValHisIleu 120
Db 889 GACTGTTTCTCACTGACTTCTGGGTAACTGGAGAAAGCTTCACTGTTCACTG 948
QY 121 LeuAlaGlyGlyPheAlaGlnPheSerArgCysPheProGlyLeuCysGluGlyIleSer 140
Db 949 CTTCGAGAGTGGGTGCTGATGTTCTCTGTTGTTCCCTGGCTCTGTGAAGAAATCC 1008
QY 141 ThrLeuValProThrCysIleSerGlnProCysLeuProValAlaAsnIleGlyProThr 160
Db 1009 ACTCTAGTCCCTACCTGCACTTCTCAGCTTGCTTACCTGTTGCCAACTTGGGCCCAAC 1068
QY 161 AcGlyIleLeuProAsnLeuThrLeuGluIleCysGlnArgAspValLeuAsnIleGlyLeuIle 180
Db 1069 GGAATTTCTTCCCACTTATCTTATCTGCGCAGAGAAATGTCCTCAACAAGAGCTGAT- 1127
QY 181 -GlnGlnGlnGlyIleGlyTyrValLeuAsnAlaSerTyr-ThrCysProIleProAsp 200
Db 1128 GCAGAGAAATGGATGGTATGATTAAATGCCAGAA-TACCTGTCCAAAGCTGACT 1186
QY 200 heIleProGlnSerHisPheLeuArgValProValaAsnAspSerPheCysGluIleIle 220
Db 1187 TTATCCCGAGTCCATATTTCTCGGTGCTGCTGATGACACCTTTTGGAAATTT 1246
QY 220 euProIleAspIleValSerValAspPheIleGluIleValIleValAsnGlnIleCysVal 240
Db 1247 TGCCGTGGTGGCAAAATCAGTATGATTTCAATGAAAGCAAAAGCTCCAAATGATGTG 1306
QY 240 alleuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
Db 1307 TTCTAGTGCACGTGTTAGCTGGATCTCCGCTCCGCAACATCGCTATCGCTTACATCA 1366
QY 260 eIleValArgMetAspMetSerLeuAspGluAlaTyrThrPheValIleGluIleValArgProT 280
Db 1367 TGAAGAGATGAGCATGCTTTAGATGAAGCTTTACGATTGTGAAAGAAAAAGACCTTA 1426
QY 280 hrlIleSerProAsnPheAsnPheLeuGlyGlnLeuLeuAspTyrGlnIleValIleIleVal 300
Db 1427 CTATATCTCCAACTTCAATTTTCTGGGCCAATCTCTGGAATGAAAGAAAGATTAAAGA 1486
QY 300 snGlnThrGlyAlaSerGlyProIleValSerIleValLeuLeuHisIleGluIleValProA 320
Db 1487 ACCAGACTGGAGCATACAGGCCAAAGAGCAAACTCAAGCTCTCACTGAGAAAGCAAA 1546
QY 320 snGluProValProAlaValSerGluGlyGlnIleValSerGluThrProIleuSerProp 340
Db 1547 ATGAACCTGTCTCCTCTGCTCAAGAGGTGAGCAAGAAAGGAAAGCCCTCTCACTGTCAC 1606
QY 340 roCysAlaAspSerAlaThrSerGluAlaAlaGlyGlnIleValProValHisIleProAlaSerVal 360
Db 1607 CCTGAGCCGACTCTCTACCTCAAGAGGAGCAAGAAAGCCCGTGCATCCGCCAGCG 1666
QY 360 alProSerValProSerValGlnProSerLeuLeuGluIleAspSerProIleValGlnAla 380
Db 1667 TGCCAGAGGTGCCAGCGTGCAGCGTCTGTTAAGAGCAAGCCCGCTGTTGTAAGAGCGC 1726

QY 380 euSerGlyLeuHisIleuSerAlaAspArgLeuGluAspSerAsnIleuValArgSerP 400
Db 1727 TCAGTGGGCTGCACCTGCTCCGAGACAGGCTGGAAAGACGAAATTAAGCTCAAGCGTTCT 1786
QY 400 heSerLeuAspIleIleValSerValSerTyrSerAlaSerMetAlaIleSerLeuHisGlyP 420
Db 1787 TCTCTCTGAAATACAAATACATGTTTCAATATTCAGCCAGCATGGCAGCATCTTACATGCT 1846
QY 420 heSerSerSerGluAspAlaLeuGluIleTyrTyrIleProSerThrThrIleuAspGlyThr 440
Db 1847 TCTCCATCAGAAAGATGTTTGGAAATCTAACAATCTTCACTACTCTGATGAGCA 1906
QY 440 snIleValCysGlnPheSerProValGlnGluLeuSerGluGlnThrProGluThrSerP 460
Db 1907 ACAGGTTATGCAAGTCTCTCCCTGTTGAGAACTATCGAGACAGATCCCGAAACGATC 1966
QY 460 roAspIleGluGluAlaSerIleProIleValLeuGluIleThrAlaArgProSerAspSerG 480
Db 1967 CTGATTAAGAGAGAACCGACATCCCAAGAAAGCTGCAAGCCGCGAGCTTTCAGACAGCC 2026
QY 480 InsIleValArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500
Db 2027 AAAGCAAGCTGATGATTCGCTCAGAACAGACAGCAATGACACCGCCAGAGTCTCTT 2086
QY 500 euSerProLeuHisArgSerGlySerValGlnAspAsnTyrHisThrSerPheLeuPheG 520
Db 2087 TATCTCCATCAGATCGAAAGTGGAGCTGGAGAGCAATTAACAACAGCTCTTCTTTCG 2146
QY 520 IlyLeuSerThrSerGlnGlnHisIleuThrIleValSerAlaGlyLeuGlyLeuIleValIle 540
Db 2147 GCTTTTCCACAGCCAGACAGACACCTCAAGAGTCTGCTGGCTGGCTTAAAGGCTGAC 2206
QY 540 IsSerAspIleLeuAlaProGlnThrSerThrProSerIleuThrSerSerTyrPheA 560
Db 2207 ACTCGATATCTTGCCCCCAACCTCTACCTTCTGACAGCAAGCTGATTTTGG 2266
QY 560 lathrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyIleValAsnIleVal 580
Db 2267 CCACAGAGTCTCAGACTTCTACTGCTGCTGACCATCTACGAGAGCAGTCCAGTTACT 2326
QY 580 eAlaTyrSerCysSerGlnLeuProThrCysGlyAspGlnValIleSerValArgArg 600
Db 2327 CTGCCTACAGCTGCACCGCTGCCCATCTTCCCTGACAGCAAGCTTATCTGTGCGACAGC 2386
QY 600 rGlnIleProSerAspArgAlaAspSerArgArgSerThrHisGluGluIleuSerPheG 620
Db 2387 GGCAGAAAGCCAAAGTACAGAGCTGACTCGCGCGAGAGCTGGCATGAAAGAGGCCCCCTT 2446
QY 620 IuIleGlnPheIleValArgArgSerCysGlnMetGluPheGlyIleSerIleMetSerGlu 640
Db 2447 AAAAGCAATTTAAAGCAGAAAGCTGCCAAATGGAAATTTGGAGAGATCATGTCAGAGA 2506
QY 640 snArgSerArgGluIleuLeuGlyIleValGlyIleSerGlnSerSerPheSerGlySerMetG 660
Db 2507 ACAGGTACAGGGAGAGAGCTGGGAAAGTGGGAGATCACTAGCTTTTTCGCGAGCATG 2566
QY 660 IuIleIleGluValSer 665
Db 2567 AAATCATTAAGAGTCTCC 2583

RESULT 31
US-10-072-012-255
/ Sequence 255, Application US/10072012
/ Publication No. US2004003493A1
/ GENERAL INFORMATION:
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Zernusen, Bryan
/ APPLICANT: Paturajan, Meera
/ APPLICANT: Shimkets, Richard
/ APPLICANT: Li, Li
/ APPLICANT: Gangoli, Beha


```

RESULT 32
US-10-072-012-257
; Sequence 257, Application US/10072012
; Publication No. US2004003493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zetruksen, Bryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangoli, Baha
; APPLICANT: Padigaru, Muradidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Coleman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; REMAINING PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 257
; LENGTH: 2071
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-072-012-257

Alignment Scores:
Pred. No.: 6,8e-295 Length: 2071
Score: 304.00 Matches: 658
Percent Similarity: 98.65% Conservative: 0
Best Local Similarity: 98.65% Mismatches: 7
Query Match: 45.71% Indels: 9
DB: 17 Gaps: 0

US-10-029-345A-109 (1-665) x US-10-072-012-257 (1-2071)
QY 1 Metalahisglumeti1eglyThrglml1evalThrglunrgueuValalaleuLeuglu 20

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Db 61 ATGCCCATGAGATGATGAACTCAAAATTGTACTGAGAGAGGTGGCTCGCTGGAA 120
QY 21 SerGIThrglunysValleu1leu1leapSerArpPropheValgluThrsnThser 40
Db 121 AGTGAACGGAAAAAGTGGCTGCTAATGTATACCCGCCATTGTGAAATACATACATCC 180
QY 41 His1leleuGlunAlalean1leapnysSerlyseuMetlysarArgLeugl1ng1n 60
Db 181 CACATTTTGAAGCCATTATATCAACTGCTCCAAAGCTTATGAAGCGAAGGTGCAACAG 240
QY 61 AsplysValleu1leThrgluleu1leglnHisserAlalysh1elysValaspl1eap 80
Db 241 GACAAAGTGTATATACAGAGCTATCCAGCATTCAGGAACATTAAGTTGACATTGAT 300
QY 81 CysSerGlnysValval1y1y1rApGlnSerSerGlnAspVal1aserLeuSerSer 100
Db 301 TGCAGTCAGAGGTGTGTAGTTACGATCAAGCTCCCAAGATGTGCTCTCTCTTCA 360
QY 101 AspCysPheLeuThrValleuLeuGlylyseuGlnysSerPheAsnSerValH1sleu 120
Db 361 GACTGTTTTCACATGCTCTCTGAGTAACTGAGAGAGCTTCAACTCTGTTCACTG 420
QY 121 leu1aglyglyPhealagluPheSerArgCysPheProGlyleuGlylysser 140
Db 421 CTTCAGAGTGGGTGTGCTGAGTCTCTCGTTTCCCTGCTCTGAGGAAATCC 480
QY 141 ThrleuValProThrCys11eserGlnProCysleuProVal1alasn1leglyProThr 160
Db 481 ACTCTAGTCCCTACCTCACTTCTCGAGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 161 Arg1leleuProAsnleuThrleuGlyCysGlnArgAspValleuAsnysgluleu1le 180
Db 541 CGAATTCCTCCCACTTTATCTTGCTGCGACGAGAGAGTCTCAACAAGAGCTGAT 599
QY 181 -GlnGlnAsnGly11eglyThrValleuAsn1aserTy-ThrCysProlyProAsp 200
Db 600 GCAGCAGAAATGGATGGTATGTGTAAATCCAGCA-TCCTGCTCCAAAGCTGACT 658
QY 200 he1leProGlnSerH1sPheleuArgValProValAsnAspSerPheCysGlyly1le 220
Db 659 TTATCCCGAGCTCACTTCTCGCGTGCCCTGTGAAGACAGCTTTGTGAAATTT 718
QY 220 euProThreAsnysSerValasPhe1leglylyal1y1alaserAsnGlyCysV 240
Db 719 TCCCGGTGGCAAAATCAGTAGATTCAATTGAGAAAGCAAAAGCTCCCAATGAGATG 778
QY 240 alleuValH1sCysleu1agly1leserArgSerAlaThr1leal1leal1y11leu 260
Db 779 TTCTAGTGACATGTTAGCTGGATCTCCGCTCCGACCAATGCTATGCTTACATCA 838
QY 260 eflysArgMetAspMetSerleuAspGluAlaTy1rArgPheVal1y1y1y1y1y1y1 280
Db 839 TAAAGAGATGACATGCTTAAATGATGAACTTCAAGATTGTGAAGAAAAAGAACTTA 898
QY 280 hr1leSerProAsnPheAsnPheleuGlyGlnleuAspTy1y1y1y1y1y1y1y1y1 300
Db 899 CTATATCTCAAACTTCAATTTTCTGGGCCAACTCTGAGCTATGAGAAAGAAATTAAG 958
QY 300 snGlnThrglYAlaserGlyProlySerlyseu1y1leuH1sleuGlylyyPro 320
Db 959 ACCAGACTGAGACATCAGGGCCAAAGAGCAAACTCAAGCTGCTGACCTCGAAGAACCA 1018
QY 320 snGluProVal1ProAl1ValaserGlylyGlyGlnysSerGlylyThrProleuSerProp 340
Db 1019 ATGAACCTGCTCCGCTGCTCTCAAGAGGTGGAAGAAAGCGAGAGCCCTTCACTGAC 1078
QY 340 roCyAlaAspSerAlaThrSerGlnAla1aglyGlnArgProValH1sProAlaserV 360
Db 1079 CCTGTGCCGACTGCTGCTACCTCAGAGGCGAGGAGCAAGAGCCCGTGCATC--C--C-G 1132
QY 360 alProSerValProSerValGlnProSerleuLeuGlyAspSerProleuValGlnAlal 380

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Db 1133 --CC-AGCGTACCAGCGTGCAGCCGCTGTTAGAGCAGACCCGCTGTACAGGCGC 1189
QY 380 euSerGlyLeuHisLeuSerAlaAspArgLeuGluAspSerAsnValLeuValArgSerP 400
Db 1190 TCAGTGGCGTGCACCTGCTCCGAGACAGGTGGAAACAGCAATTAAGCTCAACGCTTCCCT 1249
QY 400 heserLeuAspIleValSerValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyP 420
Db 1250 TCTCTGTGATATCAATCAATCACTTTCATATTACAGCAGCATGAGCATCTTACATGCT 1309
QY 420 heserSerSerGluAspAlaLeuGluTyrTyrIleAspProSerThrThrIleAspGlyThrA 440
Db 1310 TCTCCTCATCAGAAAGATGCTTGGAAATACCAAACTTCCATCACTGATGATGGAGCA 1369
QY 440 enuValLeuCyArgIlePheSerProValGlnGluLeuSerGluGlnThrProGluThrSerP 460
Db 1370 ACAAGATATGCCAGTTCCTCCCTGTTCAAGAACTATCGAGCACTCCCGAAACCAAGTC 1429
QY 460 roAspArgGluGluAlaSerIleProIleValLeuGlnThrAlaArgProSerAspSerG 480
Db 1430 CTGATTAAGAGAAAGCCAGCATCCCAAGAACTGCAAGCCAGCCGCTTCCAGACAGCC 1489
QY 480 InSerValArgLeuHisSerValArgThrSerSerSerGlyThrAlaGlnArgSerLeu 500
Db 1490 AGAGCAAGCGATTCGATTCGGTCAGAACCAAGCAGCAGTGGCACCGCCAGAGGCTCCCTTT 1549
QY 500 euSerProLeuHisArgSerGlySerValGluAspAsnTyrHisThrSerPheLeuPheG 520
Db 1550 TATCTCAGCTGCAATCAAGGTGGAGCGTGGAGACAAATTAACACACAGCTTCTCTTTTG 1609
QY 520 ILeuSerThrSerGlnGlnHisLeuThrIleValSerAlaGlyLeuGlyLeuValTyrP 540
Db 1610 GCTTTTCCACACCCAGCAGCAGCAGCTCAAGAGTCTGCTGGCTTGGCTTAAAGGCTGGC 1669
QY 540 IAspSerAlaIleLeuAlaProGlnThrSerThrProSerLeuThrSerSerTyrPheA 560
Db 1670 ACTCGGATATCTTGGCCCCCAGACCTTACCTCCCTTCCGACAGCAGCTGATTTTGG 1729
QY 560 IAThrGluSerSerHisPheTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrS 580
Db 1730 CCAACAGATCTTCACTACTTCTGCTGCTCAGCCATCTACAGAGCAGCAGCTGATTA 1789
QY 580 erAlaTyrSerCySerGlnLeuProThrCyArgIleAspGlnValTyrSerValArgArgA 600
Db 1790 CTGCCCTAAGCTGACAGCTGCTCCCACTTGGGAAACCAAGTCTATCTGTCGAGAGC 1849
QY 600 rGlnIleAspProSerAspArgAlaAspSerArgArgSerTyrHisGluGluSerProPheG 620
Db 1850 GCGAGAAAGCCAACTGACAGAGCTGACTCGCGCGGAGCTGGCATGAAGAGAGCCCTTGG 1909
QY 620 IuValGlnPheValArgArgSerCyArgIleMetGluPheGlyGluSerIleMetSerGluA 640
Db 1910 AAAAGAGATTAAACCAAGAGCTGCCAAATGGAATTTGAGAGACATCATGTCAGAGA 1969
QY 640 snArgSerArgGluGluLeuGlyValValGlySerGlnSerSerPheSerGlySerMetG 660
Db 1970 ACGAGTACAGGAAAGAGCTGGGGAAAGTGGGCACTAGCTTTCGGGAGCATGG 2029
QY 660 IuIleIleGluValSer 665
Db 2030 AATCATTTAGAGCTCTCC 2046
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RESULT 33

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US-10-108-260A-2429
; Sequence 2429, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
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; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2429
; LENGTH: 1916
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-2429

Alignment Scores:
pred. No.: 2 866-168 Length: 1916
Score: 178.00 Matches: 278
Percent Similarity: 99.29% Conservative: 0
Best Local Similarity: 99.29% Mismatches: 1
Query Match: 26.77% Indels: 2
DB: 17 Gaps: 0

US-10-029-345A-109 (1-665) x US-10-108-260A-2429 (1-1916)
QY 387 AlaAspArgLeuGluAspSerAsnValLeuValArgSerPheSerLeuAspIleValSer 406
Db 142 GCAGACAGGCTGGAGAGACAGCATTAAGCTCAAGCGTCTTCTCTGTGATATCAATCA 201
QY 407 ValSerTyrSerAlaSerMetAlaAlaSerLeuHisGlyPheSerSerSerGluAspAla 426
Db 202 GTTTCATATTACAGCAGCATGCGAGCATCTTACATGCGCTTCTCCATCAGAAAGATGCT 261
QY 427 LeuGluTyrTyrIleProSerThrThrIleAspGlyThrAsnValLeuCyArgIlePheSer 446
Db 262 TTGGAATATTAACAACCTTCACTCTGAGTGGAGCAACAAGCTATATGCAAGTCTCC 321
QY 447 ProValGlnGluLeuSerGluGlnThrAlaArgProSerAspSerGlnSerIleValArgLeuHis 466
Db 322 CCGTTTCAAGAACTATCCGAGCAGACTCCGAAACCAAGTCTGATTAAGAGAGAGCAGC 381
QY 467 ILeuProValLeuGlnThrAlaArgProSerAspSerGlnSerIleValArgLeuHisSer 486
Db 382 ATCCCAAGAAAGCTGAGAGCCCGCAGGCTTCAAGCAGCAGCAGCATGATTCGATTCG 441
QY 487 ValArgThrSerSerSerGlyThrAlaArgProSerLeuLeuSerProLeuHisArgSer 506
Db 442 GTTCAGAAACAGAGCAGGTGGACCCGCAAGAGTCTTATATCTCAGCTGATCCAGAT 501
QY 507 GlySerValGluAspAsnTyrHisThrSerPheLeuPheGlyLeuSerThrSerGlnG 526
Db 502 GGGAGCGTGGAGAGCAATTAACACAGCAGCTTCTTTGGCTTCCATCAGCCAGCA 560
QY 526 nHisLeuThrIleValSerAlaGlyLeuGlyLeuValGlyTyrPheIleAspIleLeuAlaP 546
Db 561 GCACCTCAGAGAGTCTGCTGGCTGGCTTAAAGGCTGGCACTCGATATCTTGGCCCC 620
QY 546 OGlnThrSerThrProSerLeuThrSerSerTyrPheAlaThrGluSerSerHisPhe 566
Db 621 CCAAGACTTACCTCTTCCCTTCAACAGCAGCTGGATTTTGGCCAGAGTCTCCACACTT 680
QY 566 eTyrSerAlaSerAlaIleTyrGlyGlySerAlaSerTyrSerAlaTyrSerCySerG 586
Db 681 CTACTCTGCTCAGGCATTTACGAGGAGCGAGTCCAGTTACTCTGCTTACAGCTGAGCCA 740
QY 586 nLeuProThrCyArgIleAspGlnValTyrSerValArgArgGlnLeuAspSerAspArg 606
Db 741 GCTGCCCACTTGCAGAGACCAAGTCTATTCTGCGCAGGCGGAGAAACCAAGTACAG 800
QY 606 gAlaAspSerArgArgSerTyrHisGluGluSerProPheGlyValGlnPheValArgArg 626
Db 801 AACTGACTGCGCGGAGCTGGCATGAAGAGAGCCCTTTGAAAGAGCAATTAACAGCAG 860
QY 626 gSerCyArgIleMetGluPheGlyGluSerIleMetSerGluAsnArgSerArgGluGlu 646
Db 861 AAGCTGCCAAATGGAATTTGGAGAGAGCATATGTCAGAAACAGTCAAGGGAAGAGCT 920
QY 646 uGlyIleValGlySerGlnSerSerPheSerGlySerMetGluIleIleGluValSer 665
Db 921 GGGGAAAGGTGGCAGTCAAGTCTTTCGGGAGCAGATGAATCAATTAAGAGTCTCC 978
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RESULT 34

US-10-357-930-10717/C
Sequence 10717, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10717
LENGTH: 425
TYPE: DNA
ORGANISM: Homo sapiens
US-10-357-930-10717

Alignment Scores:

Pred. No.: 1,18e-128 Length: 425
Score: 138.00 Matches: 138
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.75% Indels: 0
Gaps: 0

US-10-029-345a-109 (1-665) x US-10-357-930-10717 (1-425)

QY 240 ValLeuValHisCySleuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrlle 259
DB 423 GTTCTAGTGACACTGTTAGCTGGGATCTCCGCTCCGACCATGCTATCGCTACATC 364
QY 260 MetIlyArgMetAspMetSerIleuAspGluAlaTyArgPheValIlyGluIlyArgPro 279
DB 363 ATGAAGAGATGACATGCTTCTTAGTAGAGCTTACAGATTGTAAGAAAAAGAAAGACCT 304
QY 280 ThrIleSerProAsnPhelaAsnPheluGlyGlnLeuLeuAspTyArgIlyIlyIleIys 299
DB 303 ACTATATCTCCAAACTTCAATTTCTGGGCCAACTCTGAGCTATGAGAAAGATTAAAG 244
QY 300 AaGlnThrGlyAlaSerGlyProIlySerIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIly 319
DB 243 AACGACACTGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACTGAGAGACCA 184
QY 320 AaGlnProValProAlaValSerGluGlyGlnIlySerGluThrProLeuSerPro 339
DB 183 AATGAACCTGCTCCTGCTGTCTCAGAGGTGAGCAGAAACCGAGACGCCCCCTTAGTCCA 124
QY 340 ProCyAlaAspSerAlaThrSerGluAlaAlaGlyIlyIlyIlyIlyIlyIlyIlyIlyIly 359
DB 123 CCTTGTGCGACTGCTGCTACTCCTCAGAGGCAAGAGCAAGAGCCCGTGCATCCGCGACGC 64
QY 360 ValProSerValProSerValGlnProSerLeuLeuGluIlyAspSerProLeuVal 377
DB 63 GTGCCACGCGGCCAGGCTGACGCTGCTGTTAGAGAGCAGCCCGCTGTGTA 10

RESULT 35

US-10-357-930-31909/C
Sequence 31909, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 31909
LENGTH: 467
TYPE: DNA
ORGANISM: Homo sapiens
US-10-357-930-31909

Alignment Scores:

Pred. No.: 1,3e-127 Length: 467
Score: 137.00 Matches: 137
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.60% Indels: 0
Gaps: 0

US-10-029-345a-109 (1-665) x US-10-357-930-31909 (1-467)

QY 241 LeuValHisCySleuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrlleMet 260
DB 465 CTAGTGACACTGTTAGCTGGGATCTCCGCTCCGACCATGCTATCGCTACATCATG 406
QY 261 IlyArgMetAspMetSerIleuAspGluAlaTyArgPheValIlyGluIlyArgProThr 280
DB 405 AAGAGGATGAGATGCTTCTTAGATGAGCTTACAGATTGTAAGAAAAAGAAAGACCTACT 346
QY 281 IleSerProAsnPhelaAsnPheluGlyGlnLeuLeuAspTyArgIlyIlyIlyIlyIlyIly 300
DB 345 AATATCTCCAAACTTCAATTTCTGGGCCAACTCTGAGCTATGAGAAAGATTAAAGAAC 286
QY 301 GlnThrGlyAlaSerGlyProIlySerIlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIly 320
DB 285 CAGACTGAGCATCAGGGCCAAAGAGCAAACTCAAGCTGCTGCACTGAGAGACCAAT 226
QY 321 GlnProValProAlaValSerGluGlyGlnIlySerGluThrProLeuSerProPro 340
DB 225 GAACCTGCTCCTGCTGTCTCAGAGGTTGACAGAAAAAGCAAGCGCCCTCACTCCACCC 166
QY 341 CyAlaAspSerAlaThrSerGluAlaAlaGlyIlyIlyIlyIlyIlyIlyIlyIlyIlyIly 360
DB 165 TGTGCCACTGCTGCTACTCCTCAGAGGCAAGAGCAAGAGCCCGTGCATCCGCGACGCG 106
QY 361 ProSerValProSerValGlnProSerLeuLeuGluIlyAspSerProLeuVal 377

Db 105 CCCAGCGTCCGAGCGTGCAGCCGCTGTTAGAGACAGCCCGCTGTA 55
RESULT 36
US-10-357-930-40868/c
Sequence 40868, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 40868
LENGTH: 467
TYPE: DNA
ORGANISM: Homo sapiens
US-10-357-930-40868
Alignment Scores:
Pred. No.: 1,3e-127 Length: 467
Score: 137.00 Matches: 137
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.60% Indels: 0
Gaps: 0
DB: 18
US-10-029-345A-109 (1-665) x US-10-357-930-40868 (1-467)
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
Db 465 CTAGTCACCTGTTTACCTGGATCTCCGCTCCGCCACCATCGCTACATCATG 406
QY 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValIleGluLysArgProthr 280
Db 405 AAGAGATGACATGCTTAGATGAAGCTTACAGATTGTGTAAGAAAAAGAACTACT 346
QY 281 IleSerProAsnPheAsnIleLeuGlyIleLeuLeuAspTyrGluLysIleLysIleLysAsn 300
Db 345 ATATCTCCAACTCAATTCTTGCGCCAACTCTGACTATGAGAAGAAATTAAAGAAC 286
QY 301 GlnThrGlyAlaSerGlyProLysSerIleValLeuIleLeuHisIleLeuGluLysProAsn 320
Db 285 CAGACTGAGCATCAGGGCCAAAGCAAACTCAAGCTGCTGACCTGGAAGAACCAAT 226
QY 321 GluProValProAlaValSerGluGlyIleGlnLysSerGluThrProLeuSerProPro 340
Db 225 GAACCTGTCCTCTGCTCTCAGAGGGTGAAGAAAAAGGAGAGCGCCCTCAGTCAACC 166
QY 341 CysAlaAspSerAlaThrSerGluAlaIleAlaGlyIleArgProValHisProAlaSerVal 360
Db 165 TGTGCCAGACTGTGCTACTCCTCAGAGGAGAGCAAAAGGCCCTGTCATCCCGCCAGCGTG 106
QY 361 ProSerValProSerValGlnProSerLeuLeuGluAspSerProLeuVal 377

Db 105 CCCAGCGTCCGAGCGTGCAGCCGCTGTTAGAGACAGCCCGCTGTA 55
RESULT 37
US-10-357-930-41017/c
Sequence 41017, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 41017
LENGTH: 467
TYPE: DNA
ORGANISM: Homo sapiens
US-10-357-930-41017
Alignment Scores:
Pred. No.: 1,3e-127 Length: 467
Score: 137.00 Matches: 137
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.60% Indels: 0
Gaps: 0
DB: 18
US-10-029-345A-109 (1-665) x US-10-357-930-41017 (1-467)
QY 241 LeuValHisCysLeuAlaGlyIleSerArgSerAlaThrIleAlaIleAlaTyrIleMet 260
Db 465 CTAGTCACCTGTTTACCTGGATCTCCGCTCCGCCACCATCGCTACATCATG 406
QY 261 LysArgMetAspMetSerLeuAspGluAlaTyrArgPheValIleGluLysArgProthr 280
Db 405 AAGAGATGACATGCTTAGATGAAGCTTACAGATTGTGTAAGAAAAAGAACTACT 346
QY 281 IleSerProAsnPheAsnIleLeuGlyIleLeuLeuAspTyrGluLysIleLysIleLysAsn 300
Db 345 ATATCTCCAACTCAATTCTTGCGCCAACTCTGACTATGAGAAGAAATTAAAGAAC 286
QY 301 GlnThrGlyAlaSerGlyProLysSerIleValLeuIleLeuHisIleLeuGluLysProAsn 320
Db 285 CAGACTGAGCATCAGGGCCAAAGCAAACTCAAGCTGCTGACCTGGAAGAACCAAT 226
QY 321 GluProValProAlaValSerGluGlyIleGlnLysSerGluThrProLeuSerProPro 340
Db 225 GAACCTGTCCTCTGCTCTCAGAGGGTGAAGAAAAAGGAGAGCGCCCTCAGTCAACC 166
QY 341 CysAlaAspSerAlaThrSerGluAlaIleAlaGlyIleArgProValHisProAlaSerVal 360
Db 165 TGTGCCAGACTGTGCTACTCCTCAGAGGAGAGCAAAAGGCCCTGTCATCCCGCCAGCGTG 106

Db	137	ACCTCAGAGGACAGGACAAAGGCCCGTGCATCCCGCCAGCGTGGCCAGCGTGCCAGC	78
Qy	366	VaIGlnProSerLeuLeuGluAaspSerProLeuVal	377
Db	77	GTGCAAGCCGTGCTGTTAGAGAACAGCCCGCTGGTA	42

Search completed: February 14, 2005, 16:00:26
Job time : 974 secs

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